

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions **.rnpm** and **.rnpn**

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions **.rapm** and **.rapn**

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2005, 11:13:06 ; Search time 17 Seconds
(without alignments)
39.520 Million cell updates/sec

Title: US-09-761-636A-14

Perfect score: 52

Sequence: 1 CISVPLVPC 9

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 99282

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	51.9	9	4	US-09-535-852-1681
2	26	50.0	9	3	US-09-187-859-2726
3	26	50.0	9	4	US-09-839-542B-2726
4	24	46.2	6	4	US-09-368-670C-17
5	24	46.2	7	1	US-08-261-206A-18
6	23	44.2	8	1	US-08-189-331-147
7	23	44.2	8	1	US-08-189-331-148
8	23	44.2	8	1	US-08-189-331-149
9	23	44.2	8	1	US-08-189-331-150
10	23	44.2	8	1	US-08-633-760-9
11	23	44.2	8	2	US-08-471-068-147
12	23	44.2	8	2	US-08-471-068-148
13	23	44.2	8	2	US-08-471-068-149
14	23	44.2	8	2	US-08-471-068-150
15	23	44.2	9	3	US-08-891-271-4
16	23	44.2	9	3	US-09-258-754-373
17	23	44.2	9	3	US-09-042-107-373
18	23	44.2	9	4	US-09-723-250D-373
19	23	44.2	9	4	US-09-676-475A-373
20	23	44.2	9	4	US-10-038-407-29
21	22	42.3	4	3	US-09-357-952-69
22	22	42.3	4	3	US-09-521-650-69
23	22	42.3	4	3	US-09-168-888-69
24	22	42.3	4	4	US-09-947-387-69
25	22	42.3	5	3	US-09-357-952-68
26	22	42.3	5	3	US-09-357-952-116
27	22	42.3	5	3	US-09-521-650-68

28	22	42.3	5	3	US-09-521-650-116	Sequence 116, Appl
29	22	42.3	5	3	US-09-168-888-68	Sequence 68, Appl
30	22	42.3	5	3	US-09-168-888-116	Sequence 116, Appl
31	22	42.3	5	4	US-09-947-387-68	Sequence 68, Appl
32	22	42.3	5	4	US-09-947-387-116	Sequence 116, Appl
33	22	42.3	5	4	US-09-368-670C-10	Sequence 10, Appl
34	22	42.3	6	3	US-09-357-952-67	Sequence 67, Appl
35	22	42.3	6	3	US-09-357-952-115	Sequence 115, Appl
36	22	42.3	6	3	US-09-521-650-67	Sequence 67, Appl
37	22	42.3	6	3	US-09-521-650-115	Sequence 115, Appl
38	22	42.3	6	3	US-09-168-888-67	Sequence 67, Appl
39	22	42.3	6	3	US-09-168-888-115	Sequence 115, Appl
40	22	42.3	6	4	US-09-947-387-67	Sequence 67, Appl
41	22	42.3	6	4	US-09-947-387-115	Sequence 115, Appl
42	22	42.3	6	4	US-09-368-670C-1	Sequence 1, Appl
43	22	42.3	6	4	US-09-368-670C-8	Sequence 8, Appl
44	22	42.3	6	4	US-09-368-670C-9	Sequence 9, Appl
45	22	42.3	6	4	US-09-368-670C-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-09-535-852-1681
; Sequence 1681, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND ENTHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1681
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclicized modulating agent comprising
; OTHER INFORMATION: desmocollin-2 cell adhesion recognition sequence
US-09-535-852-1681

Query Match 51.9%; Score 27; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CISVPLVPC 9
|||:
Db 1 CIAFATTPC 9

RESULT 2

US-09-187-859-2726
; Sequence 2726, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2726
; LENGTH: 9
; TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-09-187-859-2726

Query Match          50.0%; Score 26; DB 3; Length 9;
Best Local Similarity 44.4%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 C1SVPLVPC 9
Db 1 CFALDLVTC 9

RESULT 3
US-09-839-542B-2726
; Sequence 2726, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2726
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-09-839-542B-2726

Query Match          50.0%; Score 26; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 C1SVPLVPC 9
Db 1 CFALDLVTC 9

RESULT 4
US-09-368-670C-17
; Sequence 17, Application US/09368670C
; Patent No. 6767991
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim (Canada) Ltd.
; TITLE OF INVENTION: Hepatitis C Inhibitor Peptides
; FILE REFERENCE: 13/063-2-C2
; CURRENT APPLICATION NUMBER: US/09/368,670C
; CURRENT FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,945
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/055,186
; PRIOR FILING DATE: 1997-08-11
; PRIOR APPLICATION NUMBER: 09/131,758
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Hepatitis C
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 1
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; OTHER INFORMATION: Asp is acetylated
US-09-368-670C-17

Query Match          46.2%; Score 24; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LVPC 9
Db 3 LVPC 6

RESULT 5
US-08-261-206A-18
; Sequence 18, Application US/08261206A
; Patent No. 5574007
; GENERAL INFORMATION:
; APPLICANT: Zushi, Mitichitaka
; APPLICANT: Gomi, Komakazu
; APPLICANT: Yamamoto, Shuji
; APPLICANT: Suzuki, Koji
; APPLICANT: Matsuda, Akio
; TITLE OF INVENTION: A Polypeptide Capable of Interacting
; TITLE OF INVENTION: with Thrombin
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261,206A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/740,492
; FILING DATE: 03-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 216-275P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-261-206A-18

Query Match          46.2%; Score 24; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLVPC 9
Db 2 PVAPC 6

RESULT 6
US-08-189-331-147
; Sequence 147, Application US/08189331
; Patent No. 5747334
```

```
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189.331
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 147:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-189-331-147

Query Match 44.2%; Score 23; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 C1SVP 5
Db 4 CVSAP 8

RESULT 7
US-08-189-331-148
; Sequence 148, Application US/08189331
; Patent No. 5747334
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189.331
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 149:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-189-331-149

Query Match 44.2%; Score 23; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 C1SVP 5
Db 4 CVSAP 8
```

```
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189.331
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-189-331-148

Query Match 44.2%; Score 23; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 C1SVP 5
Db 3 CVSAP 7

RESULT 8
US-08-189-331-149
; Sequence 149, Application US/08189331
; Patent No. 5747334
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189.331
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 149:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-189-331-149

Query Match 44.2%; Score 23; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 C1SVP 5
Db 3 CVSAP 7
```

Db 2 CVSAP 6

RESULT 9
US-08-189-331-150
; Sequence 150, Application US/08189331
; Patent No. 5747334
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189,331
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-189-331-150

Query Match 44.2%; Score 23; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CISVP 5
| : |
| : |
Db 1 CVSAP 5

RESULT 10
US-08-633-760-9
; Sequence 9, Application US/08633760
; Patent No. 5804429
; GENERAL INFORMATION:
; APPLICANT: NIWA, MINEO
; APPLICANT: SAITO, YOSHIMASA
; APPLICANT: FUJIMURA, TAKAO
; APPLICANT: ISHII, YOSHINORI
; APPLICANT: NOGUCHI, YUJI
; TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA

ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,760
; FILING DATE: 01-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 18-929-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-633-760-9

Query Match 44.2%; Score 23; DB 1; Length 8;
Best Local Similarity 42.9%; Pred. No. 4.1e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CISVPLV 7
| : |
| : |
Db 2 CAAPVPL 8

RESULT 11
US-08-471-068-147
; Sequence 147, Application US/08471068
; Patent No. 5948635
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; APPLICANT: Fowlkes, D. M.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,068
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/189,331
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 147:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-471-068-147

Query Match 44.2%; Score 23; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CUSVP 5
Db 4 CVSAP 8

RESULT 12

US-08-471-068-148
; Sequence 148, Application US/08471068
; Patent No. 5948635
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,068
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/189,331
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 148:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-471-068-148

Query Match 44.2%; Score 23; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CUSVP 5
Db 3 CVSAP 7

RESULT 13

US-08-471-068-149

; Sequence 149, Application US/08471068
; Patent No. 5948635
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,068
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/189,331
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 149:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-471-068-149

Query Match 44.2%; Score 23; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CUSVP 5
Db 2 CVSAP 6

RESULT 14

US-08-471-068-150
; Sequence 150, Application US/08471068
; Patent No. 5948635
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-471-068-150

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,068
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/189,331
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-471-068-150

Query Match 44.2%; Score 23; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CUSVP 5
|:|
Db 1 CUSAP 5

RESULT 15
US-08-891-271-4
; Sequence 4, Application US/08891271
; Patent No. 6165476
; GENERAL INFORMATION:
; APPLICANT: Strom, Terry B.
; APPLICANT: Sytkowski, Arthur J.
; APPLICANT: Zheng, Xin Xiao
; TITLE OF INVENTION: Fusion Proteins with an Immunoglobulin
; TITLE OF INVENTION: Hing Region Linker
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,271
; FILING DATE: 10-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hogle, Doreen M.
; REGISTRATION NUMBER: 36,361
; REFERENCE/DOCKET NUMBER: BIH97-07
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
US-08-891-271-4

Query Match 44.2%; Score 23; DB 3; Length 9;
Best Local Similarity 44.4%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 1;

QY 1 CUSVPLVPC 9
|:|
Db 2 CUECP-PC 8

Search completed: April 1, 2005, 11:24:41
Job time : 17 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2005, 12:02:21 ; Search time 44 Seconds
(without alignments)
16.966 Million cell updates/sec

Title: US-09-761-636A-13
Perfect score: 56
Sequence: 1 CISVPLSVPC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 115750

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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5: /cgn2_6/prodata/1/1aa/PCTUS-COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	64.3	9	1	US-08-331-383-33
2	36	64.3	9	1	US-08-549-008-43
3	36	64.3	9	3	US-08-802-981-143
4	33	58.9	9	1	US-08-331-383-31
5	33	58.9	9	1	US-08-549-008-42
6	33	58.9	9	3	US-08-802-981-142
7	32	57.1	10	4	US-09-671-089-13
8	25	44.6	10	1	US-08-212-190A-5
9	25	44.6	10	2	US-08-900-321-5
10	25	44.6	10	3	US-09-461-697-21
11	25	44.6	10	4	US-09-436-469-5
12	25	44.6	10	5	PCT-US95-03610-5
13	24	42.9	5	4	US-09-886-135A-5
14	24	42.9	6	1	US-08-483-434A-21
15	24	42.9	6	3	US-08-476-134A-30
16	24	42.9	6	6	5190920-26
17	24	42.9	6	6	5506208-28
18	24	42.9	6	6	5190920-26
19	24	42.9	6	6	5506208-28
20	24	42.9	8	4	US-09-239-043D-9
21	24	42.9	8	4	US-09-239-043D-675
22	24	42.9	8	4	US-09-239-043D-1515
23	24	42.9	9	1	US-08-331-383-35
24	24	42.9	9	1	US-08-549-008-40
25	24	42.9	9	3	US-08-802-981-1
26	24	42.9	9	4	US-09-239-043D-169
27	24	42.9	10	1	US-08-033-857A-5

28	24	42.9	10	1	US-08-374-983A-5
29	24	42.9	10	3	US-08-377-781A-17
30	24	42.9	10	4	US-09-239-043D-10
31	24	42.9	10	4	US-09-239-043D-15
32	24	42.9	10	4	US-09-239-043D-676
33	24	42.9	10	4	US-09-239-043D-686
34	24	42.9	10	4	US-09-239-043D-1336
35	24	42.9	10	4	US-09-239-043D-1516
36	24	42.9	10	4	US-09-239-043D-1786
37	23	41.1	6	1	US-07-994-133-3
38	23	41.1	6	1	US-08-221-078A-8
39	23	41.1	6	1	US-08-221-171A-8
40	23	41.1	8	1	US-08-189-331-147
41	23	41.1	8	1	US-08-189-331-148
42	23	41.1	8	1	US-08-189-331-149
43	23	41.1	8	1	US-08-189-331-150
44	23	41.1	8	2	US-08-471-068-147
45	23	41.1	8	2	US-08-471-068-148

ALIGNMENTS

RESULT 1
US-08-331-383-33
; Sequence 33, Application US/08331383
; Patent No. 5605809
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of
; TITLE OF INVENTION: Proteases in Biological Samples and Methods and Use
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,383
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 16865-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-331-383-33

Query Match 64.3%; Score 36; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLSVPC 10

Db 2 AIPMSIPC 9

```
RESULT 2
US-08-549-008-43
; Sequence 43, Application US/08549008
; Patent No. 5714342
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of
; TITLE OF INVENTION: Protease in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 27-OCT-1995
; CLASSIFICATION: 435
; APPLICATION NUMBER: US/08/549,008
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,383
; FILING DATE: 28-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 016865-0001100S
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-549-008-43

Query Match 64.3%; Score 36; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLSVPC 10
Db 2 AIPMSIPC 9

RESULT 3
US-08-802-981-143
; Sequence 143, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 424
; APPLICATION NUMBER: US/08/331,383
; FILING DATE: 28-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 16865-1
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,981
FILING DATE: 20-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 016865-0003000S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-802-981-143

Query Match 64.3%; Score 36; DB 3; Length 9;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLSVPC 10
Db 2 AIPMSIPC 9

RESULT 4
US-08-331-383-31
; Sequence 31, Application US/08331383
; Patent No. 5605809
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of
; TITLE OF INVENTION: Proteases in Biological Samples and Methods of Use
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,383
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 16865-1
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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;
; TOPOLOGY: linear
; MOLECULE TYPE: peptid
; FEATURE:
; NAME/KEY: Region
; LOCATION: One-Of(5)
; OTHER INFORMATION: /note= "Xaa is norleucine."
US-08-331-383-31

Query Match 58.9%; Score 33; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 SVPLSVPC 10
DB 2 AIPXSIPC 9

RESULT 5

US-08-549-008-42
; Sequence 42, Application US/08549008
; Patent No. 5714342
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; TITLE OF INVENTION: Compositions for the Detection of
; TITLE OF INVENTION: Protease in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/549,008
; FILING DATE: 27-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,383
; FILING DATE: 28-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 016865-000110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptid
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /product= "Nle"
US-08-549-008-42

Query Match 58.9%; Score 33; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 SVPLSVPC 10
DB 2 AIPXSIPC 9

RESULT 6

US-08-802-981-142
; Sequence 142, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-000300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 142:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptid
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /product= "Nle"
US-08-802-981-142

Query Match 58.9%; Score 33; DB 3; Length 9;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 SVPLSVPC 10
DB 2 AIPXSIPC 9

RESULT 7

US-09-671-089-13
; Sequence 13, Application US/09671089
; Patent No. 6780846
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20018
; CURRENT APPLICATION NUMBER: US/09/671,089
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13

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; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: membrane translocating peptide, cyclic
US-09-671-089-13

Query Match          57.1%; Score 32; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 29;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTSVPLSVPC 10
   | : | : | : |
Db 1 CLPVLUAAPC 10

RESULT 8
US-08-212-190A-5
; Sequence 5, Application US/08212190A
; Patent No. 5652223
; GENERAL INFORMATION:
; APPLICANT: KOHN, ELISE C.
; APPLICANT: LIOTTA, LANCE A.
; APPLICANT: KIM, YOUNG S.
; TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Stuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,190A
; FILING DATE: 14-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 15280-204US
; TELEPHONE: (415) 543-5043
; TELEFAX: (415) 543-9600
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-212-190A-5

Query Match          44.6%; Score 25; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLSVPC 10
   | : | : |
Db 3 PAPVPC 8

RESULT 9
US-08-900-321-5
; Sequence 5, Application US/08900321
; Patent No. 5981712
```

```
; GENERAL INFORMATION:
; APPLICANT: Kohn, Elise C.
; APPLICANT: Liotta, Lance A.
; APPLICANT: Kim, Young S.
; TITLE OF INVENTION: DNA Encoding CAI Resistance Proteins and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/900,321
; FILING DATE: 25-JUL-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,190
; FILING DATE: 14-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-204100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-900-321-5

Query Match          44.6%; Score 25; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLSVPC 10
   | : | : |
Db 3 PAPVPC 8

RESULT 10
US-09-461-697-21
; Sequence 21, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 10
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-461-697-21

Query Match 44.6%; Score 25; DB 3; Length 10;
Best Local Similarity 44.4%; Pred. No. 3.8e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTSVPLSVP 9
| : |||
Db 2 CVMTHSLP 10

RESULT 11

US-09-436-469-5
; Sequence 5, Application US/09436469
; Patent No. 6790936
; GENERAL INFORMATION:
; APPLICANT: Kohn, Elise C. A.
; Liotta, Lance A.
; Kim, Young S.
; TITLE OF INVENTION: DNA Encoding CAI Resistance Proteins and
; Uses Thereof

; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Cr w LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/436,469
; FILING DATE: 08-NO. 6790936-1999
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/900,321
; FILING DATE: 25-JUL-1997
; APPLICATION NUMBER: US 08/212,190
; FILING DATE: 14-MAR-1994
; ATTORNEY/AGENT INFORMATION:

; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-204100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-436-469-5

Query Match 44.6%; Score 25; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLSVPC 10
| : |||
Db 3 PAPVPC 8

RESULT 12

PCT-US95-03610-5

; Sequence 5, Application PC/TUS9503610
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND
; NUMBER OF SEQUENCES: 10
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03610
; FILING DATE: 14-MAR-1995
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US 08/212,190
; FILING DATE: 14-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 15280-204000PC
; REFERENCE/DOCKET NUMBER: DHHS Ref. No. E-112-94/0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-03610-5

Query Match 44.6%; Score 25; DB 5; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLSVPC 10
| : |||
Db 3 PAPVPC 8

RESULT 13

US-09-886-135A-5
; Sequence 5, Application US/09886135A
; Patent No. 6790647
; GENERAL INFORMATION:
; APPLICANT: PRITSYN, Leonid R
; APPLICANT: ALTMAN, Irina B
; APPLICANT: SMIRNOV, Sergey V
; APPLICANT: ROSTOVA, Yulia G
; APPLICANT: YAMPOLSKAYA, Tatyana A
; APPLICANT: LEONOVA, Tatyana V
; APPLICANT: GUSYATINER, Mikhail M
; TITLE OF INVENTION: NEW MUTANT-ACETYLGLUTAMATE SYNTHASE AND METHOD FOR L-ARGININE PROI
; FILE REFERENCE: 209873USO
; CURRENT APPLICATION NUMBER: US/09/886,135A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: RUSSIAN FEDERATION 2000116481
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: RUSSIAN FEDERATION 2001112869
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-886-135A-5

Query Match 42.9%; Score 24; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SVPC 10
Db 2 SVPC 5

RESULT 14
US-08-483-434A-21
; Sequence 21, Application US/08483434A
; Patent No. 5648461
; GENERAL INFORMATION:
; APPLICANT: EVAL, Jacob
; APPLICANT: HAMILTON, Bruce K.
; APPLICANT: TUSZYNSKI, George P.
; TITLE OF INVENTION: Synthetic Analogs of Thrombospondin and
; TITLE OF INVENTION: Therapeutic Use Thereof
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,434A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/450,738
; FILING DATE: 25-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/185,614
; FILING DATE: 24-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/024,436
; FILING DATE: 01-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/597,197
; FILING DATE: 24-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/483,527
; FILING DATE: 22-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary Ph.D., Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9598-306 (9049)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 567-2020
; TELEFAX: (215) 567-2991
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-483-434A-21

Query Match 42.9%; Score 24; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SVPC 10
Db 2 SVPC 5

RESULT 15
US-08-476-134A-30
; Sequence 30, Application US/08476134A
; Patent No. 6239110
; GENERAL INFORMATION:
; APPLICANT: EVAL, JACOB
; APPLICANT: HAMILTON, BRUCE K.
; APPLICANT: TUSZYNSKI, GEORGE P.
; TITLE OF INVENTION: SYNTHETIC ANALOGS OF THROMBOSPONDIN AND THERAPEUTIC USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 07206-0009
; CURRENT APPLICATION NUMBER: US/08/476,134A
; CURRENT FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/587,197
; PRIOR FILING DATE: 1990-09-24
; PRIOR APPLICATION NUMBER: 07/483,527
; PRIOR FILING DATE: 1990-02-22
; PRIOR APPLICATION NUMBER: 08/450,738
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: 08/185,614
; PRIOR FILING DATE: 1994-01-24
; PRIOR APPLICATION NUMBER: 08/024,436
; PRIOR FILING DATE: 1993-03-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: analog of thrombospondin
US-08-476-134A-30

Query Match 42.9%; Score 24; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SVPC 10
Db 2 SVPC 5

Search completed: April 1, 2005, 12:10:00
Job time : 44 secs

GenCore version 5.1.6
Copyright (C) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2005, 11:19:07 ; Search time 11.5 Seconds
(without alignments)
75.300 Million cell updates/sec

Title: US-09-761-636A-14

Perfect score: 52

Sequence: 1 CISVPLVPC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 791

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	42.3	6	2 165546	MHC H2-L antigen -
2	19	36.5	5	2 A60521	glycogen phosphory
3	19	36.5	9	2 A60356	118K stomach cancer
4	18	34.6	9	2 A61620	locustamyotropin I
5	17	32.7	8	2 S10783	enamelin f - bovin
6	17	32.7	9	2 S66419	tetrameric protein
7	16	30.8	4	2 I51049	metallothionein-A
8	16	30.8	9	2 S13636	coat protein beta
9	15	28.8	6	2 H48394	glycoprotein compo
10	15	28.8	8	2 G31098	205K exoantigen -
11	15	28.8	8	4 I54017	granulocyte-colony
12	15	28.8	9	2 PT0080	60K Ca binding pro
13	14	26.9	7	2 I48105	dihydrofolate redu
14	14	26.9	8	2 S21288	lectin - potato (f
15	14	26.9	9	2 PH0943	T-cell receptor be
16	14	26.9	9	2 D48186	ATPase R1 subunit
17	13	25.0	5	2 E42364	flagellar protein
18	13	25.0	7	2 S42620	aggreccan - bovine
19	13	25.0	8	2 B39745	endoglycosylcerami
20	13	25.0	8	2 A42689	major postsynaptic
21	13	25.0	9	2 B28495	conopressin S - co
22	13	25.0	9	2 PT0247	Ig heavy chain CRD
23	13	25.0	9	2 PT0268	Ig heavy chain CRD
24	13	25.0	9	2 S26508	collagen alpha 2IV
25	12	23.1	5	2 B22565	R-phycocerythrin al
26	12	23.1	6	2 B34835	dnaA protein - Pse
27	12	23.1	6	2 B26206	alpha-1,4-glucan-p
28	12	23.1	6	4 A35039	hypothetical colla
29	12	23.1	7	2 E61491	seed protein ws-5

30	12	23.1	7	2 PH1602	Ig H chain V-D-J r
31	12	23.1	7	2 PH0932	T-cell receptor be
32	12	23.1	7	2 ECMUCR	catch-relaxing pep
33	12	23.1	8	2 S16324	hypothetical prote
34	12	23.1	8	2 PH0934	T-cell receptor be
35	12	23.1	8	2 A35180	neutral proteinase
36	12	23.1	9	2 A53797	3',5'-cyclic-GMP p
37	12	23.1	9	2 PH0935	T-cell receptor be
38	12	23.1	9	2 PH0937	T-cell receptor be
39	12	23.1	9	2 PH0902	T-cell receptor be
40	12	23.1	9	2 PH0917	T-cell receptor be
41	12	23.1	9	2 PH0918	T-cell receptor be
42	12	23.1	9	2 PH0921	T-cell receptor be
43	12	23.1	9	2 GS8502	kidney and bladder
44	12	23.1	9	2 S55696	phosphoenolpyruvac
45	12	23.1	9	2 S39437	D-amino-acid oxida

ALIGNMENTS

RESULT 1

I65546
MHC H2-L antigen - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I65546
Cell 44, 261-272, 1986
R:Kimura, A.; Israel, A.; Le Bail, O.; Kourileky, P.
A>Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and their
A:Reference number: I52778; MUID:86106202; PMID:3510743
A:Accession: I65546
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: GB:M12483; NID:g199565; PIDN:AAA39663.1; PID:g554234

Query Match 42.3%; Score 22; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 LVPC 9
:||||
Db 1 MVPC 4

RESULT 2

A60521
glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
N:Alternate names: glycogen phosphorylase b
C:Species: Liza ramada
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Mar-2004
C:Accession: A60521
R:Bonamusa, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A>Title: Purification and characterization of glycogen phosphorylase B from skeletal muscle
A:Reference number: A60521; MUID:90227907; PMID:2109669
A:Accession: A60521
A:Molecule type: protein
A:Residues: 1-5 <EON>
C:Keywords: Glycosyltransferase; hexosyltransferase; phosphoprotein
F:3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experime

Query Match 36.5%; Score 19; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVP 5
:||||
Db 2 ISVP 5

RESULT 3

A60356
118K stomach cancer antigen - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: A60356
R:Shiraishi, Y.
Int. J. Cancer 45, 783-787, 1990
A:Title: Western blotting analysis for malignant lymphoma and stomach cancer antigens fr
A:Reference number: A60356; MUID:90216080; PMID:2323853
A:Accession: A60356
A:Molecule type: protein
A:Residues: 1-9 <SH1>
A:Cross-references: UNIPROT:Q7M4R6
C:Keywords: glycoprotein

Query Match 36.5%; Score 19; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VPLVP 8
:|:|
Db 1 IPLKP 5

RESULT 4
A61620
locustamyotropin III - migratory locust
C:Species: Locusta migratoria (migratory locust)
C:Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
C:Accession: A61620
R:Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.
Insect Biochem. Mol. Biol. 22, 447-452, 1992
A:Title: Isolation, identification and synthesis of locustamyotropin III and IV, two add
A:Reference number: A61620
A:Accession: A61620
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <SCH>
A:Cross-references: UNIPROT:P41489
C:Keywords: amidated carboxyl end; neuropeptide
F:9/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 34.6%; Score 18; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLVP 8
|:|
Db 4 PVP 7

RESULT 5
S10783
enamelin f - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C:Accession: S10783
R:Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu
A:Reference number: S10780; MUID:90336641; PMID:2379503
A:Accession: S10783
A:Molecule type: protein
A:Residues: 1-8 <STR>
C:Keywords: enamel; phosphoprotein

Query Match 32.7%; Score 17; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VPLVP 8
:|:|
Db 1 MPLPP 5

us-09-761-636a-14.closed.rpr

RESULT 6

S66419
tetrameric proteinase precursor, 60K, dithiothreitol-sensitive - spinach (fragment)
C:Species: Spinacia oleracea (spinach)
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C:Accession: S66419
R:Kuwabara, T.
FEBS Lett. 371, 195-198, 1995
A:Title: The 60-kDa precursor to the dithiothreitol-sensitive tetrameric protease of spir
A:Reference number: S66419; MUID:95402209; PMID:7672127
A:Accession: S66419
A:Molecule type: protein
A:Residues: 1-9 <KUM>
A:Cross-references: UNIPROT:Q9T2K8; UNIPROT:Q41388

Query Match 32.7%; Score 17; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLVP 8
|:|
Db 2 PLVP 5

RESULT 7

I51049
metallothionein-A - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I51049
R:Olsson, P.E.; Kling, P.; Erkel, L.J.; Kille, P.
Eur. J. Biochem. 230, 344-349, 1995
A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) met
A:Reference number: I51049; MUID:95324545; PMID:7601121
A:Accession: I51049
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <OLS>
A:Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328

Query Match 30.8%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PC 9
|:|
Db 3 PC 4

RESULT 8

SI3636
coat protein beta chain, Golgi-derived - rabbit (fragment)
N:Alternate names: beta-COP protein
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: SI3636
R:Serafini, T.; Stenbeck, G.; Brecht, A.; Lottspeich, F.; Orsi, L.; Rothman, J.E.; Wieler
Nature 349, 215-220, 1991
A:Title: A coat subunit of Golgi-derived non-clathrin-coated vesicles with homology to t
A:Reference number: SI3636; MUID:91101693; PMID:1898984
A:Accession: SI3636
A:Molecule type: protein
A:Residues: 1-9 <SER>
A:Cross-references: UNIPROT:Q7M2R5
C:Superfamily: coatomer complex beta chain
C:Keywords: Golgi apparatus; protein transport

Query Match 30.8%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPLV 7
:|:|
Db 5 IPIV 8

RESULT 9

H48394
glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C:Accession: H48394
R:Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A:Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
II-like sequences.
A:Reference number: A48394; MUID:93250576; PMID:8485470
A:Accession: H48394
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-6 <MAP>
A:Experimental source: milk
A:Note: sequence extracted from NCBI backbone (NCBIP:131518)
C:Keywords: glycoprotein

Query Match 28.8%; Score 15; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 VPLVPC 9
:|:|
Db 1 VELLGC 6

RESULT 10

G33098
205K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C:Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C:Accession: G33098
R:Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A:Reference number: A33098
A:Accession: G33098
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <NIC>

Query Match 28.8%; Score 15; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPL 6
:|:|
Db 2 VPL 4

RESULT 11

I54017
granulocyte-colony stimulating factor precursor - synthetic (fragment)
C:Species: synthetic
A:Note: human gene engineered and expressed in Escherichia coli
C:Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 28-Jan-2000
C:Accession: I54017
R:Devlin, P.E.; Drummond, R.J.; Toy, P.; Mark, D.F.; Watt, K.W.; Devlin, J.J.
Gene 65, 13-22, 1988
A:Title: Alteration of amino-terminal codons of human granulocyte-colony-stimulating fac
i.

A:Reference number: I54017; MUID:88284374; PMID:2456256
A:Accession: I54017
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-8 <DEV>
A:Cross-references: GB:M20922; NID:9806638; PIDN:AAA66353.1; PID:g183043

Query Match 28.8%; Score 15; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLVP 8
:|:|
Db 3 PLGP 6

RESULT 12

PT0080
60K Ca binding protein - edible frog (fragment)
C:Species: Rana esculenta (edible frog)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: PT0080
R:Trevoso, S.; Zorzato, F.; Chiozzi, P.; Melandri, P.; Volpe, P.; Pozzan, T.
Biochem. Biophys. Res. Commun. 175, 444-450, 1991
A:Title: Frog brain expresses a 60 kDa Ca²⁺ binding protein similar to mammalian calretic
A:Reference number: PT0080; MUID:91207333; PMID:2018493
A:Accession: PT0080
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <TRE>
A:Cross-references: UNIPROT:Q7LZT5

Query Match 28.8%; Score 15; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLV 7
:|:|
Db 2 PLV 4

RESULT 13

I48105
dihydrofolate reductase - Chinese hamster (fragment)
C:Species: Crictetus griseus (Chinese hamster)
C:Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999
C:Accession: I48105
R:Aziakhan, J.C.; Vaughn, J.P.; Christy, R.J.; Hamlin, J.L.
Biochemistry 25, 6228-6236, 1986
A:Title: Nucleotide sequence and nuclease hypersensitivity of the Chinese hamster dihydr
A:Reference number: I48105; MUID:87076541; PMID:3024702
A:Accession: I48105
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7 <RES>
A:Cross-references: GB:M14771; NID:gl91055; PIDN:AAA36975.1; PID:gl91056

Query Match 26.9%; Score 14; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLV 7
:|:|
Db 4 PLI 6

RESULT 14

S21288
lectin - potato (fragment)
C:Species: Solanum tuberosum (potato)
C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C:Accession: S21288
R:Willar, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.
Biochem. J. 283, 813-821, 1992
A:Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization
A:Reference number: S21288; MUID:92272683; PMID:1590771
A:Accession: S21288
A:Molecule type: protein
A:Residues: 1-8 <ML>

A;Cross-references: UNIPROT:Q7M1V6
A;Experimental source: var. Ulster Sceptre
C;Function:
A;Description: may be involved in defence mechanism of the plant
C;Keywords: hydroxyproline; lectin

Query Match 26.9%; Score 14; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 SVPLVP 8
| | | |
Db 3 STPSPP 8

RESULT 15
PH0943
T-cell receptor beta chain V-D-J region (clone 14) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0943
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0943
A;Molecule type: mRNA
A;Residues: 1-9 <GOL>
A;Experimental source: complete Freund's adjuvant-immunized lymph node
A;Note: the authors translated the codon GAC for residue 8 as Glu
C;Keywords: T-cell receptor

Query Match 26.9%; Score 14; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CISVPLV 7
| | | |
Db 1 CASTDTV 7

Search completed: April 1, 2005, 11:25:15
Job time : 11.5 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 11:12:11 ; Search time 46.5 Seconds
(without alignments)
99.112 Million cell updates/sec

Title: US-09-761-636A-14
Perfect score: 52
Sequence: 1 CISVPLVPC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1455

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	20	38.5	9	1	MGMT_BOVIN	P29177 bos taurus
2	20	38.5	9	2	Q9P8E5	Q9P8E5 kluyveromyc
3	19	36.5	7	2	Q42564	Q42564 fugu rubrip
4	19	36.5	8	2	Q56140	Q56140 streptococ
5	19	36.5	9	2	Q7M4R6	Q7M4R6 homo sapien
6	18	34.6	8	1	CON2_CONPU	P58785 conus purpu
7	18	34.6	9	1	LMT3_LOCFMI	P41489 locusta mig
8	18	34.6	9	2	Q8AUM7	Q8AUM7 carassius a
9	18	34.6	9	2	Q8AYL5	Q8AYL5 carassius a
10	17	32.7	8	2	Q6LD23	P61d23 mus musculu
11	17	32.7	9	1	UPA3_HUMAN	P30089 homo sapien
12	17	32.7	9	2	Q7X6A3	Q7X6A3 zea mays (m
13	16	30.8	8	1	PPK2_PERAM	P93233 lycopersico
14	16	30.8	8	1	PPK2_PERAM	P82692 periplaneta
15	16	30.8	8	2	Q02831	O02831 oryctolagus
16	16	30.8	8	2	Q9TRY3	Q9TRY3 sus sp. ins
17	16	30.8	8	2	Q6UA69	Q6UA69 carassius c
18	16	30.8	9	2	Q16220	Q16220 homo sapien
19	16	30.8	9	2	Q9UMF3	Q9UMF3 homo sapien
20	16	30.8	9	2	Q7M2R5	Q7M2R5 oryctolagus
21	16	30.8	9	2	Q8QVD3	Q8QVD3 ovine respi
22	15	28.8	7	2	Q07624	Q07624 rous sarcom
23	15	28.8	8	1	PPK3_PERAM	P82618 periplaneta
24	15	28.8	8	2	Q6LDS6	Q6LDS6 homo sapien
25	15	28.8	9	1	UPA7_HUMAN	P30093 homo sapien
26	15	28.8	9	2	Q6LEK1	Q6LEK1 homo sapien
27	15	28.8	9	2	Q71GU0	Q71GU0 andrena vul
28	15	28.8	9	2	Q71H00	Q71H00 andrena iso
29	15	28.8	9	2	Q9S8J8	Q9S8J8 oryza sativ
30	15	28.8	9	2	Q712A6	Q712A6 sinorhizobi
31	15	28.8	9	2	O35953	O35953 mus musculu

32	15	28.8	9	2	Q7LZT5	Q7LZT5 rana esculc
33	14	26.9	7	2	O07354	O07354 synechococ
34	14	26.9	8	2	Q9TRX8	Q9TRX8 bos taurus
35	14	26.9	8	2	Q7M1V6	Q7M1V6 solanum tub
36	14	26.9	8	2	P83532	P83532 lactobacill
37	14	26.9	8	2	Q6LDP8	Q6LDP8 pseudomonas
38	14	26.9	8	2	Q9X3K1	Q9X3K1 prochloroco
39	14	26.9	9	2	Q6QF45	Q6QF45 homo sapien
40	14	26.9	9	2	Q6PT73	Q6PT73 zizania aqu
41	14	26.9	9	2	Q6PT74	Q6PT74 streptococ
42	14	26.9	9	2	Q6PT75	Q6PT75 sorghum bic
43	14	26.9	9	2	Q6PT76	Q6PT76 lolium pere
44	14	26.9	9	2	Q6PT77	Q6PT77 danthonia s
45	14	26.9	9	2	Q6PT78	Q6PT78 chasmanthiu

ALIGNMENTS

RESULT 1

MGMT_BOVIN
ID MGMT_BOVIN STANDARD; PRT; 9 AA.
AC P29177;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-methylguanine-DNA methyltransferase) (MGMT) (O-6-methylguanine-DNA-alkyltransferase) (Fragment).
GN Name=MGMT;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=90174912; PubMed=2308022;
RA Rydberg B., Hall J., Karan P.;
RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA methyltransferase.";
RL Nucleic Acids Res. 18:17-21(1990).
CC -!- FUNCTION: Involved in the cellular defense against the biological effects of O6-methylguanine (O6-MeG) in DNA. Repairs alkylated guanine in DNA by stoichiometrically transferring the alkyl group at the O-6 position to a cysteine residue in the enzyme. This is a suicide reaction: the enzyme is irreversibly inactivated.
CC -!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) + protein L-cysteine = DNA (without 6-O-methylguanine) + protein S-methyl-L-cysteine.
CC -!- SIMILARITY: Belongs to the MGMT family.
DR InterPro: IPR001497; Methyltransf_1.
DR PROSITE: PS00374; MGMT; PARTIAL.
KW Direct protein sequencing; DNA repair; Methyltransferase; Transferase.
FT NON_TER 1
FT ACT_SITE 9 9 Alkyl group acceptor (By similarity).
FT NON_TER 9
SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 38.5%; Score 20; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 LVPC 9
DB 6 LTPC 9

RESULT 2

Q9P8E5
ID Q9P8E5 PRELIMINARY; PRT; 9 AA.
AC Q9P8E5;

```
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DE 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE HIS4 protein (Fragment)
GN Name=HIS4;
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL-Y1140;
RX MEDLINE=99448382; PubMed=10518937; DOI=10.1016/S0014-5793(99)01105-9;
RA Lamas-Maceliras M., Esperanza Cerdan E., Freire-Picos M.A.;
RT "Kluyveromyces lactis HIS4 transcriptional regulation: similarities
RT and differences to Saccharomyces cerevisiae HIS4 gene.";
RL FEBS Lett. 458:72-76(1999).
DR EMBL; AJ238494; CAB87125.1; -.
FT NON TER 9
SQ SEQUENCE 9 AA; 1015 MW; 5770D2D772D2D767 CRC64;

Query Match 38.5%; Score 20; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPLVP 8
DB 2 LPVP 6

RESULT 3
O42564 PRELIMINARY; PRT; 7 AA.
AC O42564;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Truncated voltage-gated sodium channel alpha subunit (Fragment).
GN Name=Scn8a;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neoceratopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97442476; PubMed=9295353; DOI=10.1074/jbc.272.38.24008;
RA Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
RT two-domain protein in fetal brain and non-neuronal cells.";
RL J. Biol. Chem. 272:24008-24015(1997).
DR EMBL; U97673; AAB80916.1; -.
DR GO; GO:0005216; F:ion channel activity; IEA.
KW Ionic channel.
FT NON TER 1
SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

Query Match 36.5%; Score 19; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPLV 7
DB 1 VPLV 4

RESULT 4
Q56140 PRELIMINARY; PRT; 8 AA.
ID Q56140;
AC Q56140;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE STP6 protein (Fragment).
GN Name=STP6;
OS Streptococcus thermophilus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1308;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ST11;
RX MEDLINE=95047254; PubMed=7958782;
RA Constable A., Mollet B.;
RT "Isolation and characterisation of promoter regions from Streptococcus
RT thermophilus.";
RL FEMS Microbiol. Lett. 122:85-90(1994).
DR EMBL; X78210; CAA55045.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 846 MW; ED086772D5B045B6 CRC64;

Query Match 36.5%; Score 19; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVP 5
DB 3 ISVP 6

RESULT 5
Q7M4R6 PRELIMINARY; PRT; 9 AA.
ID Q7M4R6;
AC Q7M4R6;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE 118K stomach cancer antigen (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=90216080; PubMed=2323853;
RA Shiraishi Y.;
RT "Western blotting analysis for malignant lymphoma and stomach cancer
RT antigens from carcinogen-transformed bloom syndrome cells.";
RL Int. J. Cancer 45:783-787(1990).
DR PIR; A60356; A60356.
FT NON TER 1
FT NON TER 9
SQ SEQUENCE 9 AA; 949 MW; 3D057042D7633737 CRC64;

Query Match 36.5%; Score 19; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VPLVP 8
DB 1 IPLKP 5

RESULT 6
COW2 CONPU STANDARD; PRT; 8 AA.
ID COW2 CONPU;
AC P58785;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leu-contryphan-P.
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
```

OX	NCBI_TaxID=41690;
RN	[1]
RP	SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC	STRAN=Cliperton Island; TISSUE=Venom;
RX	MEDLINE=99388839; PubMed=10461743;
RA	Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
RA	Olivera B.M.;
RT	"A novel D-leucine-containing Conus peptide: diverse conformational
RT	dynamics in the contryphan family.";
RL	J. Pept. Res. 54:93-99(1999).
CC	-I- SUBCELLULAR LOCATION: Secreted.
CC	-I- TISSUE SPECIFICITY: Expressed by the venom duct.
CC	-I- MASS SPECTROMETRY: MW=886.4; METHOD=LSI; RANGE=1-8; NOTE=Ref.1.
KW	D-amino acid; Belongs to the contryphan family.
CC	D-amino acid; Direct protein sequencing; Toxin.
FT	DISULFID 2 8
FT	MOD RES 4 4 D-leucine.
SQ	SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;
Query Match	34.6%; Score 18; DB 1; Length 8;
Best Local Similarity	40.0%; Pred. No. 1.6e+06;
Matches	2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY	1 CISVP 5 :
DB	2 CVLLP 6
RESULT 7	
LMT3_LOCMI	
ID_LMT3_LOCMI	STANDARD; PRT; 9 AA.
AC	P41489;
DT	01-NOV-1995 (Rel. 32, Created)
DT	01-NOV-1995 (Rel. 32, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Locustamytropin 3 (LOM-WT-3).
OS	Locusta migratoria (Migratory locust).
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC	Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC	Acridoidea; Acrididae; Oedipodinae; Locusta.
OX	NCBI_TaxID=7004;
RN	[1]
RP	SEQUENCE, AND SYNTHESIS.
RC	TISSUE=Brain;
RA	Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA	de Loof A.;
RT	"Isolation, identification and synthesis of locustamytropin III and
RT	IV, two additional neuropeptides of Locusta migratoria: members of the
RT	locustamytropin peptide family.";
RT	Insect Biochem. Mol. Biol. 22:447-452(1992).
CC	-I- FUNCTION: Potent mediator of visceral muscle contractile activity
CC	(myotropic activity).
CC	-I- SIMILARITY: Belongs to the pyrokinin family.
DR	PIR; A61620; A61620.
DR	InterPro; IPR001484; Pyrokinin.
DR	PROSITE; PS00539; PYROKININ; 1.
FM	Annotation; Direct protein sequencing; Neuropeptide; Pyrokinin.
FT	MOD RES 9 9 Leucine amide.
SQ	SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;
Query Match	34.6%; Score 18; DB 1; Length 9;
Best Local Similarity	75.0%; Pred. No. 1.6e+06;
Matches	3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	5 PLVP 8
DB	4 PFVP 7
RESULT 8	
QBAUM7	
ID_QBAUM7	PRELIMINARY; PRT; 9 AA.
AC_QBAUM7	

```
RESULT 10
Q6LD23 PRELIMINARY; PRT; 8 AA.
AC Q6LD23;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Interferon alpha/beta receptor (Fragment).
GN Name=IFNAR;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RX MEDLINE=95047447; PubMed=7958966; DOI=10.1016/0378-1119(94)90710-2;
RA Lutfalla G., Uze G.;
RT "Structure of the murine interferon alpha/beta receptor-encoding gene:
RT high-frequency rearrangements in the interferon-resistant Li210 cell
RT line.";
RL Gene 148:343-346(1994).
DR EMBL; U06237; AAA65003.1; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 999 MW; CSBB59D76059D76A CRC64;

Query Match 32.7%; Score 17; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLVP 8
DB 2 PFIP 5

RESULT 11
UPA3_HUMAN STANDARD; PRT; 9 AA.
AC P30089;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of plasma (Spot 11) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -I- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 4.6, its MW is: 46 kDa.
DR SWISS-2DPAGE; P30089; HUMAN.
KW Direct protein sequencing.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1056 MW; 26F2B1EAF769C737 CRC64;

Query Match 32.7%; Score 17; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLVP 8
DB 1 PFIP 5

RESULT 12
Q7X6A3 PRELIMINARY; PRT; 9 AA.
AC Q7X6A3;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Isoamylase (Fragment).
GN Name=sui;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]_TaxID=4577;
RP SEQUENCE FROM N.A.
RA Wilson L.M., Whitt S.R., Ibanez A.M., Rocheford T.R., Goodman M.M.,
RA Buckler E.S. IV.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY290305; AAP45331.1; -.
DR EMBL; AY290311; AAP45337.1; -.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 976 MW; DF9BCEA76736CDD CRC64;

Query Match 32.7%; Score 17; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 VPC 9
DB 5 LPC 7

RESULT 13
P93233 PRELIMINARY; PRT; 7 AA.
AC P93233;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
DE (Fragment).
GN Name=LE-ACS1B;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]_TaxID=4081;
RP SEQUENCE FROM N.A.
RX MEDLINE=97351561; PubMed=9207843; DOI=10.1023/A:1005800511372;
RA Oetiker J.H., Olson D.C., Shiu O.Y., Yang S.F.;
RT "Differential induction of seven 1-aminocyclopropane-1-carboxylate
RT synthase genes by elicitor in suspension cultures of tomato
RT (Lycopersicon esculentum).";
RL Plant Mol. Biol. 34:275-286(1997).
DR EMBL; U75692; AAC49682.1; -.
DR GO; GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . .; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
KW Lyase.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 828 MW; 71B412C7377415D0 CRC64;

Query Match 30.8%; Score 16; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SVPLV 7
DB 1 SRPLV 5
```

```
RESULT 14
PPK2_PERAM STANDARD; PRT; 8 AA.
AC PPK2_PERAM 8 AA; 1028 MW; B859C7272EA77371 CRC64;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pyrokinin-2 (Pea-PK-2) (FXPRI-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattellidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=97353923; PubMed=9210163; DOI=10.1016/S0196-9781(97)00067-3;
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of two pyrokinins from the
RL retrocerebral complex of the American cockroach.";
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RL the American cockroach.";
RN [3]
RP J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -!- TISSUE SPECIFICITY: Corpora cardiaca.
CC -!- MASS SPECTROMETRY: MW=883; METHOD=WALDI; RANGE=1-8; NOTE=Ref.1.
CC -!- SIMILARITY: Belongs to the pyrokinin family.
DR InterPro: IPR001484; Pyrokinin.
DR PROSITE: PS00539; PYROKININ; FALSE_NEG.
KW Amidation; Direct protein sequencing; Neuropeptide; Pyrokinin.
FT MOD_RES 8 Leucine amide.
SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;
Query Match 30.8%; Score 16; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 SVPLVP 8
DB 1 SPFPAP 6
RESULT 15
O02831 PRELIMINARY; PRT; 8 AA.
AC O02831;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Pro alpha 1 type III collagen protein (Fragment).
GN Name-pro alpha 1 type III collagen;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96377339; PubMed=8793186; DOI=10.1016/S0945-053X(96)90125-0;
RA Metzaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
RA Vuorio E.;
RT "Evidence for insufficient chondrocytic differentiation during repair
RT of full-thickness defects of articular cartilage.";
RL Matrix Biol. 15:39-47(1996).
DR EMBL; S83371; AAD14433.1; -.
KW Collagen.
```

```
FT NON_TER 8
SQ SEQUENCE 8 AA; 1028 MW; B859C7272EA77371 CRC64;
Query Match 30.8%; Score 16; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 PC 9
DB 3 PC 4
Search completed: April 1, 2005, 11:23:57
Job time : 47.5 secs
```

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2005, 11:11:16 ; Search time 58.5 Seconds
(without alignments)
59.502 Million cell updates/sec

Title: US-09-761-636A-14

Perfect score: 52

Sequence: 1 CISVPLVPC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 330156

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	9	AAU04533	AAU04533 VEGF base
2	27	51.9	9	ABG35134	Abg35134 Pancreat
3	27	51.9	9	ABB46931	Abb46931 Desmocol
4	27	51.9	9	ABG60522	Abg60522 Selective
5	27	51.9	9	ABR56920	AbR56920 Pancreat
6	27	51.9	9	ADM35404	Adm35404 Human LY
7	27	51.9	9	ADM35430	Adm35430 Human LY
8	27	51.9	9	ADM35441	Adm35441 Human LY
9	27	51.9	9	ADM35456	Adm35456 Human LY
10	27	51.9	9	ADM35435	Adm35435 Human LY
11	27	51.9	9	ADM35451	Adm35451 Human LY
12	27	51.9	9	ADM35434	Adm35434 Human LY
13	27	51.9	9	ADM35426	Adm35426 Human LY
14	27	51.9	9	ADM35397	Adm35397 Human LY
15	27	51.9	9	AD112322	Ad112322 Human BCY
16	27	51.9	9	AD112363	Ad112363 Human BCY
17	27	51.9	9	AD112336	Ad112336 Human BCY
18	27	51.9	9	AD112323	Ad112323 Human BCY
19	26	50.0	7	AAy84998	Aay84998 Amino aci
20	26	50.0	7	ADC44293	Adc44293 Endotheli
21	26	50.0	9	AAy63242	Aay63242 Protocach
22	26	50.0	9	AAE07204	Aae07204 Modified
23	26	50.0	9	AAm24655	Aam24655 Human MHC
24	26	50.0	9	ABG35050	Abg35050 Endostati
25	26	50.0	9	ADK07023	Adk07023 Hepatitis

ALIGNMENTS

RESULT 1

AAU04533

ID AAU04533 standard; peptide; 9 AA.

XX AC AAU04533;

XX DT 26-SEP-2001 (first entry)

XX DE VEGF based monocyclic peptide 11.

XX KW Human; VEGF; vascular endothelial growth factor; angiogenesis;

KW neovascularisation; lymphangiogenesis; psoriasis; tumour;

KW diabetes induced neovascular sequelae; rheumatoid arthritis;

KW diabetic retinopathy; chronic inflammation; cyclic.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Disulfide-bond 1..9

FT /note= "This bond cyclises the peptide"

XX PN WO200152875-A1.

XX PD 26-JUL-2001.

XX PF 18-JAN-2001; 2001WO-US001533.

XX PR 18-JAN-2000; 2000US-0176293P.

XX PR 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX PI Achen MG, Hughes RA, Stacker S, Cendron A;

XX DR WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

XX Claim 49; Page 32; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9
 DB 1 CISVPLVPC 9

RESULT 2
 ABG35134
 ID ABG35134 standard; peptide; 9 AA.

AC ABG35134;
 XX
 DT 15-JUL-2002 (first entry)
 DE Pancreatic islet targeting peptide #10.
 XX
 KW Targeting peptide; cancer; Hodgkin's disease; cytostatic;
 KW immunosuppressive; anti-inflammatory; antiarthritic; antiviral;
 KW antiatherosclerotic; antidiabetic; antibacterial; diabetes mellitus;
 KW inflammatory disease; arthritis; atherosclerosis; cancer;
 KW autoimmune disease; bacterial infection; viral infection.

OS Unidentified.
 XX
 XX WO200220722-A2.
 PN
 PD 14-MAR-2002.
 XX
 PF 07-SEP-2001; 2001WO-US027702.
 XX
 PR 08-SEP-2000; 2000US-0231266P.
 PR 17-JAN-2001; 2001US-00765101.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.

PI Arap W, Pasqualini R;
 XX
 DR WPI; 2002-383050/41.
 XX
 XX Identifying targeting peptides useful for treating e.g. diabetes
 PT mellitus, inflammatory diseases, cancer, or autoimmune diseases.
 PT comprises exposing a sample to a phase display library and recovering
 PT phase bound to the sample.
 XX
 XX Claim 56; Page 288; 298pp; English.

XX This invention relates to a novel method for identifying disease
 CC targeting peptides. The method comprises exposing a sample from an organ,
 CC tissue or cell type of interest, to a phase display library and
 CC recovering phase bound to the sample (the phase expresses targeting
 CC peptides). The peptides identified by the method of the invention may
 CC have cytostatic, immunosuppressive, anti-inflammatory, antiarthritic,
 CC antiatherosclerotic, antidiabetic, antibacterial and antiviral
 CC activities. The methods and composition are useful for identifying
 CC targeting peptides and one or more receptors for a targeting peptide. The
 CC targeting peptides are used for selective delivery of therapeutic agents,
 CC including gene therapy vectors and fusion proteins, to specific organs,
 CC tissues, or cell types in subject. The targeting peptide may also be used
 CC for treating diseases such as diabetes mellitus, inflammatory diseases,
 CC arthritis, atherosclerosis, cancer, autoimmune diseases, bacterial and
 CC viral infections and Hodgkin's disease. The present sequence represents a
 CC targeting peptide of the invention
 XX
 SQ Sequence 9 AA;

Query Match 51.9%; Score 27; DB 5; Length 9;
 Best Local Similarity 55.6%; Pred. No. 1.8e+06;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9
 DB 1 CMSSPGVAC 9

RESULT 3
 ABB46931
 ID ABB46931 standard; peptide; 9 AA.

AC ABB46931;
 XX
 DT 30-JAN-2002 (first entry)
 DE Desmocollin-2 CAR cyclic peptide 13.
 XX
 KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;
 KW organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.

OS Synthetic.
 XX
 PN WO200172956-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-IB001400.
 PR
 PR 27-MAR-2000; 2000US-00535852.
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 PI Blaschuk OW, Symonds JM, Gour BJ;
 XX
 DR WPI; 2002-025778/03.

XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis.
 XX
 PS Claim 23; Page 111; 127pp; English.

XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have

CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
CC facilitate wound healing and/or reduce scar tissue, for enhancing
CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
CC treating an autoimmune blistering disorder and to treat cancer (e.g.
CC carcinoma, leukaemia or melanoma) and induce apoptosis
XX
SQ Sequence 9 AA;

Query Match 51.9%; Score 27; DB 5; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9
||: ||
Db 1 CIAFATTPC 9

RESULT 4
ABG60522
ID ABG60522 standard; peptide; 9 AA.

XX AC ABG60522;
XX DT 30-JUL-2002 (first entry)
XX DE Selective targeting peptide #197.
XX KW Targeting peptide; cancer; arthritis; diabetes; inflammatory disease;
XX KW atherosclerosis; autoimmune disease; bacterial infection; apoptosis;
XX KW viral infection; cardiovascular disease; degenerative disease; ischaemia;
XX KW inflammation; macular degeneration; antiinflammatory; antidiabetic;
XX KW cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic;
XX KW gene therapy.

XX OS Synthetic.

XX FN WO200220769-A1.

XX PD 14-MAR-2002.

XX PF 07-SEP-2001; 2001WO-US027692.

XX PR 08-SEP-2000; 2000US-0231266P.

XX PR 17-JAN-2001; 2001US-00765101.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Arap W, Pasqualini R;

XX WPI; 2002-415731/44.

XX Targeting peptides identified by phage display, useful for targeting
PT delivery to an organ or tissue, particularly for treating a disease, e.g.
PT cancer, inflammatory or autoimmune diseases, infections or cardiovascular
PT disease.

PS Claim 22; Page 121; 317pp; English.

XX The invention relates to an isolated peptide of 100 amino acids or less
CC in size useful for targeting delivery to an organ or tissue, particularly
CC for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory
CC disease, atherosclerosis, autoimmune disease, bacterial infection, viral
CC infection, cardiovascular disease or degenerative disease. The peptide is
CC also useful for inducing apoptosis, particularly to a subject with
CC ischaemia, cancer, arthritis, diabetes, cardiovascular disease.
CC inflammation or macular degeneration. Furthermore, the peptide is useful
CC for diagnosing the diseases cited above. Targeting peptides of the
CC invention can also be used to deliver an agent to a foetus, by attaching
CC a peptide to the agent and administering the peptide to a pregnant
CC subject. Sequences ABG60326-ABG60574 represent selective targeting
CC peptides of the invention

XX SQ Sequence 9 AA;

Query Match 51.9%; Score 27; DB 5; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9
||: ||
Db 1 CMSSPGVAC 9

RESULT 5
ABR56920
ID ABR56920 standard; peptide; 9 AA.

XX AC ABR56920;

XX DT 30-JUL-2003 (first entry)

XX DE Pancreatic targeting peptide SEQ ID NO:137.

XX KW Targeting peptide; obesity; lipodystrophy; anorectic; antilipaeamic;
XX KW peptide therapy; gene therapy; infection; human immunodeficiency virus;
XX KW HIV; placental delivery; teratogenic; placenta; adipose; pancreatic;
XX KW beta-3 integrin; beta-5 integrin; spleen; aminopeptidase A.

XX OS Mus musculus.

XX OS Synthetic.

XX PN WO2003022991-A2.

XX PD 20-MAR-2003.

XX PF 30-AUG-2002; 2002WO-US027836.

XX PR 07-SEP-2001; 2001WO-US027692.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Pasqualini R, Arap W, Kolonin MG;

XX WPI; 2003-371749/35.

XX Treating obesity or a lipodystrophy comprises obtaining a targeting
PT peptide selective for adipose tissue, attaching the peptide to a
PT therapeutic agent to form a complex, and administering the complex to a
PT subject.

XX Example 9; Page 114; 247pp; English.

XX The present invention describes a method for treating obesity or a
CC lipodystrophy, which comprises: (a) obtaining a targeting peptide
CC selective for adipose tissue; (b) attaching the peptide to a therapeutic
CC agent to form a complex; (c) administering the complex to a subject; and
CC (d) inducing weight loss in the subject or treating lipodystrophy. The
CC adipose targeting peptides have anorectic and antilipaeamic activities,
CC and can be used in peptide and gene therapy. The method is used for
CC treating obesity or a lipodystrophy that is related to infection with
CC human immunodeficiency virus (HIV). The peptides used in the method can
CC also be used for targeting delivery to an organ or tissue, such as
CC placental delivery. A receptor that binds to a placenta targeting peptide
CC is used to screen compounds for teratogenic activity. ABR56806 to
CC ABR56927 and ACC79106 to ACC79111 represent sequences used in the
CC exemplification of the present invention

XX SQ Sequence 9 AA;

Query Match 51.9%; Score 27; DB 6; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9
||: ||
Db 1 CMSSPGVAC 9

Human LY148P cancer related peptide for cancer detection method.

cytostatic; T-cell vaccine; detection; cancer;
chronic lymphocytic leukemia.

RESULT 6

ADM35404

ID ADM35404 standard; peptide; 9 AA.

XX AC

ADM35404;

XX DT 03-JUN-2004 (first entry)

XX DE Human LY148P cancer related peptide for cancer detection method.

XX KW cytostatic; T-cell vaccine; detection; cancer;
chronic lymphocytic leukemia.

XX OS Homo sapiens.

XX FN WO2003077836-A2.

XX PD 25-SEP-2003.

XX PF 06-NOV-2002; 2002WO-US035728.

XX PR 06-NOV-2001; 2001US-00040862.

XX PR 23-MAY-2002; 2002US-00154884.

XX PA (CORI-) CORIXA CORP.

XX PI Gaiger A, Algate PA, Mannion J, Retter M;

XX WPI; 2003-756941/71.

XX DR Detecting cancer in a patient comprises contacting a biological sample
from the patient with a binding agent that binds to a cancer-associated
polypeptide and comparing the amount of polypeptide to a predetermined
cutoff value.

XX PS Disclosure; SEQ ID NO 11228; 419pp; English.

XX CC The invention relates to a method of detecting (M1) cancer in a patient
by: (i) contacting a biological sample from the patient with an agent
that binds to any of three polypeptides given in the specification; (ii)
detecting in a sample an amount of the peptide that binds to the binding
agent; and (iii) comparing the amount of polypeptide present in the
patient's sample to a predetermined cutoff value. The specification also
discloses a separate method for detecting (M2) cancer in a patient by a
method similar to M1, except that the detection agent is an
oligonucleotide that binds to any of three polynucleotides given in the
specification. M1 and M2 are useful for detecting the presence of cancer
in a patient, especially chronic lymphocytic leukemia. The applicants
have identified specific human polypeptides overexpressed in one or more
types of hematological malignancies. This sequence corresponds to a
peptide used in the method of the invention.

XX SQ Sequence 9 AA;

Query Match 51.9%; Score 27; DB 7; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.8e+06;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 C1SVPL 6

Db 4 CLSVPL 9

RESULT 7

ADM35430

ID ADM35430 standard; peptide; 9 AA.

XX AC

ADM35430;

XX DT 03-JUN-2004 (first entry)

XX

DE

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KW

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Human LY148P cancer related peptide for cancer detection method.

cytostatic; T-cell vaccine; detection; cancer;
chronic lymphocytic leukemia.

Homo sapiens.

WO2003077836-A2.

25-SEP-2003.

06-NOV-2002; 2002WO-US035728.

06-NOV-2001; 2001US-00040862.

23-MAY-2002; 2002US-00154884.

(CORI-) CORIXA CORP.

Gaiger A, Algate PA, Mannion J, Retter M;

WPI; 2003-756941/71.

Detecting cancer in a patient comprises contacting a biological sample
from the patient with a binding agent that binds to a cancer-associated
polypeptide and comparing the amount of polypeptide to a predetermined
cutoff value.

Disclosure; SEQ ID NO 11254; 419pp; English.

The invention relates to a method of detecting (M1) cancer in a patient
by: (i) contacting a biological sample from the patient with an agent
that binds to any of three polypeptides given in the specification; (ii)
detecting in a sample an amount of the peptide that binds to the binding
agent; and (iii) comparing the amount of polypeptide present in the
patient's sample to a predetermined cutoff value. The specification also
discloses a separate method for detecting (M2) cancer in a patient by a
method similar to M1, except that the detection agent is an
oligonucleotide that binds to any of three polynucleotides given in the
specification. M1 and M2 are useful for detecting the presence of cancer
in a patient, especially chronic lymphocytic leukemia. The applicants
have identified specific human polypeptides overexpressed in one or more
types of hematological malignancies. This sequence corresponds to a
peptide used in the method of the invention.

Sequence 9 AA;

Query Match 51.9%; Score 27; DB 7; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.8e+06;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 C1SVPL 6

Db 4 CLSVPL 9

RESULT 8

ADM35441

ID ADM35441 standard; peptide; 9 AA.

XX AC

ADM35441;

XX DT 03-JUN-2004 (first entry)

XX DE Human LY148P cancer related peptide for cancer detection method.

XX KW cytostatic; T-cell vaccine; detection; cancer;
chronic lymphocytic leukemia.

XX OS Homo sapiens.

XX FN WO2003077836-A2.

XX PD 25-SEP-2003.

XX	
PF	06-NOV-2002; 2002WO-US035728.
XX	
PR	06-NOV-2001; 2001US-00040862.
PR	23-MAY-2002; 2002US-00154884.
XX	
PA	(CORI-) CORIXA CORP.
XX	
PI	Gaiger A, Algate PA, Mannion J, Retter M;
XX	
DR	WPI; 2003-756941/71.
XX	
PT	Detecting cancer in a patient comprises contacting a biological sample
PT	from the patient with a binding agent that binds to a cancer-associated
PT	polypeptide and comparing the amount of polypeptide to a predetermined
XX	cutoff value.
XX	
PS	Disclosure; SEQ ID NO 11265; 419pp; English.
XX	
CC	The invention relates to a method of detecting (M1) cancer in a patient
CC	by: (i) contacting a biological sample from the patient with an agent
CC	that binds to any of three polypeptides given in the specification; (ii)
CC	detecting in a sample an amount of the peptide that binds to the binding
CC	agent; and (iii) comparing the amount of polypeptide present in the
CC	patient's sample to a predetermined cutoff value. The specification also
CC	discloses a separate method for detecting (M2) cancer in a patient by a
CC	method similar to M1, except that the detection agent is an
CC	oligonucleotide that binds to any of three polynucleotides given in the
CC	specification. M1 and M2 are useful for detecting the presence of cancer
CC	in a patient, especially chronic lymphocytic leukemia. The applicants
CC	have identified specific human polypeptides overexpressed in one or more
CC	types of hematological malignancies. This sequence corresponds to a
CC	peptide used in the method of the invention.
XX	
SQ	Sequence 9 AA;
Query Match	51.9%; Score 27; DB 7; Length 9;
Best Local Similarity	66.7%; Pred. NO. 1.8e+06;
Matches	4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Oy	1 C1SVPL 6
	: :
Db	4 CLSVPV 9
RESULT 9	
ADM35456	
ID	ADM35456 standard; peptide; 9 AA.
XX	
AC	ADM35456;
AC	
DT	03-JUN-2004 (first entry)
XX	
DE	Human LY1448P cancer related peptide for cancer detection method.
XX	
KW	cytostatic; T-cell vaccine; detection; cancer;
KW	chronic lymphocytic leukemia.
XX	
OS	Homo sapiens.
XX	
PN	WO2003077836-A2.
XX	
PD	25-SEP-2003.
XX	
PF	06-NOV-2002; 2002WO-US035728.
XX	
PR	06-NOV-2001; 2001US-00040862.
PR	23-MAY-2002; 2002US-00154884.
XX	
PA	(CORI-) CORIXA CORP.
XX	
PI	Gaiger A, Algate PA, Mannion J, Retter M;
XX	

CC by: (i) contacting a biological sample from the patient with an agent
CC that binds to any of three polypeptides given in the specification; (ii)
CC detecting in a sample an amount of the peptide that binds to the binding
CC agent; and (iii) comparing the amount of polypeptide present in the
CC patient's sample to a predetermined cutoff value. The specification also
CC discloses a separate method for detecting (M2) cancer in a patient by a
CC method similar to M1, except that the detection agent is an
CC oligonucleotide that binds to any of three polynucleotides given in the
CC specification. M1 and M2 are useful for detecting the presence of cancer
CC in a patient, especially chronic lymphocytic leukemia. The applicants
CC have identified specific human polypeptides overexpressed in one or more
CC types of hematological malignancies. This sequence corresponds to a
CC peptide used in the method of the invention.

XX Sequence 9 AA;

Query Match 51.9%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 C1SVPL 6
|:|:|:
Db 4 CLSPVP 9

RESULT 11

ADM35451
ID ADM35451 standard; peptide; 9 AA.

XX
AC ADM35451;

XX 03-JUN-2004 (first entry)

XX Human LY1448P cancer related peptide for cancer detection method.

XX cytostatic; T-cell vaccine; detection; cancer;

KW chronic lymphocytic leukemia.

XX Homo sapiens.

XX WO2003077836-A2.

XX 25-SEP-2003.

XX 06-NOV-2002; 2002WO-US035728.

XX 06-NOV-2001; 2001US-00040862.

PR 23-MAY-2002; 2002US-00154884.

XX (CORI-) CORIXA CORP.

XX Gaiger A, Algate PA, Mannion J, Retter M;

XX WPI; 2003-756941/71.

XX Detecting cancer in a patient comprises contacting a biological sample
XX from the patient with a binding agent that binds to a cancer-associated
XX polypeptide and comparing the amount of polypeptide to a predetermined
XX cutoff value.

XX Disclosure; SEQ ID NO 11275; 419pp; English.

XX The invention relates to a method of detecting (M1) cancer in a patient
XX by: (i) contacting a biological sample from the patient with an agent
XX that binds to any of three polypeptides given in the specification; (ii)
XX detecting in a sample an amount of the peptide that binds to the binding
XX agent; and (iii) comparing the amount of polypeptide present in the
XX patient's sample to a predetermined cutoff value. The specification also
XX discloses a separate method for detecting (M2) cancer in a patient by a
XX method similar to M1, except that the detection agent is an
XX oligonucleotide that binds to any of three polynucleotides given in the
XX specification. M1 and M2 are useful for detecting the presence of cancer
XX in a patient, especially chronic lymphocytic leukemia. The applicants

CC have identified specific human polypeptides overexpressed in one or more
CC types of hematological malignancies. This sequence corresponds to a
CC peptide used in the method of the invention.

XX Sequence 9 AA;

Query Match 51.9%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 C1SVPL 6
|:|:|:
Db 4 CLSPVP 9

RESULT 12

ADM35434
ID ADM35434 standard; peptide; 9 AA.

XX
AC ADM35434;

XX 03-JUN-2004 (first entry)

XX Human LY1448P cancer related peptide for cancer detection method.

XX cytostatic; T-cell vaccine; detection; cancer;

KW chronic lymphocytic leukemia.

XX Homo sapiens.

XX WO2003077836-A2.

XX 25-SEP-2003.

XX 06-NOV-2002; 2002WO-US035728.

XX 06-NOV-2001; 2001US-00040862.

PR 23-MAY-2002; 2002US-00154884.

XX (CORI-) CORIXA CORP.

XX Gaiger A, Algate PA, Mannion J, Retter M;

XX WPI; 2003-756941/71.

XX Detecting cancer in a patient comprises contacting a biological sample
XX from the patient with a binding agent that binds to a cancer-associated
XX polypeptide and comparing the amount of polypeptide to a predetermined
XX cutoff value.

XX Disclosure; SEQ ID NO 11258; 419pp; English.

XX The invention relates to a method of detecting (M1) cancer in a patient
XX by: (i) contacting a biological sample from the patient with an agent
XX that binds to any of three polypeptides given in the specification; (ii)
XX detecting in a sample an amount of the peptide that binds to the binding
XX agent; and (iii) comparing the amount of polypeptide present in the
XX patient's sample to a predetermined cutoff value. The specification also
XX discloses a separate method for detecting (M2) cancer in a patient by a
XX method similar to M1, except that the detection agent is an
XX oligonucleotide that binds to any of three polynucleotides given in the
XX specification. M1 and M2 are useful for detecting the presence of cancer
XX in a patient, especially chronic lymphocytic leukemia. The applicants
XX have identified specific human polypeptides overexpressed in one or more
XX types of hematological malignancies. This sequence corresponds to a
XX peptide used in the method of the invention.

XX Sequence 9 AA;

Query Match 51.9%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CUSVPL 6
DB 4 CLSVPV 9

RESULT 13
ADM35426
ID ADM35426 standard; peptide; 9 AA.
XX AC ADM35426;
XX DT 03-JUN-2004 (first entry)
XX DE Human LY1448P cancer related peptide for cancer detection method.
XX KW cytostatic; T-cell vaccine; detection; cancer;
XX KW chronic lymphocytic leukemia.
XX OS Homo sapiens.
XX PN WO2003077836-A2.
XX PD 25-SEP-2003.
XX PF 06-NOV-2002; 2002WO-US035728.
XX PR 06-NOV-2001; 2001US-00040862.
XX PR 23-MAY-2002; 2002US-00154884.
XX PA (CORI-) CORIXA CORP.
XX PI Gaiger A, Algate PA, Mannion J, Retter M;
XX DR WPI; 2003-756941/71.
XX PT Detecting cancer in a patient comprises contacting a biological sample from the patient with a binding agent that binds to a cancer-associated polypeptide and comparing the amount of polypeptide to a predetermined cutoff value.
XX PS Disclosure; SEQ ID NO 11250; 419pp; English.
XX CC The invention relates to a method of detecting (M1) cancer in a patient by: (i) contacting a biological sample from the patient with an agent that binds to any of three polypeptides given in the specification; (ii) detecting in a sample an amount of the peptide that binds to the binding agent; and (iii) comparing the amount of polypeptide present in the patient's sample to a predetermined cutoff value. The specification also discloses a separate method for detecting (M2) cancer in a patient by a method similar to M1, except that the detection agent is an oligonucleotide that binds to any of three polynucleotides given in the specification. M1 and M2 are useful for detecting the presence of cancer in a patient, especially chronic lymphocytic leukemia. The applicants have identified specific human polypeptides overexpressed in one or more types of hematological malignancies. This sequence corresponds to a peptide used in the method of the invention.

XX SQ Sequence 9 AA;
Query Match 51.9%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CUSVPL 6
DB 4 CLSVPV 9

RESULT 14
ADM35397
ID ADM35397 standard; peptide; 9 AA.
XX AC ADM35397;

XX 03-JUN-2004 (first entry)
XX DE Human LY1448P cancer related peptide for cancer detection method.
XX KW cytostatic; T-cell vaccine; detection; cancer;
XX KW chronic lymphocytic leukemia.
XX OS Homo sapiens.
XX PN WO2003077836-A2.
XX PD 25-SEP-2003.
XX PF 06-NOV-2002; 2002WO-US035728.
XX PR 06-NOV-2001; 2001US-00040862.
XX PR 23-MAY-2002; 2002US-00154884.
XX PA (CORI-) CORIXA CORP.
XX PI Gaiger A, Algate PA, Mannion J, Retter M;
XX DR WPI; 2003-756941/71.
XX PT Detecting cancer in a patient comprises contacting a biological sample from the patient with a binding agent that binds to a cancer-associated polypeptide and comparing the amount of polypeptide to a predetermined cutoff value.
XX PS Disclosure; SEQ ID NO 11221; 419pp; English.
XX CC The invention relates to a method of detecting (M1) cancer in a patient by: (i) contacting a biological sample from the patient with an agent that binds to any of three polypeptides given in the specification; (ii) detecting in a sample an amount of the peptide that binds to the binding agent; and (iii) comparing the amount of polypeptide present in the patient's sample to a predetermined cutoff value. The specification also discloses a separate method for detecting (M2) cancer in a patient by a method similar to M1, except that the detection agent is an oligonucleotide that binds to any of three polynucleotides given in the specification. M1 and M2 are useful for detecting the presence of cancer in a patient, especially chronic lymphocytic leukemia. The applicants have identified specific human polypeptides overexpressed in one or more types of hematological malignancies. This sequence corresponds to a peptide used in the method of the invention.

XX SQ Sequence 9 AA;
Query Match 51.9%; Score 27; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CUSVPL 6
DB 2 CLSVPV 7

RESULT 15
ADM12322
ID ADM12322 standard; peptide; 9 AA.
XX AC ADM12322;
XX DT 06-MAY-2004 (first entry)
XX DE Human BCY1 immunogenic peptide.
XX KW cancer; BFA4; BCY1; immunisation; tumour antigen; cytostatic; vaccine;
XX KW gene therapy; immunotherapeutic; human.
XX OS Homo sapiens.
OS Synthetic.

XX WO2004005463-A2.
XX
XX
PD 15-JAN-2004.
XX
XX
PF 01-JUL-2003; 2003WO-US020636.
XX
XX
PR 03-JUL-2002; 2002US-0394346P.
PR 09-JUL-2002; 2002US-0394503P.
PR 18-SEP-2002; 2002US-0411833P.
PR 06-FEB-2003; 2003US-0445342P.
XX
XX (AVET) AVENTIS PASTEUR INC.
XX
XX Berinstitute N, Lovitt C, Parrington M, Pedyczak A, Radvanyi L;
PI Gallichan S, Singh-Sandhu D;
XX
XX WPI; 2004-099378/10.
XX
XX New expression vector useful for preventing and/or treating cancer or for
PT the insertion and expression of foreign genes encoding tumor antigens for
PT use in the immunotherapeutic treatment of cancer.
XX
XX
PS Claim 38; Page 44; 58pp; English.
XX
XX The present invention describes an expression vector comprising a
CC nucleotide sequence of 3847 (S1) or 1203 (S3) base pairs (bp), see SEQ ID
CC NO:1 (AD11211) or SEQ ID NO:3 (AD112113), or its fragment. Also
CC described: (1) a composition comprising the expression vector in a
CC pharmaceutical carrier; (2) a method for preventing or treating cancer,
CC comprising administering to a host the expression vector described above;
CC (3) peptides derived from BFA4 or BCY1 as listed in the specification;
CC and (4) methods for immunizing a host against the tumour antigen BFA4 or
CC BCY1, comprising administering to the patient the peptides described
CC above, either alone or in combination with another agent, where the
CC individual components of the combination are administered simultaneously
CC or separately from one another. The compositions and peptides have
CC cytostatic activities, and can be used in vaccines and in gene therapy.
CC The composition and methods are useful for preventing or treating cancer.
CC In particular, the vector is used for the insertion and expression of
CC foreign genes encoding tumour antigens for use in the immunotherapeutic
CC treatment of cancer. The present sequence represents a human BCY1
CC immunogenic peptide, which is used in the exemplification of the present
CC invention. The human BFA4 gene is located on chromosome 8.
XX
SQ Sequence 9 AA;
Query Match 51.9%; Score 27; DB 8; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 ISVPLVPC 9
DB 2 VTALVPC 9
Search completed: April 1, 2005, 11:22:13
Job time : 59.5 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 11:24:02 ; Search time 67 Seconds
(without alignments)
44,542 Million cell updates/sec

Title: US-09-761-636A-14

Perfect score: 52

Sequence: 1 CISVPLVPC 9

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 135600

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	27	51.9	9	15	Sequence 11221, A
3	27	51.9	9	15	Sequence 11228, A
4	27	51.9	9	15	Sequence 11250, A
5	27	51.9	9	15	Sequence 11254, A
6	27	51.9	9	15	Sequence 11258, A
7	27	51.9	9	15	Sequence 11259, A
8	27	51.9	9	15	Sequence 11265, A
9	27	51.9	9	15	Sequence 11275, A
10	27	51.9	9	15	Sequence 11280, A
11	27	51.9	9	15	Sequence 242, App
12	27	51.9	9	16	Sequence 206, App
13	27	51.9	9	16	Sequence 203, App

14	27	51.9	9	16	US-10-611-440-207	Sequence 207, App
15	26	50.0	7	14	US-10-286-457-21	Sequence 21, App
16	26	50.0	9	9	US-09-780-053-148	Sequence 148, App
17	26	50.0	9	14	US-10-006-869-2726	Sequence 2726, App
18	26	50.0	9	15	US-10-395-032-2726	Sequence 2726, App
19	26	50.0	9	15	US-10-363-208-137	Sequence 137, App
20	25	48.1	5	14	US-10-286-457-36	Sequence 36, App
21	24.5	47.1	9	15	US-10-428-335-52	Sequence 52, App
22	24	46.2	9	10	US-09-932-165-439	Sequence 439, App
23	24	46.2	9	10	US-09-932-165-636	Sequence 636, App
24	24	46.2	9	14	US-10-286-457-216	Sequence 216, App
25	24	46.2	9	15	US-10-428-335-90	Sequence 90, App
26	24	46.2	9	15	US-10-611-440-208	Sequence 208, App
27	24	46.2	9	16	US-10-611-440-209	Sequence 209, App
28	23	44.2	7	9	US-09-761-636A-11	Sequence 11, App
29	23	44.2	9	11	US-09-977-579-19	Sequence 19, App
30	23	44.2	9	14	US-10-038-407-29	Sequence 29, App
31	23	44.2	9	14	US-10-254-446A-123	Sequence 123, App
32	23	44.2	9	14	US-10-286-457-165	Sequence 165, App
33	23	44.2	9	14	US-10-286-457-500	Sequence 500, App
34	23	44.2	9	14	US-10-164-279-15	Sequence 15, App
35	23	44.2	9	15	US-10-363-208-147	Sequence 147, App
36	23	44.2	9	15	US-10-363-208-236	Sequence 236, App
37	23	44.2	9	16	US-10-777-053-304	Sequence 304, App
38	23	44.2	9	16	US-10-363-204-197	Sequence 197, App
39	23	44.2	9	17	US-10-838-289-450	Sequence 450, App
40	23	44.2	9	17	US-10-838-289-526	Sequence 526, App
41	22	42.3	4	9	US-09-947-387-69	Sequence 69, App
42	22	42.3	4	15	US-10-138-375-69	Sequence 69, App
43	22	42.3	4	16	US-10-829-381-69	Sequence 69, App
44	22	42.3	5	9	US-09-947-387-68	Sequence 68, App
45	22	42.3	5	9	US-09-947-387-116	Sequence 116, App

ALIGNMENTS

RESULT 1
US-09-761-636A-14
; Sequence 14, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-14

Query Match 100.0%; Score 52; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9

Db 1 CISVPLVPC 9

RESULT 2

US-10-154-884B-11221

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; Sequence 11221, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11221
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11221

Query Match 51.9%; Score 27; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C1SVPL 6
Db 2 C1SVPV 7

RESULT 3
US-10-154-884B-11228
; Sequence 11228, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11221
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11221
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; Sequence 11221, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11228
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11228

Query Match 51.9%; Score 27; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C1SVPL 6
Db 4 C1SVPV 9

RESULT 4
US-10-154-884B-11250
; Sequence 11250, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11250
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11250
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US-10-154-884B-11258
; Sequence 11258, Application US/10154884B
; Publication No. US2004005561A1
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: Aigate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.

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/ APPLICANT: Corixa Corporation
/ TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
/ TITLE OF INVENTION: Hematological Malignancies
/ FILE REFERENCE: 014058-013521US
/ CURRENT APPLICATION NUMBER: US/10/154,884B
/ CURRENT FILING DATE: 2002-05-23
/ PRIOR APPLICATION NUMBER: US 60/186,126
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: US 60/190,479
/ PRIOR FILING DATE: 2000-03-17
/ PRIOR APPLICATION NUMBER: US 60/200,545
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 60/200,303
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,779
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,999
/ PRIOR FILING DATE: 2000-05-01
/ PRIOR APPLICATION NUMBER: US 60/202,084
/ PRIOR FILING DATE: 2000-05-04

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; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11259
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11259

Query Match 51.9%; Score 27; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CISVPL 6
|:|:|:
Db 4 CLSVPV 9

RESULT 8
US-10-154-884B-11265
; Sequence 11265, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11265
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11265

Query Match 51.9%; Score 27; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CISVPL 6

Db 4 CLSVPV 9
|:|:|:

RESULT 9
US-10-154-884B-11275
; Sequence 11275, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11275
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11275

Query Match 51.9%; Score 27; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CISVPL 6
|:|:|:
Db 4 CLSVPV 9

RESULT 10
US-10-154-884B-11280
; Sequence 11280, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126

; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11280
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11280

Query Match 51.9%; Score 27; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTSVPL 6
|:|:|:
Db 4 CLSVPV 9

RESULT 11
US-10-363-208-242
; Sequence 242, Application US/10363208
; Publication No. US20040048243A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774.P005PCT
; CURRENT APPLICATION NUMBER: US/10/363,208
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 242
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(9)
; OTHER INFORMATION: synthetic construct
US-10-363-208-242

Query Match 51.9%; Score 27; DB 15; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTSVPLVPC 9
|:|:|:|:
Db 1 CMSSPGVAC 9

RESULT 12
US-10-363-204-203
; Sequence 203, Application US/10363204
; Publication No. US20040170955A1
; GENERAL INFORMATION:

; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: US/10/363,204
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 203
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(9)
; OTHER INFORMATION: synthetic construct
US-10-363-204-203

Query Match 51.9%; Score 27; DB 16; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTSVPLVPC 9
|:|:|:|:
Db 1 CMSSPGVAC 9

RESULT 13
US-10-611-440-206
; Sequence 206, Application US/10611440
; Publication No. US20040197912A1
; GENERAL INFORMATION:
; APPLICANT: Berinstitute, Neil
; APPLICANT: Gallichan, Scott
; APPLICANT: Lovitt, Corey
; APPLICANT: Parrington, Mark
; APPLICANT: Pedyczak, Artur
; APPLICANT: Radvanyi, Laszlo
; APPLICANT: Singh-Sandhu, Devender
; APPLICANT: Oomen, Raymond P
; APPLICANT: Cao, Shi-Xian
; TITLE OF INVENTION: Tumor Antigens BPA4 and BCY1 for Prevention and/or Treatment of
; FILE REFERENCE: API-02-11-US
; CURRENT APPLICATION NUMBER: US/10/611,440
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 60/394,346
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/394,503
; PRIOR FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US 60/411,833
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/445,342
; PRIOR FILING DATE: 2003-02-06
; NUMBER OF SEQ ID NOS: 218
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 206
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: CLP-2916
US-10-611-440-206

Query Match 51.9%; Score 27; DB 16; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISVPLVPC 9
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Db 2 VTAALVPC 9

RESULT 14

US-10-611-440-207
; Sequence 207, Application US/10611440
; Publication No. US20040197912A1
; GENERAL INFORMATION:
; APPLICANT: Berinstein, Neil
; APPLICANT: Gallichan, Scott
; APPLICANT: Lovitt, Corey
; APPLICANT: Parrington, Mark
; APPLICANT: Pedyczak, Artur
; APPLICANT: Radvanyi, Laszlo
; APPLICANT: Singh-Sandhu, Devender
; APPLICANT: Comen, Raymond P
; APPLICANT: Cao, Shi-Xian
; TITLE OF INVENTION: Tumor Antigens BFA4 and BCY1 for Prevention and/or Treatment of
; FILE REFERENCE: API-02-11-US
; CURRENT APPLICATION NUMBER: US/10/611,440
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 60/394,346
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/394,503
; PRIOR FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US 60/411,833
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/445,342
; PRIOR FILING DATE: 2003-02-06
; NUMBER OF SEQ ID NOS: 218
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 207
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: CLP-2917
US-10-611-440-207

US-10-611-440-207
; Sequence 207, Application US/10611440
; Publication No. US20040197912A1
; GENERAL INFORMATION:
; APPLICANT: Berinstein, Neil
; APPLICANT: Gallichan, Scott
; APPLICANT: Lovitt, Corey
; APPLICANT: Parrington, Mark
; APPLICANT: Pedyczak, Artur
; APPLICANT: Radvanyi, Laszlo
; APPLICANT: Singh-Sandhu, Devender
; APPLICANT: Comen, Raymond P
; APPLICANT: Cao, Shi-Xian
; TITLE OF INVENTION: Tumor Antigens BFA4 and BCY1 for Prevention and/or Treatment of
; FILE REFERENCE: API-02-11-US
; CURRENT APPLICATION NUMBER: US/10/611,440
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 60/394,346
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/394,503
; PRIOR FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US 60/411,833
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/445,342
; PRIOR FILING DATE: 2003-02-06
; NUMBER OF SEQ ID NOS: 218
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 207
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: CLP-2917
US-10-611-440-207

Query Match 51.9%; Score 27; DB 16; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISVPLVPC 9
DB 1 VTALVPC 8

RESULT 15
US-10-286-457-21
; Sequence 21, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-21

Query Match 50.0%; Score 26; DB 14; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLVP 8

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OM protein - protein search, using sw model

Run on: April 1, 2005, 11:47:34 ; Search time 43 Seconds
(without alignments)
10.416 Million cell updates/sec

Title: US-09-761-636A-12

Perfect score: 38

Sequence: 1 CVPLTC 6

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

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Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*

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- 3: /cgn2_6/prodata/1/aaa/6A COMB.pep.*
- 4: /cgn2_6/prodata/1/aaa/6B COMB.pep.*
- 5: /cgn2_6/prodata/1/aaa/PCTUS COMB.pep.*
- 6: /cgn2_6/prodata/1/aaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	26	68.4	6	4	US-09-839-542B-1374
3	25	65.8	6	3	US-09-187-859-1798
4	25	65.8	6	3	US-09-187-859-3970
5	25	65.8	6	3	US-09-187-859-4046
6	25	65.8	6	4	US-09-839-542B-1798
7	25	65.8	6	4	US-09-839-542B-3970
8	25	65.8	6	4	US-09-839-542B-4046
9	24	63.2	6	3	US-09-187-859-3573
10	24	63.2	6	4	US-09-839-542B-3573
11	23	60.5	6	3	US-09-187-859-2154
12	23	60.5	6	3	US-09-187-859-4040
13	23	60.5	6	4	US-09-839-542B-2154
14	23	60.5	6	4	US-09-839-542B-4040
15	22	57.9	4	2	US-08-429-964-41
16	22	57.9	4	4	US-09-665-362A-35
17	22	57.9	4	4	US-09-665-637-35
18	22	57.9	4	5	PCT-US93-08062-41
19	22	57.9	6	3	US-09-187-859-1737
20	22	57.9	6	3	US-09-187-859-2719
21	22	57.9	6	4	US-09-839-542B-1737
22	22	57.9	6	4	US-09-839-542B-2719
23	21	55.3	5	4	US-09-082-358B-90
24	21	55.3	5	4	US-09-050-861B-24
25	21	55.3	6	3	US-09-187-859-1885
26	21	55.3	6	3	US-09-187-859-2747
27	21	55.3	6	4	US-09-839-542B-1885

28	21	55.3	6	4	US-09-839-542B-2747	Sequence 2747, Ap
29	20	52.6	4	1	US-08-548-540-120	Sequence 120, App
30	20	52.6	4	5	PCT-US96-09809-120	Sequence 120, App
31	20	52.6	5	3	US-09-322-791-4	Sequence 4, Appli
32	20	52.6	5	3	US-09-322-791-6	Sequence 6, Appli
33	20	52.6	5	3	US-09-394-610-13	Sequence 13, Appl
34	20	52.6	6	3	US-08-750-142B-21	Sequence 21, Appl
35	20	52.6	6	3	US-09-187-859-1591	Sequence 1591, Ap
36	20	52.6	6	4	US-09-839-542B-1591	Sequence 1591, Ap
37	20	52.6	6	4	US-09-535-852-1344	Sequence 1344, Ap
38	20	52.6	6	4	US-09-535-852-1670	Sequence 1670, Ap
39	19	50.0	5	3	US-09-248-588-109	Sequence 109, App
40	19	50.0	5	4	US-09-721-908-102	Sequence 102, App
41	19	50.0	5	4	US-09-721-341-13	Sequence 13, Appl
42	19	50.0	5	4	US-09-721-495B-13	Sequence 13, Appl
43	19	50.0	6	1	US-08-201-046A-4	Sequence 4, Appli
44	19	50.0	6	1	US-08-433-318A-181	Sequence 181, App
45	19	50.0	6	2	US-08-922-048-181	Sequence 181, App

ALIGNMENTS

RESULT 1

US-09-187-859-1374
; Sequence 1374, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1374
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence

Query Match 68.4%; Score 26; DB 3; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.1e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 2;

QY 1 CVPLTC 6
| | | |
Db 1 CEPKTC 6

RESULT 2

US-09-839-542B-1374
; Sequence 1374, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1374
; LENGTH: 6
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
US-09-839-542B-1374

Query Match 68.4%; Score 26; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CVPLTC 6
| | | |
Db 1 CDPKTC 6

RESULT 3

US-09-187-859-1798
; Sequence 1798, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1798
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence
US-09-187-859-1798

Query Match 65.8%; Score 25; DB 3; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CVPLTC 6
| | | |
Db 1 CDPKTC 6

RESULT 4

US-09-187-859-3970
; Sequence 3970, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3970
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-14 cell adhesion recognition sequence
US-09-187-859-3970

Query Match 65.8%; Score 25; DB 3; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CVPLTC 6
| | | |
Db 1 CDPKTC 6

RESULT 5
US-09-187-859-4046
; Sequence 4046, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4046
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-09-187-859-4046

Query Match 65.8%; Score 25; DB 3; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CVPLTC 6
| | | |
Db 1 CDPKTC 6

RESULT 6

US-09-839-542B-1798
; Sequence 1798, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1798
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence
US-09-839-542B-1798

Query Match 65.8%; Score 25; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CVPLTC 6
| | | |
Db 1 CDPKTC 6

RESULT 7

US-09-839-542B-3970

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; Sequence 3970, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3970
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-14 cell adhesion recognition sequence
US-09-839-542B-3970

Query Match      65.8%; Score 25; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 1 CDPKTC 6

RESULT 8
US-09-839-542B-4046
; Sequence 4046, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4046
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-09-839-542B-4046

Query Match      65.8%; Score 25; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 1 CDPKTC 6

RESULT 9
US-09-187-859-3573
; Sequence 3573, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3573
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
US-09-187-859-3573

Query Match      63.2%; Score 24; DB 3; Length 6;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 1 CDPVSC 6

RESULT 10
US-09-839-542B-3573
; Sequence 3573, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3573
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
US-09-839-542B-3573

Query Match      63.2%; Score 24; DB 4; Length 6;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 1 CDPVSC 6

RESULT 11
US-09-187-859-2154
; Sequence 2154, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2154
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; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-15 cell adhesion recognition sequence
US-09-187-859-2154

Query Match 60.5%; Score 23; DB 3; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
| | | |
Db 1 CDELTC 6

RESULT 12
US-09-187-859-4040
; Sequence 2154, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4040
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-09-187-859-4040

Query Match 60.5%; Score 23; DB 3; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
| | | |
Db 1 CDELTC 6

RESULT 13
US-09-839-542B-2154
; Sequence 2154, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2154
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-15 cell adhesion recognition sequence
US-09-839-542B-2154

Query Match 60.5%; Score 23; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
| | | |
Db 1 CDELTC 6

RESULT 14
US-09-839-542B-4040
; Sequence 4040, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4040
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-09-839-542B-4040

Query Match 60.5%; Score 23; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
| | | |
Db 1 CDELTC 6

RESULT 15
US-08-429-964-41
; Sequence 41, Application US/08429964
; Patent No. 5962243
; GENERAL INFORMATION:
; APPLICANT: BROWN, MICHAEL S.
; APPLICANT: GOLDSTEIN, JOSEPH L.
; APPLICANT: REISS, YUVAL
; APPLICANT: JAMES, GUY L.
; TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL
; TITLE OF INVENTION: TRANSFERASE INHIBITORS
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/429,964
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/021,625
; FILING DATE: 16-FEB-1993


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; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/822,011
; FILING DATE: ABANDONED
; CLASSIFICATION: 435
; APPLICATION NUMBER: PCT/US/91/02650
; FILING DATE: 18-APR-1991
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/615,715
; FILING DATE: 20-NOV-1990
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/510,706
; FILING DATE: 18-APR-1990 (ABANDONED)
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PARKER, DAVID L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTSD:432/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-429-964-41

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Query Match          57.9%; Score 22; DB 2; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 CVPL 4
Db 1 CVPW 4

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Search completed: April 1, 2005, 11:55:14
Job time : 43 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 12:01:21 ; Search time 38 Seconds
(without alignments)
25.320 Million cell updates/sec

Title: US-09-761-636A-13

Perfect score: 56

Sequence: 1 CISVPLSVPC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1102

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: pir1.*
- 2: pir2.*
- 3: pir3.*
- 4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	35.7	6	2 I65546	MHC H2-L antigen -
2	19	33.9	5	2 A60521	glycogen phosphory
3	19	33.9	10	2 C39111	Ig heavy chain C r
4	18	32.1	9	2 PT0247	Ig heavy chain CRD
5	17	30.4	10	2 A61622	vitellogenin, 190K
6	17	30.4	10	2 PH0944	T-cell receptor be
7	16	28.6	4	2 I51049	metallothionein-A
8	16	28.6	8	2 G33098	205K exoantigen -
9	16	28.6	10	2 PH0926	T-cell receptor be
10	16	28.6	10	2 S62880	polygalacturonase
11	15	26.8	8	2 A42689	major postsynaptic
12	15	26.8	9	2 B49712	ATP-binding protel
13	15	26.8	10	2 S43630	cytochrome-c oxida
14	15	26.8	10	2 E86128	hypothetical prote
15	14	25.0	5	2 B22565	R-phycocerythrin al
16	14	25.0	7	2 A28340	myomodulin - Calif
17	14	25.0	8	2 I57018	gene Ctrr protein
18	14	25.0	9	2 A60356	118K stomach cance
19	14	25.0	9	2 S26508	collagen alpha 2(V
20	14	25.0	10	2 C39745	sphingomyelinase -
21	14	25.0	10	2 S65715	aryl hydrocarbon (
22	14	25.0	10	2 A32195	Na+/K+-exchanging
23	14	25.0	10	2 A24407	amicyanin - Paraco
24	14	25.0	10	2 D28027	protein P7 - curie
25	14	25.0	10	2 A61218	alpha-gliadin 4Ha
26	14	25.0	10	2 B61218	alpha-gliadin 6Ha
27	13	23.2	5	2 E42364	flagellar protein
28	13	23.2	9	2 B28495	conopressin S - co
29	13	23.2	9	2 PT0268	Ig heavy chain CRD

30	13	23.2	9	2 S77984	cytochrome-c oxida
31	13	23.2	10	2 S51912	hemagglutinin - in
32	13	23.2	10	2 B45482	platelet activatin
33	13	23.2	10	2 C93398	Fc mu (IgM) recept
34	12	21.4	5	2 S11127	phosphoprotein, bo
35	12	21.4	6	2 B34835	dnaA protein - Pse
36	12	21.4	6	2 B62205	alpha-1,4-glucan-p
37	12	21.4	6	4 A35039	hypothetical colla
38	12	21.4	7	2 E61491	seed protein ws-5
39	12	21.4	7	2 S42620	aggrecan - bovine
40	12	21.4	7	2 PH1602	Ig H chain V-D-J r
41	12	21.4	7	2 A39690	neural cell adhesi
42	12	21.4	7	2 PH0932	T-cell receptor be
43	12	21.4	7	2 A61081	tryptophyllin, bas
44	12	21.4	8	2 S68802	nitrate reductase
45	12	21.4	8	2 S10783	enamelin f - bovin

ALIGNMENTS

RESULT 1

I65546
MHC H2-L antigen - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I65546
R:Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
Cell 44, 261-272, 1986
A:Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and their
A:Reference number: I52778; MUID:86106202; PMID:3510743
A:Accession: I65546
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: GB:M12483; NID:gl9565; PIDN:AAA39663.1; PID:G554234

Query Match 35.7%; Score 20; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPC 10
DB 2 VPC 4

RESULT 2

A60521
Glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
N:Alternate names: glycogen phosphorylase b
C:Species: Liza ramada
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Mar-2004
C:Accession: A60521
R:Bonamusa, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A:Title: Purification and characterization of glycogen phosphorylase B from skeletal muscle
A:Reference number: A60521; MUID:90227907; PMID:2109669
A:Accession: A60521
A:Molecule type: protein
A:Residues: 1-5 <BON>
C:Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F:3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experiment

Query Match 33.9%; Score 19; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVP 5
DB 2 ISVP 5

RESULT 3

C39111

Ig heavy chain C region - Pacific hagfish (fragment)
 C:Species: Eptatretus stoutii (Pacific hagfish)
 C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
 C:Accession: C39111
 R:Varner, J.; Neame, P.; Litman, G.W.
 Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991
 A:Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural similarity
 A:Reference number: A39111; MUID:91156684; PMID:2000382
 A:Accession: C39111
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <VAR>
 C:Keywords: heterotetramer; immunoglobulin

Query Match 33.9%; Score 19; DB 2; Length 10;
 Best Local Similarity 71.4%; Pred. No. 2.4e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISVPLSV 8
 DB 4 ISSPLVV 10

RESULT 4

PT0247
 Ig heavy chain CRD3 region (clone 2-106A) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0247
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A:Reference number: PT0222; MUID:91108337; PMID:1899102
 A:Accession: PT0247
 A:Molecule type: DNA
 A:Residues: 1-9 <VAR>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 32.1%; Score 18; DB 2; Length 9;
 Best Local Similarity 42.9%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 SVPLSV 9
 DB 2 SAPIDSP 8

RESULT 5

A61622
 vitellogenin, 190k chain - gypsy moth (fragment)
 N:Contains: vitellin
 C:Species: Lymantria dispar (gypsy moth)
 C:Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 15-Oct-1999
 C:Accession: A61622
 R:Hiremath, S.; Eshita, S.
 Insect Biochem. Mol. Biol. 22, 605-611, 1992
 A:Title: Purification and characterization of vitellogenin from the gypsy moth, Lymantria
 A:Reference number: A61622
 A:Accession: A61622
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <HIR>
 C:Keywords: egg yolk; hemolymph

Query Match 30.4%; Score 17; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLSVP 9
 DB 2 PLTEP 6

RESULT 6

PH0944
 T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
 C:Accession: PH0944
 R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
 J. Exp. Med. 174, 1467-1476, 1991
 A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
 A:Reference number: PH0891; MUID:92078857; PMID:1836012
 A:Accession: PH0944
 A:Molecule type: mRNA
 A:Residues: 1-10 <GOL>
 A:Experimental source: complete Freund's adjuvant-immunized lymph node
 A:Note: the authors translated the codon GAC for residue 9 as Glu
 C:Keywords: T-cell receptor

Query Match 30.4%; Score 17; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVP 5
 DB 1 CASSP 5

RESULT 7

I51049
 metallothionein-A - rainbow trout (fragment)
 C:Species: Oncorhynchus mykiss (rainbow trout)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
 C:Accession: I51049
 R:Olsson, P.E.; Kling, P.; Erkel, L.J.; Kille, P.
 Eur. J. Biochem. 230, 344-349, 1995
 A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) met
 A:Reference number: I51049; MUID:95324545; PMID:7601121
 A:Accession: I51049
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 1-4 <OLS>
 A:Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328

Query Match 28.6%; Score 16; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PC 10
 DB 3 PC 4

RESULT 8

G33098
 25K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
 C:Species: Plasmodium falciparum
 C:Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
 C:Accession: G33098
 R:Nichols, J.H.; Hager, L.P.
 submitted to the Protein Sequence Database, May 1990
 A:Reference number: A33098
 A:Accession: G33098
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-8 <NIC>

Query Match 28.6%; Score 16; DB 2; Length 8;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VPLSV 8
 DB 1 1 1

Db 2 VPLXL 6

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CJSVP 5
| | |
Db 1 CASRP 5

RESULT 10

S62880
polygalacturonase (EC 3.2.1.15) IV - Aspergillus sp. (fragment)
C:Species: Aspergillus sp.
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S62880
R:Stratillova, E.; Dzurova, M.; Markovic, O.; Joernvall, H.
PDBS Lett. 382, 164-166, 1996
A:Title: An essential tyrosine residue of Aspergillus polygalacturonase.
A:Reference number: S62880; MUID:96196586; PMID:8612742
A:Accession: S62880
A:Molecule type: protein
A:Residues: 1-10 <STR>
A:Cross-references: UNIPROT:Q7M500
C:Keywords: glycosidase; hydrolase
F:4/Active site: Tyr #status predicted

Query Match 28.6%; Score 16; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CJSVP 5
| | |
Db 1 CASRP 5

RESULT 11

A42689
major postsynaptic density protein - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C:Accession: A42689
R:Wu, K.; Huang, Y.; Adler, J.; Black, I.B.
Proc. Natl. Acad. Sci. U.S.A. 89, 3015-3019, 1992
A:Title: On the identity of the major postsynaptic density protein.
A:Reference number: A42689; MUID:92212958; PMID:1313576
A:Accession: A42689
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <WUA>
A:Cross-references: UNIPROT:Q7M041

Query Match 26.8%; Score 15; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 LSVP 9
| | |
Db 2 LKVP 5

RESULT 12

B49712
ATP-binding protein p46 - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C:Accession: B49712
R:Nigam, S.K.; Goldberg, A.L.; Ho, S.; Rohde, M.F.; Bush, K.T.; Sherman, M.Y.
J. Biol. Chem. 269, 1744-1749, 1994
A:Title: A set of endoplasmic reticulum proteins possessing properties of molecular chaperone
A:Reference number: A49712; MUID:94124514; PMID:8294423
A:Accession: B49712
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <NIG>
C:Keywords: ATP; endoplasmic reticulum; molecular chaperone

Query Match 26.8%; Score 15; DB 2; Length 9;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 VPLSVP 9
| | |
Db 1 IPXXYP 6

RESULT 13

S43630
cytochrome-c oxidase (EC 1.9.3.1) chain VIC, hepatic - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)
C>Date: 20-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C:Accession: S43630
R:Freund, R.; Kadenbach, B.
Eur. J. Biochem. 221, 1111-1116, 1994
A:Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrome-c oxidase
A:Reference number: S43624; MUID:94237150; PMID:8181469
A:Accession: S43630
A:Molecule type: protein
A:Residues: 1-10 <FRE>
A:Cross-references: UNIPROT:P80331
A:Note: the source is designated as Salmo gairdneri
C:Genetics:
A:Genome: nuclear
C:Keywords: liver; membrane-associated complex; mitochondrion; oxidoreductase

Query Match 26.8%; Score 15; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 LSVP 9
| | |
Db 2 LKVP 5

RESULT 14

E86128
hypothetical protein Z5903 [imported] - Escherichia coli (strain O157:H7, substrain ED19;
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: E86128
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: E86128
A:Status: preliminary

A;Molecule type: DNA
 A;Residues: 1-10 <STO>
 A;Cross-references: UNIPROT:Q8X4E5; GB:AE005174; NID:gi2519314; PIDN:AAG59489.1; GSPDB:Q
 A;Experimental source: strain O157:H7, substrain EDL933
 C;Genetics:
 A;Gene: Z5903

Query Match 26.8%; Score 15; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 LSVPC 10
 | | |
 Db 5 LQVVC 9

RESULT 15
 B22565
 R-phycoerythrin alpha-2 chain - red alga (Gastrocloonium coulteri) (fragment)
 C;Species: Gastrocloonium coulteri
 C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
 C;Accession: B22565
 R;Klotz, A.V.; Glazer, A.N.
 J. Biol. Chem. 260, 4856-4863, 1985
 A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
 A;Reference number: A22565; MUID:85182601; PMID:3886644
 A;Accession: B22565
 A;Molecule type: protein
 A;Residues: 1-5 <KLO>

Query Match 25.0%; Score 14; DB 2; Length 5;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 LSVPC 9
 | | |
 Db 1 LQVPC 4

Search completed: April 1, 2005, 12:09:04
 Job time : 38 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 11:55:20 ; Search time 115 Seconds
(without alignments)
44,529 Million cell updates/sec

Title: US-09-761-636A-13
Perfect score: 56
Sequence: 1 CISVPLSVPC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 2548

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	26	46.4	9	1	MGMT_BOVIN	P29177 bos taurus
2	22	39.3	8	2	Q70Y88	Q70Y88 platostoma
3	21	37.5	9	2	Q7BE72	Q7BE72 rattus norv
4	20	35.7	9	2	Q35953	Q35953 mus musculus
5	20	35.7	10	2	Q85563	Q85563 moloney mur
6	20	35.7	10	2	Q85598	Q85598 moloney mur
7	20	35.7	10	2	Q85619	Q85619 moloney mur
8	19	33.9	8	2	Q56140	Q56140 streptococc
9	19	33.9	10	1	LPK2_LOCMI	P41488 locusta mig
10	19	33.9	10	2	Q7WUG2	Q7WUG2 escherichia
11	18	32.1	8	1	COM2_CONPU	P58785 conus purpu
12	17	30.4	8	2	Q9Y4X6	Q9Y4X6 homo sapien
13	17	30.4	9	2	Q7X6A3	Q7X6A3 zea mays (m
14	17	30.4	9	2	Q61754	Q61754 cynops pyr
15	17	30.4	10	2	Q96041	Q96041 oenothera b
16	17	30.4	10	2	Q7Y018	Q7Y018 zea mays (m
17	17	30.4	10	2	Q39957	Q39957 gb virus c/
18	16	28.6	8	2	Q15898	Q15898 homo sapien
19	16	28.6	8	2	O02831	O02831 oryctolagus
20	16	28.6	8	2	Q9TRY3	Q9TRY3 sus sp. ins
21	16	28.6	8	2	Q6UA69	Q6UA69 carassius c
22	16	28.6	9	2	Q6QF45	Q6QF45 homo sapien
23	16	28.6	9	2	Q8QVD3	Q8QVD3 ovine respi
24	16	28.6	9	2	Q8AUM7	Q8AUM7 carassius a
25	16	28.6	9	2	Q8AYL5	Q8AYL5 carassius a
26	16	28.6	10	2	Q7M500	Q7M500 aspergillus
27	16	28.6	10	2	Q7PHS9	Q7PHS9 anopheles g
28	16	28.6	10	2	Q8SPN8	Q8SPN8 macaca mula
29	16	28.6	10	2	Q6JVP0	Q6JVP0 wollastonia
30	16	28.6	10	2	Q6JVP3	Q6JVP3 otopappus e
31	16	28.6	10	2	Q6JVP6	Q6JVP6 elaphandra

32	16	28.6	10	2	Q6JVP8	Q6JVP8 dimerostemm
33	16	28.6	10	2	Q6JVP0	Q6JVP0 dimerostemm
34	16	28.6	10	2	Q6JVP3	Q6JVP3 baltimora r
35	16	28.6	10	2	Q6JVP5	Q6JVP5 angelphytum
36	16	28.6	10	2	Q6JVP7	Q6JVP7 angelphytum
37	16	28.6	10	2	Q85AZ9	Q85AZ9 pyrrhobryum
38	16	28.6	10	2	Q94IS6	Q94IS6 pinus taeda
39	15	26.8	7	2	Q42564	Q42564 fugu rubrip
40	15	26.8	8	2	Q7M041	Q7M041 rattus norv
41	15	26.8	9	2	Q7S3Z9	Q7S3Z9 neurospora
42	15	26.8	9	2	Q712A6	Q712A6 sinorhizobi
43	15	26.8	10	1	COXH_ONCMY	P80331 oncorhynchu
44	15	26.8	10	1	NSL_WYCTU	P81135 mycobacteri
45	15	26.8	10	1	TXL2_LOCMI	P16224 locusta mig

ALIGNMENTS

RESULT 1
MGMT_BOVIN
ID MGMT_BOVIN STANDARD; PRT; 9 AA.
AC P29177;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-methylguanine-DNA methyltransferase) (MGMT) (O-6-methylguanine-DNA-alkyltransferase) (Fragment).
GN Name=MGMT;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=90174912; PubMed=2308822;
RA Rydberg B., Hall J., Karan P.;
RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA methyltransferase."
RL Nucleic Acids Res. 18:17-21(1990).
CC -!- FUNCTION: Involved in the cellular defense against the biological effects of O6-methylguanine (O6-MeG) in DNA. Repairs alkylated guanine in DNA by stoichiometrically transferring the alkyl group at the O-6 position to a cysteine residue in the enzyme. This is a suicide reaction: the enzyme is irreversibly inactivated.
CC -!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) + protein L-cysteine = DNA (without 6-O-methylguanine) + protein S-methyl-L-cysteine.
CC -!- SIMILARITY: Belongs to the MGMT family.
CC InterPro: IPR001497; Methyltransf_1.
DR PROSITE, PS00374; MGMT; PARTIAL.
KW Direct protein sequencing; DNA repair; Methyltransferase; Transferase.
FT NON_TER 1
FT ACT_SITE 9 9 Alkyl group acceptor (By similarity).
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 46.4%; Score 26; DB 1; Length 9;
Best Local Similarity 42.9%; Pred. No. 1.6e+06;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 VPLSVPC 10
:|:|
Db 3 IPILTPC 9

RESULT 2
Q70Y88 PRELIMINARY; PRT; 8 AA.
ID Q70Y88
AC Q70Y88;

DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Ribosomal protein (Fragment).
GN Name=rp16;
OS Platyostoma fimbriatum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Platostoma.
OX NCBI_TaxID=204168;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;
RA Paton A., Springate D.A., Suddle S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simmonds M.S.J., Powell M.P., Savolainen V.,
RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505368; CAD45489.1; -;
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON_TER 1
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 789 MW; 86786772D1BBA772 CRC64;

Query Match 39.3%; Score 22; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VPLSVP 9
Db 1 VPTVTP 6

RESULT 3
Q78E72
ID Q78E72 PRELIMINARY; PRT; 9 AA.
AC Q78E72;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Decidual/trophoblast prolactin-related protein (Fragment).
GN Name=d/TPRP;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=97307698; PubMed=9165040; DOI=10.1210/en.138.6.2491;
RA Orwig K.E., Dai G., Rasmussen C.A., Soares M.J.;
RT "Decidual/trophoblast prolactin-related protein: characterization of
RT gene structure and cell-specific expression.";
RL Endocrinology 138:2491-2500(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Liver;
RA Orwig K.O., Dai G., Soares M.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U44438; AAB17697.1; -;
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA; 1088 MW; 5AED1776CSB73767 CRC64;

Query Match 37.5%; Score 21; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VPLSVP 9
Db 2 LPLSQP 7

RESULT 4
Q35953
ID Q35953 PRELIMINARY; PRT; 9 AA.
AC Q35953;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Truncated voltage-gated sodium channel alpha subunit (Fragment).
GN Name=Scn8a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIII;
RX MEDLINE=97442476; PubMed=9295353; DOI=10.1074/jbc.272.38.24008;
RA Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
RT two-domain protein in fetal brain and non-neuronal cells.";
RL J. Biol. Chem. 272:24008-24015(1997).
DR EMBL; U97672; AAB80914.1; -;
DR MGD; MGI:103169; Scn8a.
DR GO; GO:0007628; P:adult walking behavior; IMP.
DR GO; GO:0007626; P:locomotory behavior; IMP.
KW Ionic channel.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 9 AA; 898 MW; 22D92865B735B737 CRC64;

Query Match 35.7%; Score 20; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPLSV 8
Db 1 VPLSL 5

RESULT 5
Q85563
ID Q85563 PRELIMINARY; PRT; 10 AA.
AC Q85563;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Env-mos fusion protein (Fragment).
OS Moloney murine leukemia virus.
OC Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11801;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82196891; PubMed=6281735;
RA Donoghue D.J., Hunter T.;
RT "A generalized method of subcloning DNA fragments by restriction site
RT reconstruction: Application to sequencing the amino-terminal region of
RT the transforming gene of Gazdar murine sarcoma virus.";
RL Nucleic Acids Res. 10:2549-2564(1982).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83164305; PubMed=6300424;
RA Donoghue D.J., Hunter T.;
RT "Recombination junctions of variants of Moloney murine sarcoma virus:
RT Generation and divergence of a mammalian transforming gene.";
RL J. Virol. 45:607-617(1983).
DR EMBL; K03105; AAA46491.1; -;
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1062 MW; F9ECFCBEA771B5B1 CRC64;

Query Match 35.7%; Score 20; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 7.2e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 VPLSVP 9
Db 2 LPLSQP 7


```

QY      7 SVPC 10
Db      4 STPC 7

RESULT 6
Q85598      PRELIMINARY;      PRT;      10 AA.
AC Q85598;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Moloney murine sarcoma virus (strain HT1) env/mos 5' junction.
DE (Fragment).
OS Moloney murine leukemia virus.
OC Viruses; Retroviral viruses; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11801;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83164305; PubMed=6300424;
RA Donoghue D.J., Hunter T.;
RT "Recombination junctions of variants of Moloney murine sarcom virus:
RT Generation and divergence of a mammalian transforming gene.";
RL J. Virol. 45:607-617(1983).
DR EMBL: K03106; AAA46492.1; -.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1081 MW; 7BECFCBEA771B5A4 CRC64;

Query Match      35.7%; Score 20; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 7.2e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 SVPC 10
Db      4 STPC 7

RESULT 7
Q85619      PRELIMINARY;      PRT;      10 AA.
AC Q85619;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Moloney murine sarcoma virus (strain ml) env/mos 5' junction.
DE (Fragment).
OS Moloney murine leukemia virus.
OC Viruses; Retroviral viruses; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11801;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83164305; PubMed=6300424;
RA Donoghue D.J., Hunter T.;
RT "Recombination junctions of variants of Moloney murine sarcom virus:
RT Generation and divergence of a mammalian transforming gene.";
RL J. Virol. 45:607-617(1983).
DR EMBL: K03108; AAA46494.1; -.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1081 MW; 7BECFCBEA771B5A4 CRC64;

Query Match      35.7%; Score 20; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 7.2e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 SVPC 10
Db      4 STPC 7

RESULT 8
Q56140      PRELIMINARY;      PRT;      8 AA.
ID Q56140
AC Q56140;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE STP6 protein (Fragment).
DE Name=STP6;
OS Streptococcus thermophilus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1308;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ST11;
RX MEDLINE=95047254; PubMed=7958782;
RA Constable A., Mollet B.;
RT "Isolation and characterisation of promoter regions from Streptococcus
RT thermophilus.";
RL FEMS Microbiol. Lett. 122:85-90(1994).
DR EMBL: X78210; CAA55045.1; -.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 846 MW; ED086772D5B045B6 CRC64;

Query Match      33.9%; Score 19; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 ISVP 5
Db      3 ISVP 6

RESULT 9
LPK2 LOCMI
ID LPK2 LOCMI STANDARD; PRT; 10 AA.
AC P41488;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Locustapyrokinin 2 (LOM-PK-2) (FXPRL-amide).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94094539; PubMed=7903606; DOI=10.1016/0742-8413(93)90260-R;
RA Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustapyrokinin II from
RT Locusta migratoria, another member of the FXPRL-amide peptide
RT family.";
RL Comp. Biochem. Physiol. 106C:103-109(1993).
CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -!- SIMILARITY: Belongs to the pyrokinin family.
CC InterPro: IPR001484; Pyrokinin.
DR PROSITE: PS00539; PYROKININ; 1.
KW Amidation; Direct protein sequencing; Neuropeptide; Pyrokinin;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 10 10 Leucine amide.
SQ SEQUENCE 10 AA; 1145 MW; CFAFA4271A9D1B772 CRC64;

Query Match      33.9%; Score 19; DB 1; Length 10;
Best Local Similarity 57.1%; Pred. No. 1.1e+04;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 SVPLSVP 9
Db      2 SVPTFTP 8

```

```
RESULT 10
Q7WUG2
ID Q7WUG2 PRELIMINARY; PRT; 10 AA.
AC Q7WUG2;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE TnpIS1 (Fragment).
GN Name=insA;
OS Escherichia coli.
OG Plasmid p541.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
SEQUENCE FROM N.A.
RA Mariagou V., Tzouveleakis L.S., Villa L., Lebessi E., Vatopoulos A.C.,
RA Carattoli A., Tzelepi E.;
RT "CMV-13, a Novel Inducible Cephalosporinase Encoded by an Escherichia
RT coli Plasmid.";
RL Antimicrob. Agents Chemother. 48:3172-3174(2004).
DR EMBL; AY339625; AAQ16673.1; -.
KW Plasmid.
FT NON TER 10
SQ SEQUENCE 10 AA; 991 MW; 882D57A5B045A2D5 CRC64;

Query Match 33.9%; Score 19; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SVPLSVP 9
Db 3 SVSISCP 9

RESULT 11
COW2_CONPU STANDARD; PRT; 8 AA.
AC P58785;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leu-contryphan-P.
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorboconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC STRAIN=Clipperton Island; TISSUE=Venom;
RX MEDLINE=99388839; PubMed=10461743;
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
RA Olivera B.M.;
RT "A novel D-leucine-containing Conus peptide: diverse conformational
RT dynamics in the contryphan family.";
RL J. Pept. Res. 54:93-99(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=888.4; METHOD=LSI; RANGE=1-8; NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the contryphan family.
KW D-amino acid; Direct protein sequencing; Toxin.
FT DISULFID 8
FT MOD_RES 4 4 D-leucine.
FT MOD_RES 4 4
SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 32.1%; Score 18; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTSVP 5
Db 2 CVLLP 6

RESULT 12
Q9Y4X6 PRELIMINARY; PRT; 8 AA.
ID Q9Y4X6
AC Q9Y4X6;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Nuclear LIM interactor (Fragment).
GN Name=NLI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=20108806; PubMed=10640831;
RX Drechsler M., Schumacher V., Friedrich S., Wildhardt G., Giesler S.,
RX Schroth A., Bodem J., Royer-Pokora B.;
RT "Genomic structure, alternative transcripts and chromosome location of
RT the human LIM domain binding protein gene LDB1.";
RL Cytogenet. Cell Genet. 87:119-124(1999).
DR EMBL; AJ243097; CAB45408.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 767 MW; BE6EDDEB862D5B6 CRC64;

Query Match 30.4%; Score 17; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 LSVPC 10
Db 1 MSVGC 5

RESULT 13
Q7X6A3 PRELIMINARY; PRT; 9 AA.
ID Q7X6A3
AC Q7X6A3;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Isoamylase (Fragment).
GN Name=sul;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
SEQUENCE FROM N.A.
RP Wilson L.M., Whitt S.R., Ibanez A.M., Rocheford T.R., Goodman M.M.,
RA Buckler E.S., IV;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY290305; AAP45331.1; -.
DR EMBL; AY290311; AAP45337.1; -.
FT NON TER 9
SQ SEQUENCE 9 AA; 976 MW; DF9BCEA76736C6DD CRC64;

Query Match 30.4%; Score 17; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPC 10
Db 5 LPC 7

RESULT 14
Q6I754 PRELIMINARY; PRT; 9 AA.
ID Q6I754
AC Q6I754;
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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SOX2 (Fragment).
GN Name=Sox2;
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15172683; DOI=10.1016/j.mod.2004.04.010;
RA Hayashi T., Mizuno N., Ueda Y., Okamoto M., Kondoh H.;
RT "FGF2 triggers iris-derived lens regeneration in newt eye.";
RL Mech. Dev. 121:519-526(2004).
DR EMBL; AB154819; BAD24664.1; -.
FT NON_TER 1
SQ SEQUENCE 9 AA; 969 MW; 2167F5B7376731A8 CRC64;

Query Match 30.4%; Score 17; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLS 7
DB 3 TULPS 7

RESULT 15
Q96041
ID Q96041 PRELIMINARY; PRT; 10 AA.
AC Q96041;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NADH-ubiquinone oxidoreductase subunit 3 (Fragment).
GN Name=nad3;
OS Oenothera bertiana (Bertero's evening primrose).
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Onagraceae; Oenothera.
OX NCBI_TaxID=3950;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94019250; PubMed=8413195;
RA Schuster W.;
RT "Ribosomal protein gene rpl5 is cotranscribed with the nad3 gene in
RL Oenothera mitochondria.";
RL Mol. Gen. Genet. 240:445-449(1993).
DR EMBL; X69553; CAA49285.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion; Ubiquinone.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1097 MW; 723067B0476DD9CB CRC64;

Query Match 30.4%; Score 17; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CIS 3
DB 8 CIS 10

Search completed: April 1, 2005, 12:08:14
Job time : 115 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 11:54:25 ; Search time 117 Seconds
(without alignments)
33.056 Million cell updates/sec

Title: US-09-761-636A-13

Perfect score: 56
Sequence: 1 C1SVPLSVPC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 465227

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	4	Aau04532 VEGF base
2	41.5	74.1	9	4	Aau04533 VEGF base
3	36	64.3	9	2	Aar96138 Protease
4	36	64.3	9	2	Aaw82212 D-NorFES-
5	36	64.3	9	2	Aaw46562 Peptide b
6	33	58.9	9	2	Aar96137 Protease
7	33	58.9	9	2	Aaw82094 D-NorFES-
8	33	58.9	9	2	Aaw46561 Peptide b
9	33	58.9	9	4	Aag73245 Protease
10	33	58.9	9	5	Abu60357 D-NorFES-
11	33	58.9	9	8	Adn88305 Fluorogen
12	33	58.9	9	8	Adn88488 Fluorogen
13	32	57.1	10	4	Aau00643 Human mem
14	32	57.1	10	7	Adb88786 Membrane
15	32	57.1	10	8	Abg75437 Membrane
16	31.5	56.2	9	5	Aau94301 Human nov
17	31.5	56.2	10	5	Aau94201 Human nov
18	31.5	56.2	10	5	Aau94811 Human nov
19	31.5	56.2	10	5	Aau94577 Human nov
20	31	55.4	9	7	Adm35397 Human nov
21	31	55.4	10	5	Aam50003 Human D40
22	30	53.6	9	5	Aau95231 Human nov
23	30	53.6	9	5	Aau94696 Human nov
24	30	53.6	9	5	Aau95023 Human nov
25	29	51.8	10	4	Aag73418 Human gen

26	29	51.8	10	4	AAG85638	Saccharom
27	29	51.8	10	5	ABG64264	Human alb
28	29	51.8	10	8	ADL77529	Albumin f
29	28	50.0	9	6	ABR19062	Human can
30	28	50.0	9	8	ADK06442	Hepatitis
31	28	50.0	10	6	ABR19524	Human can
32	28	50.0	10	6	ABR18877	Human can
33	27	48.2	8	2	AAr74541	Protease
34	27	48.2	8	8	Adn02838	Mammalian
35	27	48.2	9	7	ADC71003	HLA motif
36	27	48.2	9	7	ADC70887	HLA motif
37	27	48.2	9	7	ADM35404	Human LV1
38	27	48.2	9	7	ADM35430	Human LV1
39	27	48.2	9	7	ADM35441	Human LV1
40	27	48.2	9	7	ADM35456	Human LV1
41	27	48.2	9	7	ADM35435	Human LV1
42	27	48.2	9	7	ADM35451	Human LV1
43	27	48.2	9	7	ADM35434	Human LV1
44	27	48.2	9	7	ADM35426	Human LV1
45	27	48.2	10	7	ADC70636	HLA motif

ALIGNMENTS

RESULT 1
AAU04532
ID AAU04532 standard; peptide; 10 AA.
XX
AC AAU04532;
XX
DT 26-SEP-2001 (first entry)
XX
DE VEGF based monocyclic peptide 10.
XX
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..10
FT /note= "This bond cyclises the peptide"
XX
PN WO200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Achen MG, Hughes RA, Stackner S, Cendron A;
XX
DR WPI; 2001-442248/47.
XX
PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
from an exposed loop of a growth factor protein by oxidizing the cysteine
residues.
XX
PS Claim 49; Page 32; 102pp; English.
XX
CC The sequence represents a monomeric monocyclic peptide of the invention,
whose 3-dimensional structure is modelled on the exposed loop of human
VEGFD (vascular endothelial growth factor). The invention relates to a
method of producing a monomeric monocyclic peptide by a measuring beta-
carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 56; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.013; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0;

QY 1 CISVPLSVPC 10
 |||||
 DB 1 CISVPLSVPC 10

RESULT 2
 ID AAU04533
 AC AAU04533 standard; peptide; 9 AA.

XX AAU04533;

DT 26-SEP-2001 (first entry)

XX VEGF based monocyclic peptide 11.

XX Human; VEGF: vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.

XX Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 1..9 /note= "This bond cyclises the peptide"

XX WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

PR 18-JAN-2000; 2000US-0176293P.

PR 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Hughes RA, Stacker S, Cendron A;

XX WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 FT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine

PT residues.
 XX Claim 49; Page 32; 102pp; English.
 XX
 CC The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the exposed loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 9 AA;

Query Match 74.1%; Score 41.5; DB 4; Length 9;
 Best Local Similarity 90.0%; Pred. No. 1.8e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CISVPLSVPC 10
 |||||
 DB 1 CISVPL-VPC 9

RESULT 3

AA96138

ID AA96138 standard; peptide; 9 AA.

XX AA96138;

XX 25-MAR-2003 (revised)

DT 18-DEC-1996 (first entry)

XX Protease substrate peptide with fluorophore at each terminus.

XX Fluorogenic substrate; fluorophore; protease activity; assay;
 KW visible fluorescence; in situ detection; frozen tissue section;
 KW histology; arthritis; emphysema; thrombosis; cancer metastasis.

XX Synthetic.

XX Key Location/Qualifiers

FT Region 1..3

FT /label= C1

FT /note= "the two conformation determining regions C1 and
 FT C2 which flank the protease recognition site peptide P
 FT are provided to position the two fluorophores within 100
 FT angstroms of each other"

FT Modified-site 1

FT /note= "labelled by donor fluorophore (Fl) 5'-
 FT carboxytetramethylrhodamine"

FT 4..7

FT /label= P

FT /note= "peptide comprising a protease recognition site"

FT Region 8..9
 FT /note= C2
 FT /note= "the two conformation determining regions C1 and
 FT C2 which flank the protease recognition site peptide P
 FT are provided to position the two fluorophores within 100
 FT angstroms of each other"
 FT Modified-site 9
 FT /note= "labelled by acceptor fluorophore F2 rhodamine X
 FT acetamide"
 FT
 PN WO9613607-A1.
 XX
 XX
 PD 09-MAY-1996.
 XX
 XX 27-OCT-1995; 95WO-US013936.
 PF
 XX 28-OCT-1994; 94US-00331383.
 PR
 XX (ONCO-) ONCOIMMUNIN INC.
 PA
 XX Komoriya A, Packard BS;
 PI
 XX WPI; 1996-239512/24.
 DR
 XX New fluorogenic peptide(s) with fluorophore at each terminus - for
 PT detecting protease(s) in biological samples, emit intense visible
 PT fluorescence when cleaved.
 FT
 XX Claim 16; Page 31; 88pp; English.
 PS
 XX The present sequence is a specific example of a fluorogenic substrate for
 CC detecting activity of a protease. The substrate agrees with the generic
 CC formula (S1)n-C1(F1)-P-C2(F2)-(S2)k in which a peptide P of 2-8 amino
 CC acids comprising a recognition site for the protease is flanked by
 CC conformation determining regions (C1 and C2) of 1-3 amino acids. C1 and
 CC C2 are labelled by fluorophore groups (F1 and F2, respectively).
 CC positioned within 100 angstroms of each other. Additional peptide spacers
 CC of 1-50 amino acids (S1 and S2) may also be present (i.e. n and k = 0 or
 CC 1). Fluorogenic substrates corresponding to the generic formula are used
 CC to detect or localise proteases in biological specimens, esp. in frozen
 CC tissue sections or to monitor protease activity in stored reagents.
 CC Changes in protease activity are associated with e.g. arthritis,
 CC emphysema, thrombosis and cancer metastasis. (Updated on 25-MAR-2003 to
 CC correct PA field.)
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 64.3%; Score 36; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SVPLSVPC 10
 Db ::|:|:
 2 AIPMSIPC 9
 RESULT 4
 AAW82212
 ID AAW82212 standard; peptide; 9 AA.
 XX
 XX AAW82212;
 AC
 XX 18-FEB-1999 (first entry)
 DT
 DE D-NorFES-A protease inhibitor peptide #2.
 XX
 XX Protease activity; fluorophore; detection; fluorogenic; cellular uptake;
 KW conformation change.
 XX
 XX Synthetic.
 OS
 XX WO9837226-A1.
 PN
 XX

PD 27-AUG-1998.
 XX
 PF 20-FEB-1998; 98WO-US003000.
 XX
 PR 20-FEB-1997; 97US-00802981.
 XX
 XX (ONCO-) ONCOIMMUNIN INC.
 PA
 XX Komoriya A, Packard BS;
 PI
 XX WPI; 1998-467579/40.
 DR
 XX New fluorogenic compositions - containing 2 fluorophores separated by a
 PT peptide comprising a protease binding site, used for detecting protease
 PT activity in samples.
 FT
 XX Example 1; Page 52; 90pp; English.
 PS
 XX AAW82023-W82240 are peptides used in the construction of a fluorogenic
 CC composition which is used for the detection of protease activity in
 CC biological samples. The products can be used for the detection of
 CC conformational changes in nucleic acids, oligosaccharides, polysaccharides,
 CC proteins, peptides, lipids, phospholipids, glycolipids, glycoproteins,
 CC steroids or polymers. In addition, attachment of a hydrophobic group to a
 CC molecule can be used to enhance uptake by cells. The composition is
 CC composed of P = peptide comprising a protease binding site for the
 CC protease, F1, F2 peptides = fluorophores where F1 is attached to the
 CC amino terminal amino acid and F2 is attached to the carboxyl terminal
 CC amino acid and S1, S2 peptides = when present, are peptide spacers where
 CC S1, when present, is attached to the amino terminal acid, and S2, when
 CC present, is attached to the carboxyl terminal amino acid
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 64.3%; Score 36; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SVPLSVPC 10
 Db ::|:|:
 2 AIPMSIPC 9
 RESULT 5
 AAW46562
 ID AAW46562 standard; peptide; 9 AA.
 XX
 XX AAW46562;
 AC
 XX 20-MAY-1998 (first entry)
 DT
 DE Peptide backbone of a protease indicator.
 XX
 XX Protease binding site; protease; protease indicator; fluorescent signal;
 KW detection; protease activity.
 XX
 XX Synthetic.
 OS
 XX US5714342-A.
 PN
 XX 03-FEB-1998.
 PD
 XX 27-OCT-1995; 95US-00549008.
 PF
 XX 28-OCT-1994; 94US-00331383.
 PR
 XX (ONCO-) ONCOIMMUNIN INC.
 PA
 XX Packard BS, Komoriya A;
 PI
 XX WPI; 1998-158345/14.
 DR
 XX Fluorogenic substrates for protease determination - having two closely
 PT

FT where F2 is the acceptor fluorophore rhodamine X
 FT acetamide (R492)"
 PN WO9837226-A1.
 XX 27-AUG-1998.
 PD
 XX 20-FEB-1998; 98WO-US003000.
 PF 20-FEB-1997; 97US-00802981.
 XX (ONCO-) ONCOIMMUNIN INC.
 XX Komoriya A, Packard BS;
 XX WPI; 1998-467579/40.
 DR New fluorogenic compositions - containing 2 fluorophores separated by a
 PT peptide comprising a protease binding site, used for detecting protease
 PT activity in samples.
 XX Disclosure; Page 10; 90pp; English.
 PS AAW82023-WB2240 are peptides used in the construction of a fluorogenic
 CC composition which is used for the detection of protease activity in
 CC biological samples. The products can be used for the detection of
 CC conformational changes in nucleic acids, oligosaccharides, polysaccharides,
 CC proteins, peptides, lipids, phospholipids, glycolipids, glycoproteins,
 CC steroids or polymers. In addition, attachment of a hydrophobic group to a
 CC molecule can be used to enhance uptake by cells. The composition is
 CC composed of P = peptide comprising a protease binding site for the
 CC protease, F1, F2 peptides = fluorophores where F1 is attached to the
 CC amino terminal amino acid and F2 is attached to the carboxyl terminal
 CC amino acid and S1, S2 peptides = when present, are peptide spacers where
 CC S1, when present, is attached to the amino terminal acid, and S2, when
 CC present, is attached to the carboxyl terminal amino acid
 XX Sequence 9 AA;
 SQ Query Match 58.9%; Score 33; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 3 SVPLSVPC 10
 Db ::|||:
 2 AIPXSIPC 9
 RESULT 8
 AAW46561
 ID AAW46561 standard; peptide; 9 AA.
 XX AAW46561;
 AC
 XX 20-MAY-1998 (first entry)
 DT Peptide backbone of a protease indicator.
 DE Protease binding site; protease; protease indicator; fluorescent signal;
 KW detection; protease activity.
 XX Synthetic.
 OS Key Location/Qualifiers
 FT Modified-site 5 /label= Nle
 FT /note= "Norleucine"
 FT
 XX US5714342-A.
 PN 03-FEB-1998.
 XX 27-OCT-1995; 95US-00549008.
 PF

XX 28-OCT-1994; 94US-00331383.
 PR (ONCO-) ONCOIMMUNIN INC.
 XX Packard BS, Komoriya A;
 PI WPI; 1998-158345/14.
 DR Fluorogenic substrates for protease determination - having two closely
 PT spaced fluorophores flanking protease binding site.
 XX Example 1; Col 23; 39pp; English.
 PS The present peptide contains a protease binding site. It is used to
 CC produce novel reagents whose fluorescence increases in the presence of
 CC particular proteases. These fluorogenic protease indicators (substrates)
 CC provide a high intensity fluorescent signal at a visible wavelength when
 CC they are digested by a protease. The fluorogenic indicators have the
 CC general formula: F1--C1--P--C2--F2 | (S1)n (S2)k where: P is a peptide
 CC containing a protease binding site e.g. AAW46520-53, AAW46554-58. n, k =
 CC 0 or 1. C1 and C2 are conformation-determining regions that introduce a
 CC bend into the composition which positions the fluorophores adjacent to
 CC each other with a separation of less than 100 Angstrom. When n is 1, S1
 CC is joined to the terminal alpha -amino group of C1 by a peptide bond, and
 CC when k is 1, S2 is joined to the terminal carboxy group of C2 by a
 CC peptide bond. The protease indicators are used for detecting protease
 CC activity in a biological sample. The sample is contacted with the
 CC indicator and any change in fluorescence is detected, an increase in
 CC fluorescence indicating protease activity
 XX Sequence 9 AA;
 SQ Query Match 58.9%; Score 33; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 3 SVPLSVPC 10
 Db ::|||:
 2 AIPXSIPC 9
 RESULT 9
 AAG73245
 ID AAG73245 standard; peptide; 9 AA.
 XX AAG73245;
 AC
 XX 14-AUG-2001 (first entry)
 DT Protease indicator peptide #1.
 DE Protease detection; peptide cleavage; enzyme activity; fluorogenic;
 KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;
 KW haemophilia.
 XX Synthetic.
 OS Key Location/Qualifiers
 FT Modified-site 1 /label= OTHER
 FT /note= "modified by fluorophore"
 FT Modified-site 9 /label= OTHER
 FT /note= "modified by fluorophore"
 FT
 XX WO200118238-A1.
 PN 15-MAR-2001.
 XX 11-SEP-2000; 2000WO-US024882.
 PF
 XX

PR 10-SEP-1999; 99US-00394019.
 XX (ONCO-) ONCOIMMUNIN INC.
 XX Komoriya A, Packard BS;
 XX WPI; 2001-389573/41.
 XX
 PT New fluorogenic compositions whose fluorescence level increases in the
 PT presence of active proteases, useful for detecting and localizing
 PT protease activity in biological samples, particularly in frozen tissue
 PT samples.
 XX
 PS Example 2; Page 53; 86pp; English.
 XX
 CC The present invention describes fluorogenic compositions which can be
 CC used for the detection of protease activity. This can be useful as an
 CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,
 CC thrombosis and arthritis. The fluorogenic compositions comprise a
 CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The
 CC peptide is cleaved by a protease and the fluorophores can then be
 CC detected. The present sequence is one of the peptides described in the
 CC exemplification of the invention
 XX
 SQ Sequence 9 AA;
 Query Match 58.9%; Score 33; DB 4; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 3 SVPLSVPC 10
 Db :|||:
 2 AIPXSIPC 9
 RESULT 10
 ABU60357
 ID ABU60357 standard; peptide; 9 AA.
 XX
 AC ABU60357;
 XX
 DT 29-APR-2003 (first entry)
 XX
 DE D-NorFES-A protease inhibitor peptide.
 XX
 KW Protease; indicator; chromophore; H-dimer; fluorescence; absorbance;
 KW nuclease; screening; fluorophore; substrate cleavage.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "F1, where F1 is a donor fluorophore 5'-
 FT carbocytetramethylrhodamine (C2211)"
 FT 5
 FT /label= Nle
 FT /note= "norleucine"
 FT 9
 FT Modified-site
 FT /note= "F2, where F2 is an acceptor fluorophore rhodamine
 FT X acetamide (R492)"
 XX
 PN WO200261038-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 21-DEC-2001; 2001WO-US049781.
 XX
 PR 22-DEC-2000; 2000US-00747287.
 XX
 PA (ONCO-) ONCOIMMUNIN INC.
 XX
 PI Packard BS, Komoriya A;
 XX

DR WPI; 2002-698548/75.
 XX
 PT Indicator composition comprising polypeptide or nucleic acid backbone
 PT joining two same chromophores resulting in quenching of fluorescence
 PT of/change in absorbance of chromophores, useful for detecting protease
 PT activity.
 XX
 PS Example 2; Page 15; 97pp; English.
 XX
 CC This invention describes a novel indicator composition (referred as homo-
 CC doubly labeled compositions) comprising a polypeptide backbone or a
 CC nucleic acid backbone joining two chromophores of the same species
 CC whereby the chromophores form an H-dimer resulting in quenching of the
 CC fluorescence of or a change in the absorbance of the chromophore, a
 CC decrease in fluorescence or a change in absorbance indicates that the
 CC first molecule and the second molecule are interacting. The indicator is
 CC useful for detecting the activity of a protease, where an increase in
 CC fluorescence or a change in absorbance indicates that the protease
 CC cleaves the polypeptide backbone. The indicator is attached to a solid
 CC support inside a mammalian, yeast or insect cell. The composition bears a
 CC hydrophobic group such as Fmoc, 9-fluorenylacetyl group, 1-
 CC fluoronecarboxylic group, 9-fluorenylacetyl group, and 9-fluorenone-1-
 CC carboxylic group, benzoyloxycarbonyl, Xanthyl (Xan), Trityl (Trt), 4-
 CC methylnitryl (Mnt), 4-methoxytrityl (Mtr), 4-methoxy-2,3,6-trimethyl-
 CC benzenesulphonyl (Mtr), Mesitylene-2-sulphonyl (Mts), 4,4'-
 CC dimethoxybenzhydryl (Mbh), etc. The method described in the invention is
 CC useful for detecting protease or nuclease activity (or the presence of
 CC nucleic acid) in histological section, cells in culture, (e.g., seeded or
 CC cultured adherent cells), a biological sample such as tissue, biopsy,
 CC lymph, embryo, or whole animal, or cell suspension derived from a
 CC biological sample such as tissue, blood, urine, saliva, lymph, or biopsy.
 CC The indicator composition is also useful for screening a test agent for
 CC the ability to modulate a protease (or a nuclease, lipase, etc.). The
 CC indicator reagents allow rapid determination of protease activity in a
 CC matter of minutes in a single-step procedure. The fluorescent indicators
 CC both absorb and emit in the visible range (400-800 nm). These signals are
 CC therefore not readily quenched by, nor is activation of the fluorophores,
 CC that is, absorption of light, interfered with by background molecules;
 CC therefore they are easily detected in biological samples. The fluorogenic
 CC protease indicators utilize high efficiency fluorophores and are able to
 CC achieve a high degree of quenching while providing a strong signal when
 CC the quench is released by cleavage of the peptide substrate. The high
 CC signal allows detection of very low levels of protease activity. Thus the
 CC fluorogenic protease indicators are particularly well suited for in situ
 CC detection of protease activity. ABU60357-ABU60477 represent peptides use
 CC to illustrate the method described in the disclosure of the invention
 XX
 SQ Sequence 9 AA;
 Query Match 58.9%; Score 33; DB 5; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 3 SVPLSVPC 10
 Db :|||:
 2 AIPXSIPC 9
 RESULT 11
 ADN88305
 ID ADN88305 standard; peptide; 9 AA.
 XX
 AC ADN88305;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Fluorogenic protease indicator peptide #1.
 XX
 KW Fluorogenic; protease detection; protease inhibitor.
 XX
 OS Synthetic.
 XX
 PN US2004096926-A1.

XX 20-MAY-2004.
XX
XX
PF 04-JUN-2001; 2001US-00874350.
XX
XX 20-FEB-1997; 97US-00802981.
PR 20-FEB-1998; 98WO-US003000.
PR 10-SEP-1999; 99US-00394019.
PR 11-SEP-2000; 2000WO-US024882.
XX
XX (ONCO-) ONCOIMMUNIN INC.
XX
XX Packard BS, Komoriya A;
XX WPI; 2004-399235/37.
XX
XX Fluorogenic composition useful for detecting protease activity and test substance modulating protease activity.
XX
XX Disclosure; SEQ ID NO 1; 114pp; English.
XX
XX The invention relates to a fluorogenic composition (I) for detecting the activity of a protease. (I) is useful for detecting the activity of a protease, which involves contacting the protease with (I), where the activity of protease is detected in a histological section, cell culture or tissue section. The cell suspension is derived from the biological sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The protease activity is detected by fluorescence microscopy, flow cytometry, microplate reader, absorption spectroscopy or confocal fluorescent microplate reader. (I) is useful for delivering a molecule into a cell, and for screening a test agent for the ability to modulate the activity of the protease. (I) is useful for detection and localisation of protease activity in biological samples. (I) also acts as a protease inhibitor, thus useful as protease inhibitors. (I) enables detection of the protease activity, and provides a high intensity fluorescent signal at a visible wavelength when they are digested by a protease. The present sequence represents a fluorogenic protease indicator peptide of the invention.
XX
SQ Sequence 9 AA;
Query Match 58.9%; Score 33; DB 8; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 3 SVPLSVPC 10
::|||
Db 2 AIPXSIPC 9
RESULT 12
ADN88488
ID ADN88488 standard; peptide; 9 AA.
XX
XX ADN88488;
XX
XX 12-AUG-2004 (first entry)
XX
XX Fluorogenic protease indicator peptide #184.
XX
XX Fluorogenic; protease detection; protease inhibitor.
XX Synthetic.
XX
XX US2004096926-A1.
XX
XX 20-MAY-2004.
XX
XX 04-JUN-2001; 2001US-00874350.
XX
XX 20-FEB-1997; 97US-00802981.
PR 20-FEB-1998; 98WO-US003000.
PR 10-SEP-1999; 99US-00394019.
XX

PR 11-SEP-2000; 2000WO-US024882.
XX
XX (ONCO-) ONCOIMMUNIN INC.
XX
XX Packard BS, Komoriya A;
XX WPI; 2004-399235/37.
XX
XX Fluorogenic composition useful for detecting protease activity and test substance modulating protease activity.
XX
XX Example 2; SEQ ID NO 184; 114pp; English.
XX
XX The invention relates to a fluorogenic composition (I) for detecting the activity of a protease. (I) is useful for detecting the activity of a protease, which involves contacting the protease with (I), where the activity of protease is detected in a histological section, cell culture or tissue section. The cell suspension is derived from the biological sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The protease activity is detected by fluorescence microscopy, flow cytometry, microplate reader, absorption spectroscopy or confocal fluorescent microplate reader. (I) is useful for delivering a molecule into a cell, and for screening a test agent for the ability to modulate the activity of the protease. (I) is useful for detection and localisation of protease activity in biological samples. (I) also acts as a protease inhibitor, thus useful as protease inhibitors. (I) enables detection of the protease activity, and provides a high intensity fluorescent signal at a visible wavelength when they are digested by a protease. The present sequence represents a fluorogenic protease indicator peptide of the invention.
XX
SQ Sequence 9 AA;
Query Match 58.9%; Score 33; DB 8; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 3 SVPLSVPC 10
::|||
Db 2 AIPXSIPC 9
RESULT 13
AAU00643
ID AAU00643 standard; peptide; 10 AA.
XX
XX AAU00643;
XX
XX 07-SEP-2001 (first entry)
XX
XX Human membrane translocating peptide (MTLP) #12.
XX
XX Membrane translocating peptide; MTLP; human; intracellular gene delivery; epithelial cell layer; gastrointestinal tract; circulatory system.
XX
XX Homo sapiens.
XX
XX WO200127154-A2.
XX
XX 19-APR-2001.
XX
XX 27-SEP-2000; 2000WO-IB001491.
XX
XX 27-SEP-1999; 99US-0156246P.
XX
XX (OMAH/) O'MAHONY D J.
XX (LAMB/) LAMBKIN I J.
XX
XX O'mahony DJ, Lambkin IJ;
XX
XX WPI; 2001-300212/31.
DR N-PSDB; AAS00637.
XX

PT Compositions for enhancing uptake of e.g. drugs or DNA across a cell
 PT membrane, comprise membrane translocating peptides having specific amino
 PT acid sequences or a derivative, fragment, motif, analog or peptidomimetic
 PT of the peptides.

XX Claim 2; Page 11; 42pp; English.

XX The sequence represents a human membrane translocated peptide (MTLP).
 CC MTLPs and their related fragments, motifs, derivatives and analogues are
 CC used for enhancing uptake of a pharmaceutically active agent into a cell,
 CC into or out of an intracellular compartment and across a cell layer (for
 CC example, an epithelial cell layer lining the gastrointestinal tract),
 CC either directly or from a pharmaceutically active agent loaded particle,
 CC into the circulatory system of an animal. This method is useful for
 CC intracellular gene delivery, as a rapid screening method for the
 CC identification of MTLPs which retain the functional activity of a full-
 CC length MTLP, as a cell-based screen for assaying the functional activity
 CC of a MTLP and characterising the properties of a MTLP, for diagnosis of a
 CC pathological disorder (by administration of a MTLP-active agent complex
 CC or MTLP-active particle comprising a diagnostic agent) and for
 CC preventing or treating a pathological disorder

XX Sequence 10 AA;

Query Match 57.1%; Score 32; DB 4; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 C1SVPLSVPC 10
 Db 1 CLPVLAAAPC 10

RESULT 14

ADB88786
 ID ADB88786 standard; peptide; 10 AA.

AC ADB88786;

DT 04-DEC-2003 (first entry)

DE Membrane translocating peptide #12.

KW Peyer's patch cell; non-Peyer's patch cell; transcription factor;
 KW upregulated protein; antigen; vaccine delivery; M cell;
 KW membrane translocating peptide.

XX Unidentified.

XX WO2003004646-A2.

XX 16-JAN-2003.

XX 04-APR-2002; 2002WO-IB003866.

XX 04-APR-2001; 2001US-0281387P.

XX 02-JUL-2001; 2001US-0302591P.

XX (OMAH/) O'MAHONY D J.

XX O'mahony DJ, Byrne D, Brayden D;

XX WPI; 2003-229409/22.

XX Increasing the levels of a protein in a Peyer's patch cell, useful for
 PT targeted vaccine or drug delivery, comprises delivering to the Peyer's
 PT patch cell a transcription factor or an activator of a transcription
 PT factor.

XX Example 6; Page 51; 147pp; English.

XX The invention relates to a novel method for increasing the levels of a
 CC protein in a Peyer's patch cell. The method comprises delivering to the

CC cell a nucleic acid coding for a protein, the level of which or its mRNA
 CC is greater than in a non-Peyer's patch cell. The preferred protein of the
 CC invention is a transcription factor or a protein that activates a
 CC transcription factor selected from Jun-B, c-jun related TF, Jun-D, STAT 3
 CC -signal transducer and activator of transcription 3, Nfkapab6g; Tf p105
 CC subunit, S-myc proto-oncogene, myc related, Nm23-W2, nucleoside
 CC diphosphate kinase B, metastasis reducing protein, and C-est-1 proto-
 CC oncogene, and p54. The preferred upregulated protein of the invention is
 CC selected from Clusterin, T-cell surface glycoprotein CD5 precursor, HSP
 CC 84, and Ca2+ dependent phospholipase A2 precursor and the mRNA is for a
 CC protein selected from the group. The method is useful for increasing or
 CC decreasing the level of a protein in a Peyer's patch cell, particularly
 CC in increasing antigen or vaccine delivery to M cells. The method may also
 CC be used to enhance transport of a drug through the gastrointestinal tract
 CC (GIT). This sequence represents a membrane translocating peptide of the
 CC invention.

XX Sequence 10 AA;

Query Match 57.1%; Score 32; DB 7; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 C1SVPLSVPC 10
 Db 1 CLPVLAAAPC 10

RESULT 15

ABG75437
 ID ABG75437 standard; peptide; 10 AA.

AC ABG75437;

DT 15-APR-2004 (first entry)

DE Membrane translocating peptide #12.

KW Membrane translocating peptide; transmembrane transport;
 KW enzymatic degradation; gastrointestinal tract.

XX Unidentified.

XX Key Location/Qualifiers

FT modified_site 2 /note= "modified by epsilon-dansyl"

FT modified_site 10

FT /note= "C-terminal amide"

XX WO2003089458-A2.

XX 30-OCT-2003.

XX 21-APR-2003; 2003WO-US012543.

XX 19-APR-2002; 2002US-00126845.

XX (SARL-) SARLAN LTD.

XX O'mahony DJ, Lambkin I, Houghten R, Pinilla C;

XX WPI; 2004-034528/03.

XX Composition, useful for treating a pathological disease in an animal,
 PT comprises a translocating peptide, consisting of a transport peptide, an
 PT extended peptide comprising the transport peptide or a transport-active
 PT fragment.

XX Claim 1; Page 24; 0pp; English.

XX The present invention relates to a composition which comprises a
 CC translocating peptide, consisting of a transport peptide, an extended
 CC peptide comprising the transport peptide or a transport-active fragment

CC of at least 4 amino acids of the transport peptide. The composition is
CC useful in treating a pathological disorder in an animal, as it protects
CC an orally delivered active agent from enzymatic degradation in the
CC gastrointestinal tract (GIT), and promotes absorption across epithelial
CC cells lining the GIT. The present sequence is a polypeptide used in the
CC exemplification of the invention
XX

SQ Sequence 10 AA;

Query Match 57.1%; Score 32; DB 8; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CISVPLSVPC 10
|:|:|:
Db 1 CLPVLLAAPC 10

Search completed: April 1, 2005, 12:06:08
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Maximum DB seq length: 10

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Maximum Match 100%
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6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	10	9 US-09-761-636A-13	Sequence 13, Appl
2	41.5	74.1	9	9 US-09-761-636A-14	Sequence 14, Appl
3	33	58.9	9	10 US-09-747-287-1	Sequence 1, Appl
4	33	58.9	9	11 US-09-874-350A-1	Sequence 1, Appl
5	33	58.9	9	11 US-09-874-350A-184	Sequence 184, Appl
6	32	57.1	10	14 US-10-126-845-13	Sequence 13, Appl
7	32	57.1	10	14 US-10-126-845-71	Sequence 71, Appl
8	32	57.1	10	15 US-10-116-275-101	Sequence 101, Appl
9	32	57.1	10	16 US-10-764-235-13	Sequence 13, Appl
10	31.5	56.2	9	10 US-09-932-165-284	Sequence 284, Appl
11	31.5	56.2	10	10 US-09-932-165-184	Sequence 184, Appl
12	31.5	56.2	10	10 US-09-932-165-560	Sequence 560, Appl
13	31.5	56.2	10	10 US-09-932-165-794	Sequence 794, Appl

14	31	55.4	9	15 US-10-154-884B-11221	Sequence 11221, A
15	31	55.4	10	15 US-10-363-791-194	Sequence 194, App
16	30	53.6	9	10 US-09-932-165-679	Sequence 679, App
17	30	53.6	9	10 US-09-932-165-1006	Sequence 1006, App
18	30	53.6	9	10 US-09-932-165-1214	Sequence 1214, App
19	29	51.8	10	11 US-09-833-245-1011	Sequence 1011, App
20	27	48.2	8	9 US-09-756-283A-66	Sequence 66, Appl
21	27	48.2	8	11 US-09-855-604-890	Sequence 890, App
22	27	48.2	9	15 US-10-154-884B-11228	Sequence 11228, A
23	27	48.2	9	15 US-10-154-884B-11250	Sequence 11250, A
24	27	48.2	9	15 US-10-154-884B-11254	Sequence 11254, A
25	27	48.2	9	15 US-10-154-884B-11258	Sequence 11258, A
26	27	48.2	9	15 US-10-154-884B-11259	Sequence 11259, A
27	27	48.2	9	15 US-10-154-884B-11265	Sequence 11265, A
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29	27	48.2	9	15 US-10-154-884B-11280	Sequence 11280, A
30	27	48.2	9	16 US-10-415-014-421	Sequence 421, App
31	27	48.2	9	16 US-10-415-014-537	Sequence 537, App
32	27	48.2	10	16 US-10-415-014-170	Sequence 170, App
33	27	48.2	10	16 US-10-415-014-187	Sequence 187, App
34	27	48.2	10	16 US-10-415-014-266	Sequence 266, App
35	27	48.2	10	16 US-10-415-014-493	Sequence 493, App
36	27	48.2	10	16 US-10-415-014-583	Sequence 583, App
37	26	46.4	9	9 US-09-852-424-32	Sequence 32, Appl
38	26	46.4	9	9 US-09-852-424-43	Sequence 43, Appl
39	26	46.4	9	15 US-10-154-884B-11276	Sequence 11276, A
40	26	46.4	9	15 US-10-154-884B-11287	Sequence 11287, A
41	26	46.4	9	15 US-10-363-208-21	Sequence 21, Appl
42	25	44.6	9	9 US-09-761-636A-10	Sequence 10, Appl
43	25	44.6	10	9 US-09-922-261-21	Sequence 21, Appl
44	24	42.9	5	10 US-09-886-135-5	Sequence 5, Appl
45	24	42.9	5	17 US-10-891-122-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-09-761-636A-13
; Sequence 13, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 10
; TYPE: PPT
; ORGANISM: Homo sapiens
US-09-761-636A-13

Query Match 100.0%; Score 56; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CISVPLSVPC 10

Db 1 CISVPLSVPC 10

RESULT 2

US-09-761-636A-14

; Sequence 14, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-14

Query Match 74.1%; Score 41.5; DB 9; Length 9;
Best Local Similarity 90.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CISVPLSVPC 10
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Db 1 CISVPL-VPC 9

RESULT 3
US-09-747-287-1
; Sequence 1, Application US/09747287
; Publication No. US20030207264A1
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; APPLICANT: PACKARD, BEVERLY S.
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide.
; NAME/KEY: misc feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: Xaa is norleucine
US-09-747-287-1

Query Match 58.9%; Score 33; DB 10; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SVPLSVPC 10
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Db 2 AIPXSIPC 9

RESULT 4
US-09-874-350A-1
; Sequence 1, Application US/09874350A
; Publication No. US20040096926A1
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S
; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: protease indicator
; NAME/KEY: misc feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: Xaa is norleucine (Nle)
US-09-874-350A-1

Query Match 58.9%; Score 33; DB 11; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SVPLSVPC 10
:|||||:
Db 2 AIPXSIPC 9

RESULT 5
US-09-874-350A-184
; Sequence 184, Application US/09874350A
; Publication No. US20040096926A1
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S
; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 184
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide substrate
; NAME/KEY: MOD_RES

; LOCATION: (5) : (5)
; OTHER INFORMATION: X is norleucine
US-09-874-350A-184

Query Match 58.9%; Score 33; DB 11; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy	3	SVPLSVPC	10
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Db	2	AIPXSIPC	9

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RESULT 6
US-10-126-845-13
; Sequence 13, Application US/10126845
; Publication No. US20030181367A1
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20058
; CURRENT APPLICATION NUMBER: US/10/126,845
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: membrane translocating peptide, cyclic
US-10-126-845-13

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Query Match          57.1%; Score 32; DB 14; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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Qy 1 C1SVPLSVPC 10
|:|:|
Db 1 C1PVLTAAPC 10

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RESULT 7
US-10-126-845-71
; Sequence 71, Application US/10126845
; Publication No. US20030181367A1
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20058
; CURRENT APPLICATION NUMBER: US/10/126,845
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 71
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D form peptide
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(10)
; OTHER INFORMATION: D form amino acid
US-10-126-845-71

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Query Match 57.1%; Score 32; DB 14; Length 10;

Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 3; Indels

Qy	1	CISVPLSVPC	10
		: :	
Db	1	CLPVLAAAPC	10

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RESULT 8
US-10-116-275-101
; Sequence 101, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Listed in Table titled "Peptides that Target to and/or Enhance t
; OTHER INFORMATION: take Across the GIT"
US-10-116-275-101

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Query Match	57.1%	Score 32;	DB 15;	Length 10;
Best Local Similarity	50.0%	Pred. No. 1.1e+02;		
Matches 5; Conservative	2;	Mismatches 3;	Indels 0;	Gaps 0;

Qy 1 C1SVPLSVPC 10
|:|:|
Db 1 CLPVLAAAPC 10

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RESULT 9
US-10-764-235-13
; Sequence 13, Application US/10764235
; Publication No. US20040138132A1
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: P26.479-B USA
; CURRENT APPLICATION NUMBER: US/10/764,235
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: 09/671,089
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: membrane translocating peptide, cyclic
US-10-764-235-13

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Query Match 57.1%; Score 32; DB 16; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 5: Conservative 2; Mismatches 3; Indels

Best Local Matches	Similarity	Seq. ID	Accession	Length	Score	Positives	Conservative	Mismatches	Indels	Gaps
5	50.0%	1	1.1E+02	100	100	100	5	2	3	0
5	50.0%	1	1.1E+02	100	100	100	5	2	3	0

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QY 1 CISVPLSVPC 10
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Db 1 CLFVLLAAPC 10

RESULT 10
US-09-932-165-284
; Sequence 284, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 284
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-284

Query Match 56.2%; Score 31.5; DB 10; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.3e+06;
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 CISVPLSVPC 10
   |:|:|
Db 1 CLT-PLSFPC 9

RESULT 11
US-09-932-165-184
; Sequence 184, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 184
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-184

Query Match 56.2%; Score 31.5; DB 10; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.3e+06;
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 CISVPLSVPC 10
   |:|:|
Db 1 CLT-PLSFPC 9

RESULT 12
US-09-932-165-560
; Sequence 560, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 560
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-560

Query Match 56.2%; Score 31.5; DB 10; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 CISVPLSVPC 10
   |:|:|
Db 1 CLT-PLSFPC 9

RESULT 13
US-09-932-165-794
; Sequence 794, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
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; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 794
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-794

Query Match 56.2%; Score 31.5; DB 10; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 CUSVPLSVPC 10
|::|||
Db 1 CUSVPLSVPC 9

RESULT 14
US-10-154-884B-11221
; Sequence 11221, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11221
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11221

Query Match 55.4%; Score 31; DB 15; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.3e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUSVPLS 7
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Db 2 CLSVPEVS 8

RESULT 15
US-10-363-791-194
; Sequence 194, Application US/10363791
; Publication No. US20040029197A1
; GENERAL INFORMATION:
; APPLICANT: TAKIMOTO, Masato
; APPLICANT: KUZUMAKI, No. US20040029197A1oru
; APPLICANT: SATO, No. US20040029197A1iyuki
; APPLICANT: SAHARA, Hiroeki
; TITLE OF INVENTION: A novel human cancer/testis-associated gene thereof
; FILE REFERENCE: 4439-4006
; CURRENT APPLICATION NUMBER: US/10/363,791
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: JP 2000-274218
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 194
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-791-194

Query Match 55.4%; Score 31; DB 15; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLSVPC 10
|::|||
Db 2 PLSAPC 7

Search completed: April 1, 2005, 12:18:44
Job time : 94 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2005, 11:32:13 ; Search time 43 seconds
(without alignments)
12.152 Million cell updates/sec

Title: US-09-761-636A-11

Perfect score: 42

Sequence: 1 CVPLTSC 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 61165

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	73.8	7	1	US-08-526-710-21
2	31	73.8	7	3	US-08-862-855-21
3	31	73.8	7	3	US-09-226-985-21
4	31	73.8	7	3	US-09-227-906-21
5	31	73.8	7	4	US-09-228-866-21
6	26	61.9	7	3	US-09-187-859-1375
7	26	61.9	7	3	US-09-839-542B-1375
8	25	59.5	7	3	US-09-187-859-1799
9	25	59.5	7	3	US-09-187-859-3971
10	25	59.5	7	3	US-09-187-859-4047
11	25	59.5	7	4	US-09-839-542B-1799
12	25	59.5	7	4	US-09-839-542B-3971
13	25	59.5	7	4	US-09-839-542B-4047
14	24	57.1	7	3	US-09-187-859-3574
15	24	57.1	7	4	US-09-839-542B-3574
16	23	54.8	6	1	US-07-947-035-13
17	23	54.8	6	1	US-08-321-585A-11
18	23	54.8	7	3	US-09-187-859-1392
19	23	54.8	7	3	US-09-187-859-1740
20	23	54.8	7	3	US-09-187-859-2155
21	23	54.8	7	3	US-09-187-859-2720
22	23	54.8	7	3	US-09-187-859-3637
23	23	54.8	7	3	US-09-187-859-4041
24	23	54.8	7	4	US-09-839-542B-1392
25	23	54.8	7	4	US-09-839-542B-1740
26	23	54.8	7	4	US-09-839-542B-2155
27	23	54.8	7	4	US-09-839-542B-2720

28	23	54.8	7	4	US-09-839-542B-3637	Sequence 3637, Ap
29	23	54.8	7	4	US-09-839-542B-4041	Sequence 4041, Ap
30	23	54.8	7	4	US-09-535-852-1826	Sequence 1826, Ap
31	22	52.4	4	2	US-08-429-964-41	Sequence 41, Appl
32	22	52.4	4	4	US-09-665-362A-35	Sequence 35, Appl
33	22	52.4	4	4	US-09-665-637-35	Sequence 35, Appl
34	22	52.4	4	5	PCT-US93-08062-41	Sequence 41, Appl
35	22	52.4	7	1	US-07-958-903A-26	Sequence 26, Appl
36	22	52.4	7	1	US-08-462-018-26	Sequence 26, Appl
37	22	52.4	7	1	US-08-823-245-26	Sequence 26, Appl
38	22	52.4	7	3	US-07-963-329A-26	Sequence 1888, Ap
39	22	52.4	7	3	US-09-187-859-1888	Sequence 1888, Ap
40	22	52.4	7	3	US-09-187-859-2750	Sequence 2750, Ap
41	22	52.4	7	3	US-09-187-859-3606	Sequence 3606, Ap
42	22	52.4	7	3	US-09-187-859-3621	Sequence 3621, Ap
43	22	52.4	7	4	US-09-839-542B-1888	Sequence 1888, Ap
44	22	52.4	7	4	US-09-839-542B-2750	Sequence 2750, Ap
45	22	52.4	7	4	US-09-839-542B-3606	Sequence 3606, Ap

ALIGNMENTS

RESULT 1
US-08-526-710-21
; Sequence 21, Application US/08526710
; Patent No. 5622699
; GENERAL INFORMATION:
; APPLICANT: Ruolahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,710
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1779
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-526-710-21

Query Match 73.8%; Score 31; DB 1; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
|:|:
Db 1 CLPVASC 7

RESULT 2
US-08-862-855-21
; Sequence 21, Application US/08862855
; Patent No. 6068829
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,855
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2621
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-862-855-21

Query Match 73.8%; Score 31; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
|:|:|
Db 1 CLPVASC 7

RESULT 3
US-09-226-985-21
; Sequence 21, Application US/09226985
; Patent No. 6296832
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules That Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/226,985
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/862,855
; FILING DATE: 23-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-226-985-21

Query Match 73.8%; Score 31; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
|:|:|
Db 1 CLPVASC 7

RESULT 4
US-09-227-906-21
; Sequence 21, Application US/09227906
; Patent No. 6306365
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997

Query Match 73.8%; Score 31; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;

US-09-187-859-1799
; Sequence 1799, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1799
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence
US-09-187-859-1799

Query Match 59.5%; Score 25; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CVPLTSC 7
| | | | |
Db 1 CDPKTGC 7

RESULT 9

US-09-187-859-3971
; Sequence 3971, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3971
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-14 cell adhesion recognition sequence
US-09-187-859-3971

Query Match 59.5%; Score 25; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CVPLTSC 7
| | | | |
Db 1 CDPKTGC 7

RESULT 10

US-09-187-859-4047
; Sequence 4047, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1

; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4047
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-09-187-859-4047

Query Match 59.5%; Score 25; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CVPLTSC 7
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Db 1 CDPKTGC 7

RESULT 11

US-09-839-542B-1799
; Sequence 1799, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1799
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence
US-09-839-542B-1799

Query Match 59.5%; Score 25; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CVPLTSC 7
| | | | |
Db 1 CDPKTGC 7

RESULT 12

US-09-839-542B-3971
; Sequence 3971, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3971
; LENGTH: 7
; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-14 cell adhesion recognition sequence

US-09-839-542B-3971

Query Match

Best Local Similarity 59.5%; Score 25; DB 4; Length 7;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVPLTSC 7

Db 1 CDPKTC 7

RESULT 13

US-09-839-542B-4047

; Sequence 4047, Application US/09839542B

; Patent No. 6569996

; GENERAL INFORMATION:

; APPLICANT: Blaschuk, Orest W.

; APPLICANT: Symonds, James Matthew

; APPLICANT: Gour, Barbara J.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

; FILE REFERENCE: 100086.407D1

; CURRENT APPLICATION NUMBER: US/09/839,542B

; NUMBER OF SEQ ID NOS: 4052

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4047

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence

US-09-839-542B-4047

Query Match

Best Local Similarity 59.5%; Score 25; DB 4; Length 7;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVPLTSC 7

Db 1 CDPKTC 7

RESULT 14

US-09-187-859-3574

; Sequence 3574, Application US/09187859A

; Patent No. 6358920

; GENERAL INFORMATION:

; APPLICANT: Blaschuk, Orest W.

; APPLICANT: Gour, Barbara J.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

; FILE REFERENCE: 100086.407C1

; CURRENT APPLICATION NUMBER: US/09/187,859A

; CURRENT FILING DATE: 1998-11-06

; NUMBER OF SEQ ID NOS: 4052

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3574

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Representative cyclic modulating agent based on

; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion

; OTHER INFORMATION: recognition sequence

US-09-187-859-3574

Query Match

Best Local Similarity 57.1%; Score 24; DB 3; Length 7;

Best Local Similarity 42.9%; Pred. No. 4.1e+05;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTSC 7

Db 1 CDPVSGC 7

RESULT 15

US-09-839-542B-3574

; Sequence 3574, Application US/09839542B

; Patent No. 6569996

; GENERAL INFORMATION:

; APPLICANT: Blaschuk, Orest W.

; APPLICANT: Symonds, James Matthew

; APPLICANT: Gour, Barbara J.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

; FILE REFERENCE: 100086.407D1

; CURRENT APPLICATION NUMBER: US/09/839,542B

; CURRENT FILING DATE: 2001-04-20

; NUMBER OF SEQ ID NOS: 4052

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3574

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Representative cyclic modulating agent based on

; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion

; OTHER INFORMATION: recognition sequence

US-09-839-542B-3574

Query Match

Best Local Similarity 57.1%; Score 24; DB 4; Length 7;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTSC 7

Db 1 CDPVSGC 7

Search completed: April 1, 2005, 11:40:32

Job time : 44 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 11:46:34 ; Search time 39 Seconds
(without alignments)
14.803 Million cell updates/sec

Title: US-09-761-636A-12

Perfect score: 38

Sequence: 1 CVPLTC 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 316

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	15	39.5	6	2 I65546	MHC H2-L antigen -
3	14	36.8	5	2 E60274	major protein anti
4	14	36.8	5	2 P22565	R-phycoerythrin ga
5	14	36.8	6	2 I49421	laminin B1 - weste
6	11	28.9	4	2 I54357	schwannomin - mous
7	11	28.9	4	2 A32039	tyrosine-melanocyt
8	11	28.9	5	2 A60521	glycogen phosphory
9	11	28.9	6	2 I37263	Y protein - human
10	11	28.9	6	2 H48394	glycoprotein compo
11	10	26.3	6	2 C22565	R-phycoerythrin be
12	9	23.7	3	2 A22565	R-phycoerythrin al
13	9	23.7	4	2 I51049	metallothionein-A
14	9	23.7	4	2 S43959	Ig mu chain V regi
15	9	23.7	4	2 S55238	pallidipin - assas
16	9	23.7	5	2 A33882	cadmium-binding pe
17	9	23.7	5	2 B37988	acid proteinase li
18	9	23.7	5	2 B45525	actin I - malaria
19	9	23.7	5	2 S65726	hemoglobin, extrac
20	9	23.7	5	2 S11127	phosphoprotein, bo
21	9	23.7	6	2 A61049	halo-toxin - Pseud
22	9	23.7	6	2 JU0355	lipopeptide WS1279
23	9	23.7	6	2 PQ0008	angiotensin-conver
24	9	23.7	6	2 I37027	protamine P1 - gor
25	9	23.7	6	2 I67345	MHC H2-K-k cell su
26	9	23.7	6	2 PT0652	T-cell receptor be
27	9	23.7	6	2 F41946	T-cell receptor ga
28	9	23.7	6	2 S29881	Na+/K+-exchanging
29	9	23.7	6	2 A27696	contraction-inhibi

30 9 23.7 6 2 B27696 contraction-inhibi
31 9 23.7 6 4 I79564 hypothetical TCL3
32 8 21.1 3 3 I78890 tyrosine protein k
33 8 21.1 5 1 HOROHA proctolin - Americ
34 8 21.1 5 2 JN0860 peptidyl-di-peptida
35 8 21.1 5 2 JN0862 peptidyl-di-peptida
36 8 21.1 5 2 PQ0009 angiotensin-conver
37 8 21.1 5 2 S53595 hypothetical prote
38 8 21.1 5 2 E42364 flagellar protein
39 8 21.1 5 2 A60411 proctolin - Atlant
40 8 21.1 6 4 A35039 hypothetical colla
41 7 18.4 3 3 RSHST hypothetical - she
42 7 18.4 3 3 A92971 thyroliberin - eas
43 7 18.4 3 3 RHTD70 thyroliberin - Bom
44 7 18.4 3 3 A43391 TRH-like tripeptid
45 7 18.4 3 3 T13892 cytochrome-c oxida

ALIGNMENTS

RESULT 1

B22565
R-phycoerythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: B22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601; PMID:3886644
A:Accession: B22565
A:Molecule type: protein
A:Residues: 1-5 <KLO>

Query Match 52.6%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVP 3
|||
Db 2 CVP 4

RESULT 2

I65546
MHC H2-L antigen - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I65546
R:Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
Cell 44, 261-272, 1986
A:Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and their
A:Reference number: I52778; MUID:86106202; PMID:3510743
A:Accession: I65546
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: GB:M12483; NID:g199565; PIDN:AAA39663.1; PID:g554234

Query Match 39.5%; Score 15; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VPLT 5
|||
Db 2 VPCT 5

RESULT 3

E60274
Major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)
C:Species: Mycobacterium tuberculosis

C>Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993

C:Accession: E60274
R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A>Title: Isolation and partial characterization of major protein antigens in the culture
A:Reference number: A60274; MUID:9109989; PMID:1898899
A:Accession: E60274
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <NAG>

Query Match 36.8%; Score 14; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PLT 5
||
Db 3 PIT 5

RESULT 4

F22565

R-phycoerythrin gamma-A chain - red alga (Gastrocionium coulteri) (fragment)
C:Species: Gastrocionium coulteri

C>Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993

C:Accession: F22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A>Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:185182601; PMID:3886644
A:Accession: F22565
A:Molecule type: protein
A:Residues: 1-5 <KLO>

Query Match 36.8%; Score 14; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TC 6
||
Db 2 TC 3

RESULT 5

I49421

laminin B1 - western wild mouse (fragment)
C:Species: Mus spretus (western wild mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C:Accession: I49421
R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
A>Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A:Reference number: I48934; MUID:94319082; PMID:8043949
A:Accession: I49421
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: EMBL:U05736; NID:9497073; PIDN:AAB60477.1; PID:G642829

Query Match 36.8%; Score 14; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TC 6
||
Db 4 TC 5

RESULT 6

I54357

schwannomin - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999

C:Accession: I54357

R:Huyh, D.P.; Nechiporuk, T.; Pulsr, S.

Hum. Mol. Genet. 3, 1075-1079, 1994

A>Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are cor

A:Reference number: I54357; MUID:95072570; PMID:7981675

C:Accession: I54357

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-4 <RES>

A:Cross-references: GB:L28839; NID:9454836; PIDN:AAA57150.1; PID:9601923

C:Genetics:

A:Gene: NF2

Query Match 28.9%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VP 3
||
Db 1 VP 2

RESULT 7

A32039

tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000

C:Accession: A32039

R:Horvath, A.; Kastin, A.J.

J. Biol. Chem. 264, 2175-2179, 1989

A>Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1

A:Reference number: A32039; MUID:89123285; PMID:2563371

C:Accession: A32039

A:Molecule type: protein

A:Residues: 1-4 <HOR>

A:Experimental source: brain

C:Superfamily: unassigned animal peptides

C:Keywords: amidated carboxyl end

F:4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.9%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PL 4
||
Db 2 PL 3

RESULT 8

A60521

glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)

N:Alternate names: glycogen phosphorylase b

C:Species: Liza ramada

C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Mar-2004

C:Accession: A60521

R:Bonamusa, L.; Baanante, I.V.

Comp. Biochem. Physiol. B 95, 295-301, 1990

A>Title: Purification and characterization of glycogen phosphorylase B from skeletal musc

A:Reference number: A60521; MUID:90227907; PMID:2109669

C:Accession: A60521

A:Molecule type: protein

A:Residues: 1-5 <BON>

C:Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein

F:3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experime

Query Match 28.9%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VP 3
||
Db 4 VP 5

```
RESULT 9
I37263
Y protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Nov-1999
C:Accession: I37263
R:Waeber, G.; Habener, J.F.
Endocrinology 131, 2010-2015, 1992
A:Title: Novel testis germ cell-specific transcript of the CREB gene contains an alternative exon
A:Reference number: I37263; MUID:93010691; PMID:1396344
A:Accession: I37263
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: EMBL:X68994; NID:g396171; PIDN:CAA48780.1; PID:g579816
C:Genetics:
A:Gene: CREB

Query Match 28.9%; Score 11; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTC 6
DB 2 LFC 4

RESULT 10
H48394
Glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr
C:Species: Bos primigenius taurus (cattle)
C>Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C:Accession: H48394
R:Wather, I.H.; Barghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A:Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
A:Note: sequence extracted from NCBI backbone (NCBIP:131518)
C:Keywords: glycoprotein

Query Match 28.9%; Score 11; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTC 6
DB 4 LFC 6

RESULT 11
C22565
R-phycoerythrin beta-1 chain - red alga (Gastrocloonium coulteri) (fragment)
C:Species: Gastrocloonium coulteri
C>Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: C22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601; PMID:3886644
A:Accession: C22565
A:Molecule type: protein
A:Residues: 1-6 <KLO>

Query Match 26.3%; Score 10; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CV 2
DB 4 CL 5

RESULT 12
A22565
R-phycoerythrin alpha-1 chain - red alga (Gastrocloonium coulteri) (fragment)
C:Species: Gastrocloonium coulteri
C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: A22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601; PMID:3886644
A:Accession: A22565
A:Molecule type: protein
A:Residues: 1-3 <KLO>

Query Match 23.7%; Score 9; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 1 C 1

RESULT 13
I51049
metallothionein-A - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I51049
R:Olsson, P.E.; Kling, P.; Ekell, L.J.; Kille, P.
Eur. J. Biochem. 230, 344-349, 1995
A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) met
A:Reference number: I51049; MUID:95324545; PMID:7601121
A:Accession: I51049
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <OLS>
A:Cross-references: EMBL:X80181; NID:gi1019799; PIDN:CAA56466.1; PID:g4379328

Query Match 23.7%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 4 C 4

RESULT 14
S43959
Ig mu chain V region (clone 13) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C:Accession: S43959
R:Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.;
Nucleic Acids Res. 22, 1389-1393, 1994
A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
A:Reference number: S43956; MUID:94248036; PMID:8190629
A:Accession: S43959
A:Molecule type: DNA
A:Residues: 1-4 <WAG>
C:Keywords: immunoglobulin

Query Match 23.7%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 C 1
|
Db 2 C 2

RESULT 15
S55238
pallidipin - assassin bug (fragment)
C/Species: Triatoma pallidipennis (assassin bug)
C/Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 19-May-2000
C/Accession: S55238
R/Handler: B.; Becker, A.; Noeske-Jungblut, C.; Kraetzschmar, J.; Donner, P.; Schleunin
Biochem. J. 307, 465-470, 1995
A/Title: Expression of active recombinant pallidipin, a novel platelet aggregation inhib
A/Reference number: S55238; MUID:95251610; PMID:7733884
A/Accession: S55238
A/Molecule type: protein
A/Residues: 1-4 <HAE>

Query Match 23.7%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1
|
Db 3 C 3

Search completed: April 1, 2005, 11:54:19
Job time : 39 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 11:40:39 ; Search time 115 Seconds
(without alignments)
26.717 Million cell updates/sec

Title: US-09-761-636A-12

Perfect score: 38

Sequence: 1 CVPLTC 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 71

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	13	34.2	6 1 EI01_LITRU	P82096 litoria rub
2	12	31.6	5 1 FARP_CHICK	P83108 gallus gall
3	11	28.9	6 1 VP19_HVIX	P23210 human herpe
4	9	23.7	5 1 AP21_EISFO	P84182 eisenia foe
5	9	23.7	5 1 EI03_LITRU	P82099 litoria rub
6	9	23.7	6 1 CIP1_WYTED	P13736 mytilus edu
7	9	23.7	6 1 CIP2_WYTED	P13737 mytilus edu
8	9	23.7	6 1 SAPP_SEPOF	P83569 sepiia offic
9	8	21.1	5 1 PRCT_CARMA	P67857 carcinus ma
10	8	21.1	5 1 PRCT_LIMPO	P67858 limulus pol
11	8	21.1	5 1 PRCT_PERAM	P67859 periplaneta
12	8	21.1	6 1 TRP1_PSEPU	P36414 pseudomonas
13	7	18.4	3 1 THYL_BOMOR	P62970 bombina ori
14	7	18.4	3 1 THYL_NOTVI	P62971 notophthalm
15	7	18.4	3 1 THYL_PIG	P62968 sus scrofa
16	7	18.4	3 1 THYL_SHEEP	P62969 ovis aries
17	7	18.4	4 1 DCML_PSECH	P19916 pseudomonas
18	7	18.4	4 1 TUFT_HUMAN	P01858 homo sapien
19	7	18.4	4 1 YLM1_YEAST	P36515 saccharomyc
20	7	18.4	4 2 Q16047	Q16047 homo sapien
21	7	18.4	5 1 B10A_CITFR	P13071 citrobacter
22	7	18.4	5 1 BP77_BOTIN	P30425 bothrops in
23	7	18.4	5 1 EI04_LITRU	P82100 litoria rub
24	7	18.4	5 1 PAP2_PARMA	P81964 pardachirus
25	7	18.4	5 1 SUGA_ACHDO	P19991 acheta dome
26	7	18.4	6 1 OVM_LEPDE	P42985 leptinotars
27	7	18.4	6 1 PYF1_PENMO	P84005 penaeus mon
28	7	18.4	6 1 TMOF_SARBU	P41495 sarcophaga
29	5	13.2	5 1 PSK_DAUCA	P58261 daucus caro
30	5	13.2	5 1 RE31_LITRU	P82072 litoria rub
31	5	13.2	5 1 RE32_LITRU	P82073 litoria rub

32	5	13.2	5	2	P83073	P83073 bacillus ce
33	5	13.2	6	1	UN06_CLOPA	P81351 clostridium
34	5	13.2	6	2	P82181	P82181 spinacia ol
35	5	13.2	6	2	P82182	P82182 spinacia ol
36	5	13.2	6	2	P82541	P82541 spinacia ol
37	5	13.2	6	2	P83533	P83533 lactobacill
38	4	10.5	4	1	E0SI_HUMAN	P02731 homo sapien
39	4	10.5	4	1	FAR3_HIRME	P42562 hirudo medi
40	4	10.5	4	1	FLRF_HIRME	P42561 hirudo medi
41	4	10.5	4	1	FLRN_ATEL	P58707 anthopleura
42	4	10.5	4	1	ILME_SEPOF	Q08433 sepiia offic
43	4	10.5	4	2	Q08433	Q08433 rattus sp.
44	4	10.5	5	1	ALI4_CARMA	P81817 carcinus ma
45	4	10.5	5	1	RE11_LITRU	P82070 litoria rub

ALIGNMENTS

RESULT 1
EI01_LITRU
ID EI01_LITRU STANDARD; PRT; 6 AA.
AC P82096;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Electrin 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylaidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE-Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
FT MOD RES 6 Methionine amide.
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;
Query Match 34.2%; Score 13; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 VPL 4
Db 2 VPI 4
RESULT 2
FARP_CHICK
ID FARP_CHICK STANDARD; PRT; 5 AA.
AC P83308;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRFamide-like neuropeptide (LPLRF-amide).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RA Dockray G.J., Reeve-J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;

RT "A novel active pentapeptide from chicken brain identified by
 RT antibodies to FWRamide.";
 RL Nature 305:328-330(1983).
 CC -!- FUNCTION: May function as a neurotransmitter or modulator.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the FARP (FWRamide related peptide)
 CC family.
 DR GO: GO:0007218; P:neuropeptide signaling pathway; TAS.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD_RES 5 5 Phenylalanine amide.
 SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 31.6%; Score 12; DB 1; Length 5;
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VPL 4
 :||
 Db 1 LPL 3

RESULT 3

VP19_HHV1K
 ID VP19_HHV1K STANDARD; PRT; 6 AA.
 AC P23210;
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Capsid assembly and DNA maturation protein (Virion protein UL38)
 DE (Capsid protein VP19C) (Fragment).
 GN Name=UL38;
 OS Human herpesvirus 1 (strain KOS) (HHV-1) (Human herpes simplex virus
 OS 1).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Simplexvirus.
 OX NCBI_TaxID=10306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91101287; PubMed=1846198;
 RA Flanagan W.M., Papavasiliou A.G., Rice M., Hecht L.B.,
 RA Silverstein S., Wagner E.K.
 RT "Analysis of the herpes simplex virus type 1 promoter controlling the
 RT expression of UL38, a true late gene involved in capsid assembly.";
 RL J. Virol. 65:769-786(1991).
 CC -!- FUNCTION: Component of the basal layer in which the capsids are
 CC embedded. Binds DNA.
 CC -!- SIMILARITY: Belongs to the herpesviruses VP19C family.

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 CC -----
 DR EMBL; M57646; AAA45830.1; -
 KW Capsid assembly; Coat protein; DNA-binding.
 FT NON_TER 6
 SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;

Query Match 28.9%; Score 11; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PL 4
 :||
 Db 5 PL 6

RESULT 4

AP21_EISFO
 ID AP21_EISFO STANDARD; PRT; 5 AA.

P84182;
 DT 25-JAN-2005 (Rel. 46, Created)
 DT 25-JAN-2005 (Rel. 46, Last sequence update)
 DE Antimicrobial peptide OEP3121.
 OS Eisenia foetida (Common branding worm) (Common dung-worm).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
 OC Lumbricina; Lumbricidae; Eisenia.
 OX NCBI_TaxID=6396;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RX PubMed=15253156;
 RA Liu Y.-Q., Sun Z.-J., Wang C., Li S.-J., Liu Y.-Z.;
 RT "Purification of a novel antibacterial short peptide in earthworm
 RT Eisenia foetida.";
 RL Acta Biochim. Biophys. Sin. 36:297-302(2004).
 CC -!- FUNCTION: Displays antimicrobial activity against E.coli, S.aureus
 CC and P.aeruginosa.
 CC -!- MASS SPECTROMETRY: MW=510.8; METHOD=WALDI; RANGE=1-5; NOTE=Ref.1.
 KW Antibiotic; Direct protein sequencing.
 SQ SEQUENCE 5 AA; 407 MW; 687DC5BEBB00000 CRC64;

Query Match 23.7%; Score 9; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
 :
 Db 2 C 2

RESULT 5

E103_LITRU
 ID E103_LITRU STANDARD; PRT; 5 AA.
 AC P82099;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Electrin 3.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE

RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RT rubella.";
 RL Aust. J. Chem. 52:639-645(1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 KW Amidation; Amphibian defense peptide; Direct protein sequencing.
 FT MOD_RES 5 5 Methionine amide.
 SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 23.7%; Score 9; DB 1; Length 5;
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PL 4
 :||
 Db 4 PM 5

RESULT 6

CIP1_MYTED
 ID CIP1_MYTED STANDARD; PRT; 6 AA.
 AC P13736;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Contraction-inhibiting peptide I (MIP I).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Pteriomorpha; Mytiloidea;
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OX Mytiloidea; Mytilidae; Mytilus.
RN [1] NCBI_TaxID=6550;
RP SEQUENCE.
RC TISSUE=Pedal ganglion;
RX MEDLINE=88240357; PubMed=3377776;
RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
RT "Structures and actions of Mytilus inhibitory peptides.";
RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC -!- FUNCTION: Inhibitory action on contractions in several molluscan
muscles.
CC -!- SIMILARITY: To MIP II.
DR PIR; A27696; A27696.
KW Amidation; Direct protein sequencing; Hormone.
FT MOD_RES 6 Valine amide.
SQ SEQUENCE 6 AA; 637 MW; 72C9C68775B81000 CRC64;
Query Match 23.7%; Score 9; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 PL 4
Db 3 PM 4
RESULT 7
CIP2_MYTED
ID CIP2_MYTED STANDARD; PRT; 6 AA.
AC P13737;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Contraction-inhibiting peptide II (MIP II).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RC TISSUE=Pedal ganglion;
RX MEDLINE=88240357; PubMed=3377776;
RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
RT "Structures and actions of Mytilus inhibitory peptides.";
RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC -!- FUNCTION: Inhibitory action on contractions in several molluscan
muscles.
CC -!- SIMILARITY: To MIP I.
DR PIR; B27696; B27696.
KW Amidation; Direct protein sequencing; Hormone.
FT MOD_RES 6 Valine amide.
SQ SEQUENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;
Query Match 23.7%; Score 9; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 PL 4
Db 3 PM 4
RESULT 8
SAPP_SEPOF
ID SAPP_SEPOF STANDARD; PRT; 6 AA.
AC P83569;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Sperm attracting peptide SepSAP.
OS Sepia officinalis (Common cuttlefish).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
OX NCBI_TaxID=6610;
RN [1]
RP SEQUENCE, FUNCTION, DEVELOPMENTAL STAGE, MASS SPECTROMETRY, AND
RP AMIDATION.
RC TISSUE=Egg;
RX MEDLINE=22197108; PubMed=12207899; DOI=10.1016/S0006-291X(02)02036-3;
RA Zatylny C., Marvin L., Gagnon J., Henry J.;
RT "Fertilization in Sepia officinalis: the first mollusk sperm-
attracting peptide.";
RL Biochem. Biophys. Res. Commun. 296:1186-1193(2002).
CC -!- FUNCTION: Attracts sperm increasing the chances of gamete
collision.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DEVELOPMENTAL STAGE: First appears in the ovarian follicles during
vitellogenesis. Accumulates in the oocytes before being secreted
during fertilization. Expression continues in the embedded oocyte.
CC Accumulates in the egg capsule after fertilization.
CC -!- MASS SPECTROMETRY: MW=596.6; METHOD=WALDI; RANGE=1-6; NOTE=Ref.1.
KW Amidation; Direct protein sequencing.
FT MOD_RES 6 Valine amide.
SQ SEQUENCE 6 AA; 597 MW; 72C8676AA0470000 CRC64;
Query Match 23.7%; Score 9; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 PL 4
Db 1 PI 2
RESULT 9
PRCT_CARMA
ID PRCT_CARMA STANDARD; PRT; 5 AA.
AC P67857; P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Proctolin.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RX MEDLINE=86232789; PubMed=2872661; DOI=10.1016/0196-9781(86)90063-X;
RA Stangier J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
pericardial organs of the shore crab, Carcinus maenas.";
RL Peptides 7:167-72(1986).
CC -!- FUNCTION: Stimulates cardiac output and hindgut motility,
modulates visceral and skeletal muscle in many arthropods.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Found in the crab pericardial organs.
KW Direct protein sequencing; Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;
Query Match 21.1%; Score 8; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 VP 3
Db 3 LP 4
RESULT 10
PRCT_LIMPO

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ID AC P67858; P01373; STANDARD; PRT; 5 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Proctolin.
OS Limulus polyphemus (Atlantic horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Limulus.
OX NCBI_TaxID=6850;
RN [1]
RP SEQUENCE.
RX MEDLINE=50287800; PubMed=2336151; DOI=10.1016/0196-9781(90)90072-D;
RA Groome J.R., Tillinghast E.K., Towley M.A., Verovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
RT horseshoe crab, Limulus polyphemus."
RL Peptides 11:203-211(1990).
CC -!- FUNCTION: Stimulates cardiac output and hindgut motility,
CC modulates visceral and skeletal muscle in many arthropods.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Found in the crab pericardial organs.
DR PIR; A60411; A60411.
KW Direct protein sequencing; Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 21.1%; Score 8; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VP 3
DB 3 LP 4

RESULT 11
PRT_PERAM STANDARD; PRT; 5 AA.
ID AC P67859; P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Proctolin.
OS Eriplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE.
RX MEDLINE=76074708; PubMed=576; DOI=10.1016/0024-3205(75)90134-4;
RA Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
RL Life Sci. 17:1253-1256(1975).
RN [2]
RP BIOLOGICAL SOURCE.
RX MEDLINE=81225865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RL "Pentapeptide (proctolin) associated with an identified neuron."
CC -!- FUNCTION: Stimulates cardiac output and hindgut motility,
CC modulates visceral and skeletal muscle in many arthropods.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Found in the lateral white neurons.
DR PIR; A01644; HOR08A.
KW Direct protein sequencing; Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 21.1%; Score 8; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

PRT_PERAM STANDARD; PRT; 5 AA.
ID AC P67859; P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Proctolin.
OS Eriplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE.
RX MEDLINE=76074708; PubMed=576; DOI=10.1016/0024-3205(75)90134-4;
RA Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
RL Life Sci. 17:1253-1256(1975).
RN [2]
RP BIOLOGICAL SOURCE.
RX MEDLINE=81225865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RL "Pentapeptide (proctolin) associated with an identified neuron."
CC -!- FUNCTION: Stimulates cardiac output and hindgut motility,
CC modulates visceral and skeletal muscle in many arthropods.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Found in the lateral white neurons.
DR PIR; A01644; HOR08A.
KW Direct protein sequencing; Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 21.1%; Score 8; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VP 3
DB 3 LP 4

RESULT 12
TRPI_PSEPU STANDARD; PRT; 6 AA.
ID AC P36414;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE HTH-type transcriptional regulator trpI (TrpBA operon transcriptional
DE activator) (Fragment).
GN Name=trpI;
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PPG1 C15;
RX MEDLINE=89335826; PubMed=2503057; DOI=10.1016/0300-9084(89)90183-1;
RA Eberly L., Crawford I.P.;
RT "DNA sequence of the tryptophan synthase genes of Pseudomonas
RT putida."
RL Biochimie 71:521-531(1989).
CC -!- FUNCTION: Activates the expression of the trpBA genes encoding the
CC two tryptophan synthase subunits. In the absence of the inducer
CC (indoleglycerol phosphate), trpI binds upstream of the trpAB
CC operon, overlapping its own promoter region.
CC -!- SIMILARITY: Contains 1 HTH lyase-type DNA-binding domain.
CC
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CC
CC EMBL; X13299; CAA31660.1; -.
DR InterPro; IPR000847; HTH_Lyase.
DR PROSITE; PS50931; HTH_Lyase; PARTIAL.
KW Activator; DNA-binding; Transcription regulation;
KW Tryptophan biosynthesis.
FT NON_TER 6
SQ SEQUENCE 6 AA; 693 MW; 77672AA1EDD6F000 CRC64;

Query Match 21.1%; Score 8; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VP 3
DB 5 LP 6

RESULT 13
THYL_BOMOR STANDARD; PRT; 3 AA.
ID AC P62970; P01151;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Thyroliberin (Thyrotropin-releasing hormone) (TRH) (Thyrotropin
DE releasing factor) (TSH-releasing factor) (Protirelin).
OS Bombina orientalis (Oriental fire-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8346;
RN [1]
```

RP SEQUENCE.
 RC TISSUE=Skin;
 RX MEDLINE=76138399; PubMed=815011;
 RA Yasuhara T., Nakajima T.;
 RT "Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
 RL Chem. Pharm. Bull. 23:3301-3303(1975).
 CC -!- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH
 CC in the anterior pituitary gland and as a neurotransmitter/
 CC neuromodulator in the central and peripheral nervous systems (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 DR PIR: A90919; RHTDFO.
 KW Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
 FT MOD_RES 3 3 Proline amide.
 SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;

Query Match 18.4%; Score 7; DB 1; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
 |
 Db 3 P 3

RESULT 14

THYL NOTVI STANDARD; PRT; 3 AA.
 AC P62571; P01151;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE Thyrotropin (Thyrotropin releasing hormone) (TRH) (Thyrotropin
 DE releasing factor) (TSH-releasing factor) (Protirelin).
 OS Notoththalmus viridescens (Eastern newt) (Triturus viridescens).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
 CC Notoththalmus.
 CC NCBI_TaxID=8316;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Brain;
 RX MEDLINE=75035605; PubMed=4214528;
 RA Grimm-Joergensen Y., McKelvy J.F.;
 RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus
 RT viridescens) brain in vitro. Isolation and characterization of
 RT thyrotropin releasing factor.";
 RL J. Neurochem. 23:471-478(1974).
 CC -!- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH
 CC in the anterior pituitary gland and as a neurotransmitter/
 CC neuromodulator in the central and peripheral nervous systems.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 DR PIR: A92971; A92971.
 KW Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
 FT MOD_RES 3 3 Proline amide.
 SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;

Query Match 18.4%; Score 7; DB 1; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
 |
 Db 3 P 3

RESULT 15

THYL_PIG STANDARD; PRT; 3 AA.
 ID THYL_PIG
 AC P62568; P01151;
 DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Thyrotropin (Thyrotropin releasing hormone) (TRH) (Thyrotropin
 DE releasing factor) (TSH-releasing factor) (Protirelin).
 GN Name=TRH;
 OS Sus scrofa (Pig).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 CC NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hypothalamus;
 RX MEDLINE=70136150; PubMed=4984938;
 RA Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;
 RT "Structure of porcine thyrotropin releasing hormone.";
 RL Biochemistry 9:1103-1106(1970).
 RN [2]
 RP SYNTHESIS.
 RX MEDLINE=70039904; PubMed=4982117;
 RA Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;
 RT "The identity of chemical and hormonal properties of the thyrotropin
 RT releasing hormone and pyroglutamy1-histidyl-proline amide.";
 RL Biochem. Biophys. Res. Commun. 37:705-710(1969).
 CC -!- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH
 CC in the anterior pituitary gland and as a neurotransmitter/
 CC neuromodulator in the central and peripheral nervous systems.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 KW Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
 FT MOD_RES 3 3 Proline amide.
 SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;

Query Match 18.4%; Score 7; DB 1; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
 |
 Db 3 P 3

Search completed: April 1, 2005, 11:53:29
 Job time : 115 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 11:39:44 ; Search time 117 Seconds
(without alignments)
19.834 Million cell updates/sec

Title: US-09-761-636A-12

Perfect score: 38

Sequence: 1 CVPLTC 6

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 78325

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A. Geneseq 16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	6	AAU04531	VEGF base
2	26	68.4	6	AAY61488	Cadherin-
3	25	65.8	6	AAY62223	Cadherin-
4	25	65.8	6	AAY62763	PB-cadher
5	25	65.8	6	AAY62006	Cadherin-
6	25	65.8	6	ADK83244	191P4D12(
7	24	63.2	6	AAY64259	Cadherin-
8	23	60.5	6	AAY65373	IL-2 deri
9	23	60.5	6	AAY62757	PB-cadher
10	23	60.5	6	AAY62488	Cadherin-
11	23	60.5	6	AAY44431	Peptide 1
12	22	57.9	4	AAR15772	Farnesyl-
13	22	57.9	4	AAR49769	Farnesyl-
14	22	57.9	4	AAR77833	Farnesyl
15	22	57.9	4	AAR04459	Farnesyl
16	22	57.9	5	AAW67428	HCV pepti
17	22	57.9	6	AAW31456	Transcrip
18	22	57.9	6	AAV63235	Protocadh
19	22	57.9	6	AAV61927	Cadherin-
20	21	55.3	6	AAV62132	Cadherin-
21	21	55.3	6	AAV63263	Protocadh
22	21	55.3	6	ADP06886	Cell adhe
23	20	52.6	4	AAR51652	Osteogeni
24	20	52.6	4	ADK42191	Antibacte
25	20	52.6	5	AAR08270	Peptide 1

26	20	52.6	5	2	AAR78749	Aar78749 Glycosyla
27	20	52.6	5	3	AAY69213	Aay69213 Peptide f
28	20	52.6	5	3	AAY56095	Aay56095 Glycohaem
29	20	52.6	5	3	AAY68185	Aay68185 Haemoglob
30	20	52.6	5	4	AAG78351	Aag78351 Haemoglob
31	20	52.6	5	5	ABB63467	Abb63467 Tissue in
32	20	52.6	5	5	AAO17897	Aao17897 Norwalk v
33	20	52.6	5	5	ABB77196	Abb77196 Haemoglob
34	20	52.6	5	5	ABB77197	Abb77197 Haemoglob
35	20	52.6	5	7	ADG46811	Adg46811 A0 peptid
36	20	52.6	5	7	ADG46813	Adg46813 A0 peptid
37	20	52.6	5	7	ADM08233	Adm08233 Canine im
38	20	52.6	5	7	ADM08205	Adm08205 Canine im
39	20	52.6	6	2	AAW08703	Aaw08703 Honeybee
40	20	52.6	6	2	AAW95842	Aaw95842 IGF-1 mut
41	20	52.6	6	2	AAW11026	Aaw11026 Immunomod
42	20	52.6	6	2	AAW44954	Aaw44954 Immunomod
43	20	52.6	6	2	AAW51950	Aaw51950 Peptide h
44	20	52.6	6	2	AAW09380	Aaw09380 Immunoact
45	20	52.6	6	2	AAW89219	Aaw89219 Tumour ne

ALIGNMENTS

RESULT 1
AAU04531
ID AAU04531 standard; peptide; 6 AA.
XX
AC AAU04531;
XX
DT 26-SEP-2001 (first entry)
XX
DE VEGF based monocyclic peptide 9.
XX
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; peoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..6 /note= "This bond cyclises the peptide"
XX
PN WO200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX
(LUDW-) LUDWIG INST CANCER RES.
XX
PI Achen MG, Hughes RA, Stackner S, Cendron A;
XX
DR WPI; 2001-442248/47.
XX
PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
from an exposed loop of a growth factor protein by oxidizing the cysteine
residues.
XX
PS Claim 49; Page 32; 102pp; English.
XX
CC The sequence represents a monomeric monocyclic peptide of the invention,
whose 3-dimensional structure is modelled on the expose loop of human
VEGPD (vascular endothelial growth factor). The invention relates to a
method of producing a monomeric monocyclic peptide by a measuring beta-
beta carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 38; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6
 Db 1 CVPLTC 6

RESULT 2

AAV61488
 ID AAY61488 standard; peptide; 6 AA.

XX
 AC AAY61488;

DT 02-MAR-2000 (first entry)

XX Cadherin-7 cell adhesion recognition cyclic peptide SEQ ID NO:1374.

XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.

XX Synthetic.
 OS Homo sapiens.

XX Key Location/Qualifiers
 FT Disulfide-bond 1..6

XX WO9957149-A2.

XX 11-NOV-1999.

XX 05-MAY-1999; 99WO-CA000363.

XX 05-MAY-1998; 98US-00073040.

PR 06-NOV-1998; 98US-00187859.

PR 20-JAN-1999; 99US-00234395.

PR 08-MAR-1999; 99US-00264516.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OW, Gour BJ, Byers S;

XX

DR WPI; 2000-038791/03.

XX New cadherin modulating agents, used for modulating nonclassical cadherin
 PT mediated functions for treating e.g. cancers, obesity, rheumatoid
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.

XX Claim 36; Page 172; 252pp; English.

XX The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MAs can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 CC related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AAY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
 CC the exemplification of the present invention

XX Sequence 6 AA;

Query Match 68.4%; Score 26; DB 3; Length 6;

Best Local Similarity 66.7%; Pred. No. 1.8e+06;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6

Db 1 CEPKTC 6

RESULT 3

AAV62223
 ID AAY62223 standard; peptide; 6 AA.

XX
 AC AAY62223;

XX 02-MAR-2000 (first entry)

XX Cadherin-14 cell adhesion recognition cyclic peptide SEQ ID NO:3970.

XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers
 FT Disulfide-bond 1..6

XX WO9957149-A2.

XX 11-NOV-1999.

XX

```
PF 05-MAY-1999; 99WO-CA000363.
XX
PR 05-MAY-1998; 98US-00073040.
PR 06-NOV-1998; 98US-00187859.
PR 20-JAN-1999; 99US-00234395.
PR 08-MAR-1999; 99US-00264516.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuk OW, Gour BJ, Byers S;
XX
DR WPI; 2000-038791/03.
XX
PT New cadherin modulating agents, used for modulating nonclassical cadherin
PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
PT arthritis, multiple sclerosis, diabetes or a neurological disease.
XX
PS Claim 54; Page 184; 252pp; English.
XX
CC The present invention describes cadherin modulating agents (MA)
CC comprising peptides which comprise a nonclassical cadherin cell adhesion
CC recognition (CAR) sequence. The MAs can be used for modulating
CC nonclassical cadherin-mediated functions. They can be used for e.g.
CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
CC mammal, enhancing delivery of a drug through the skin of a mammal,
CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
CC expressing cell, preventing or treating obesity in a mammal, stimulating
CC blood vessel regression in a mammal, enhancing drug delivery to the
CC central nervous system, treating a demyelinating neurological disease,
CC increasing vasopermeability in a mammal, enhancing adhesion of
CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
CC a mammal, or preventing pregnancy in a mammal. They can also be used for
CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
CC -related macular degeneration, multiple sclerosis and diabetes. The
CC products can also be used for detection and diagnosis and in bioreactors.
CC AAY60592 to AAY64572 represent specifically claimed peptides, and
CC AAY64573 to AAY64643 and AA233183 to AA233186 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 6 AA;
Query Match 65.8%; Score 25; DB 3; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CVPLTC 6
DB 1 CDPKTC 6
RESULT 4
AAY62763
ID AAY62763 standard; peptide; 6 AA.
XX
AC AAY62763;
XX
DT 02-MAR-2000 (first entry)
XX
DE PB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:4046.
XX
KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
KW inhibition; cadherin extracellular domain; cell adhesion recognition;
KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
KW cadherin related neuronal receptor; Li-cadherin; protocadherin;
KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
KW neurological disease; cyclic.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..6
XX
PN WO9957149-A2.
XX
PD 11-NOV-1999.
XX
PF 05-MAY-1999; 99WO-CA000363.
XX
PR 05-MAY-1998; 98US-00073040.
PR 06-NOV-1998; 98US-00187859.
PR 20-JAN-1999; 99US-00234395.
PR 08-MAR-1999; 99US-00264516.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuk OW, Gour BJ, Byers S;
XX
DR WPI; 2000-038791/03.
XX
PT New cadherin modulating agents, used for modulating nonclassical cadherin
PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
PT arthritis, multiple sclerosis, diabetes or a neurological disease.
XX
PS Claim 72; Page 193; 252pp; English.
XX
CC The present invention describes cadherin modulating agents (MA)
CC comprising peptides which comprise a nonclassical cadherin cell adhesion
CC recognition (CAR) sequence. The MAs can be used for modulating
CC nonclassical cadherin-mediated functions. They can be used for e.g.
CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
CC mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer in
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
CC expressing cell, preventing or treating obesity in a mammal, stimulating
CC blood vessel regression in a mammal, enhancing drug delivery to the
CC central nervous system, treating a demyelinating neurological disease,
CC increasing vasopermeability in a mammal, enhancing adhesion of
CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
CC a mammal, or preventing pregnancy in a mammal. They can also be used for
CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
CC -related macular degeneration, multiple sclerosis and diabetes. The
CC products can also be used for detection and diagnosis and in bioreactors.
CC AAY60592 to AAY64572 represent specifically claimed peptides, and
CC AAY64573 to AAY64643 and AA233183 to AA233186 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 6 AA;
Query Match 65.8%; Score 25; DB 3; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CVPLTC 6
DB 1 CDPKTC 6
RESULT 5
AAY62006
ID AAY62006 standard; peptide; 6 AA.
XX
AC AAY62006;
XX
DT 02-MAR-2000 (first entry)
XX
DE Cadherin-12 cell adhesion recognition cyclic peptide SEQ ID NO:1798.
```

XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
KW inhibition; cadherin extracellular domain; cell adhesion recognition;
KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
KW cadherin related neuronal receptor; Li-cadherin; protocadherin;
KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
KW neurological disease; cyclic.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..6
PN WO957149-A2.
XX
XX 11-NOV-1999.
PD
XX 05-MAY-1999; 99WO-CA000363.
PF
XX 05-MAY-1998; 98US-00073040.
PR 06-NOV-1998; 98US-00187859.
PR 20-JAN-1999; 99US-00234395.
PR 08-MAR-1999; 99US-00264516.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuk OW, Gour BJ, Byers S;
PI WPI; 2000-038791/03.
XX
XX New cadherin modulating agents, used for modulating nonclassical cadherin
PT mediated functions for treating e.g. cancers, obesity, rheumatoid
PT arthritis, multiple sclerosis, diabetes or a neurological disease.
XX
XX Claim 49; Page 180; 252pp; English.
PS
XX The present invention describes cadherin modulating agents (MA)
CC comprising peptides which comprise a nonclassical cadherin cell adhesion
CC recognition (CAR) sequence. The MA can be used for modulating
CC nonclassical cadherin-mediated functions. They can be used for e.g.
CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
CC mammal, enhancing delivery of a drug through the skin of a mammal,
CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
CC expressing cell, preventing or treating obesity in a mammal, stimulating
CC blood vessel regression in a mammal, enhancing drug delivery to the
CC central nervous system, treating a demyelinating neurological disease,
CC increasing vasopermeability in a mammal, enhancing adhesion of
CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
CC a mammal, or preventing pregnancy in a mammal. They can also be used for
CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
CC -related macular degeneration, multiple sclerosis and diabetes. The
CC products can also be used for detection and diagnosis and in bioreactors.
CC AAY60592 to AAY64572 represent specifically claimed peptides, and
CC AAY64573 to AAY64643 and AAY63183 to AAY63186 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 6 AA;

Query Match 65.8%; Score 25; DB 3; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CVPLTC 6
Db 1 CDPKTC 6

RESULT 6
ADK83244
ID ADK83244 standard; peptide; 6 AA.
XX
AC ADK83244;
XX
DT 20-MAY-2004 (first entry)
XX
DE 191P4D12(b) N-myristoylation site, SEQ ID 75.
XX
KW Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer;
KW prostate cancer; bladder cancer; kidney cancer; colon cancer;
KW lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer;
KW cervix cancer; immune response; human; chromosome 1q22-q23.2;
KW Suppression Subtractive Hybridisation; SSH.
XX
OS Homo sapiens.
XX
PN WO2004016799-A2.
XX
PD 26-FEB-2004.
XX
PF 23-APR-2003; 2003WO-US013013.
XX
PR 16-AUG-2002; 2002US-0404306P.
PR 01-NOV-2002; 2002US-0423290P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Raitano AB, Challita-Eid PM, Jakobovits A, Faris M, Ge W;
XX WPI; 2004-203808/19.
XX
PT New composition comprising 191P4D12(b) proteins and polynucleotides,
PT useful in diagnosing, preventing and treating cancer, e.g. prostate,
PT bladder, kidney, colon, lung, pancreas or ovary and in eliciting a
PT humoral or cellular immune response.
XX
PS Example 46; SEQ ID NO 75; 443pp; English.
XX
CC The present invention relates to novel compositions comprising peptides
CC (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found
CC that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly
CC expressed in a number of cancers and so the compositions of the invention
CC are useful in diagnosing, preventing and treating cancer, e.g. cancer of
CC the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast,
CC uterus or cervix and in eliciting a humoral or cellular immune response.
CC To isolate genes that are overexpressed in prostate cancer, the
CC Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
CC derived from prostate cancer tissues. The present peptide is the N-
CC myristoylation site sequence present at position 218-223 in human
CC 191P4D12(b).
XX
SQ Sequence 6 AA;
Query Match 65.8%; Score 25; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PLTC 6
Db 3 PLTC 6

RESULT 7
AAY64259
ID AAY64259 standard; peptide; 6 AA.
XX
AC AAY64259;
XX
DT 02-MAR-2000 (first entry)
XX

DE Cadherin-related neuronal receptor CAR cyclic peptide SEQ ID NO:3573.

XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;

XX inhibition; cadherin extracellular domain; cell adhesion recognition;

KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;

KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;

KW cadherin related neuronal receptor; LI-cadherin; protocadherin;

KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;

KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;

KW neurological disease; cyclic.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Disulfide-bond 1..6

XX WO9957149-A2.

PN 11-NOV-1999.

XX 05-MAY-1999; 99WO-CA000363.

XX 05-MAY-1998; 98US-00073040.

PR 06-NOV-1998; 98US-00187859.

PR 20-JAN-1999; 99US-00234395.

PR 08-MAR-1999; 99US-00264516.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OW, Gour BJ, Byers S;

XX WPI; 2000-038791/03.

DR New cadherin modulating agents, used for modulating nonclassical cadherin

PT mediated functions for treating e.g. cancers, obesity, rheumatoid

PT arthritis, multiple sclerosis, diabetes or a neurological disease.

XX Claim 102; Page 217; 252pp; English.

XX The present invention describes cadherin modulating agents (MA)

CC comprising peptides which comprise a nonclassical cadherin cell adhesion

CC recognition (CAR) sequence. The MA can be used for modulating

CC nonclassical cadherin-mediated functions. They can be used for e.g.

CC inhibiting adhesion of nonclassical-cadherin expressing cells in a

CC mammal, enhancing delivery of a drug through the skin of a mammal,

CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in

CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting

CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-

CC expressing cell, preventing or treating obesity in a mammal, stimulating

CC blood vessel regression in a mammal, enhancing drug delivery to the

CC central nervous system, treating a demyelinating neurological disease,

CC increasing vasopermeability in a mammal, enhancing adhesion of

CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in

CC a mammal, or preventing pregnancy in a mammal. They can also be used for

CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing

CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a

CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age

CC -related macular degeneration, multiple sclerosis and diabetes. The

CC products can also be used for detection and diagnosis and in bioreactors.

CC AAY60592 to AAY64572 represent specifically claimed peptides, and

CC AAY64573 to AAY64643 and AAY23183 to AAY23186 represent sequences used in

CC the exemplification of the present invention

XX Sequence 6 AA;

XX Query Match 63.2%; Score 24; DB 3; Length 6;

XX Best Local Similarity 50.0%; Pred. No. 1.8e+06;

XX Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTC 6

DB 1 CDPVSC 6

RESULT 9

AAY62757

ID AAY62757 standard; peptide; 6 AA.

XX

RESULT 8

AAY85373

ID AAY85373 standard; peptide; 6 AA.

XX

AC AAY85373;

XX

DT 19-JUN-2000 (first entry)

XX

DE IL-2 derived anti-inflammatory peptide pep11.

XX

KW Interleukin-2; IL-2; antiinflammatory; antiarthritic; antirheumatic;

KW antidiabetic; neuroprotective; dermatological; immunosuppressive;

KW ophthalmological; autoimmune disease; multiple sclerosis; uveitis;

KW systemic lupus erythematosus; Crohn's disease.

XX Synthetic.

OS Homo sapiens.

XX WO200011028-A2.

PN 02-MAR-2000.

XX

PD 19-AUG-1999; 99WO-IL000448.

XX

PR 21-AUG-1998; 98GB-00018370.

PR 31-AUG-1998; 98IL-00126009.

PR 16-MAY-1999; 99IL-00129980.

XX (YEDA) YEDA RES & DEV CO LTD.

XX

PI Lider O, Ariel A, Hershkoviz R, Yavin EJ, Fridkin M;

XX WPI; 2000-256367/22.

DR Synthetic antiinflammatory peptide derived from IL-2 and its derivatives

PT useful for treating inflammatory autoimmune diseases such as rheumatoid

PT arthritis, multiple sclerosis and systemic lupus erythematosus.

XX Claim 6; Page 35; 49pp; English.

XX The invention provides synthetic antiinflammatory peptides derived from

CC interleukin-2 (IL-2). They can be used for inhibition of adhesion of

CC activated T-cells to ECM proteins such as fibronectin, laminin, collagen

CC type-IV; inhibition of chemotactic migration of T-cell through ECM

CC proteins preferably fibronectin; inhibition of cytokine or mitogen

CC induced T-cell proliferation; inhibition of spontaneous or induced,

CC preferably TNF-alpha induced cytokine secretion (e.g. IL-8, IL-1beta) by

CC stimulated T-cells and intestinal epithelial cells. The anti-inflammatory

CC peptides and their derivatives are useful for preparing compositions for

CC treating and/or alleviating chronic or acute inflammatory disorders and

CC autoimmune diseases such as rheumatoid arthritis, diabetes type-1,

CC multiple sclerosis, systemic lupus erythematosus, bowel inflammation,

CC uveitis, and Crohn's disease. Sequences AAY85366-374 represent modified

CC anti-inflammatory derivative peptides derived from the IL-2 derived anti-

CC inflammatory peptide pep1 (AAY85363)

XX Sequence 6 AA;

XX Query Match 60.5%; Score 23; DB 3; Length 6;

XX Best Local Similarity 50.0%; Pred. No. 1.8e+06;

XX Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6

DB 1 CIVLAC 6

RESULT 9

AAY62757

ID AAY62757 standard; peptide; 6 AA.

XX

AC	AAV622757;	
XX		
DT	02-MAR-2000	(first entry)
XX		
DE	PB-cadherin	cell adhesion recognition cyclic peptide SEQ ID NO:4040.
XX		
KW	Modulation;	nonclassical cadherin mediated cell adhesion; CAR;
KW	inhibition;	cadherin extracellular domain; cell adhesion recognition;
KW	OB-cadherin;	cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
KW	cadherin-14;	cadherin-15; T-cadherin; PB-cadherin;
KW	cadherin related	neuronal receptor; II-cadherin; protocadherin;
KW	desmoglein;	desmocollin; calcium binding; cancer; tumour; obesity;
KW	rheumatoid arthritis;	multiple sclerosis; diabetes; metastasis;
KW	neurological disease;	cyclic.
XX		
OS	Synthetic.	
OS	Homo sapiens.	
XX		
EH	Key	Location/Qualifiers
FT	Disulfide-bond	1..6
XX		
FN	W09957149-A2.	
XX		
PD	11-NOV-1999.	
XX		
PF	05-MAY-1999;	99WO-CA000363.
XX		
PR	05-MAY-1998;	98US-00073040.
PR	06-NOV-1998;	98US-00187859.
PR	20-JAN-1999;	99US-00234395.
PR	08-MAR-1999;	99US-00264516.
XX		
PA	(ADHE-) ADHEREX TECHNOLOGIES INC.	
XX		
PI	Blaschuk OW,	Gour BJ, Byers S;
XX		
DR	WPI;	2000-038791/03.
XX		
PT	New cadherin	modulating agents, used for modulating nonclassical cadherin
PT	-mediated functions	for treating e.g. cancers, obesity, rheumatoid
PT	arthritis,	multiple sclerosis, diabetes or a neurological disease.
XX		
PS	Claim 72;	Page 193; 252pp; English.
XX		
CC	The present invention	describes cadherin modulating agents (MA)
CC	comprising peptides	which comprise a nonclassical cadherin cell adhesion
CC	recognition (CAR) sequence.	The MAs can be used for modulating
CC	nonclassical cadherin-mediated functions.	They can be used for e.g.
CC	inhibiting adhesion	of nonclassical-cadherin expressing cells in a
CC	mammal, enhancing	delivery of a drug through the skin of a mammal,
CC	enhancing delivery	of a drug to a tumour in a mammal, treating cancer in
CC	a mammal, inhibiting	metastasis of a cancer in a mammal, inhibiting
CC	angiogenesis in a mammal,	inducing apoptosis in a nonclassical cadherin-
CC	expressing cell, preventing	or treating obesity in a mammal, stimulating
CC	blood vessel regression	in a mammal, enhancing drug delivery to the
CC	central nervous system,	treating a demyelinating neurological disease,
CC	increasing vasopermeability	in a mammal, enhancing adhesion of
CC	nonclassical cadherin-expressing cells,	inhibiting synaptic stability in
CC	a mammal, or preventing	pregnancy in a mammal. They can also be used for
CC	e.g. enhancing or directing	neurite outgrowth, facilitating wound healing
CC	or reducing scar tissue,	or enhancing adhesion of foreign tissue in a
CC	mammal. They can also	be used for treating e.g. psoriasis, arthritis, age
CC	-related macular degeneration,	multiple sclerosis and diabetes. The
CC	products can also be used	for detection and diagnosis and in bioreactors.
CC	AAV60592 to AAV64572	represent specifically claimed peptides, and
CC	AAV64573 to AAV64643	and AAZ33183 to AAZ33186 represent sequences used in
CC	the exemplification	of the present invention
XX		
SQ	Sequence 6 AA;	
	Query Match	60.5%; Score 23; DB 3; Length 6;
	Best Local Similarity	66.7%; Pred. No. 1.8e+06;
	Matches 4; Conservative	0; Mismatches 2; Indels 0; Gaps 0;

CC products can also be used for detection and diagnosis and in bioreactors.
CC AAY60592 to AAY64572 represent specifically claimed peptides, and
CC AAY64573 to AAY64643 and AA233183 to AA233186 represent sequences used in
CC the exemplification of the present invention

XX SQ Sequence 6 AA;

Query Match 60.5%; Score 23; DB 3; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CVPLTC 6
| | | |
DB 1 CDELTC 6

RESULT 11
ID AAY4431
AAAY4431 standard; peptide; 6 AA.

XX AC AAY44431;

XX DT 22-MAR-2000 (first entry)

XX DE Peptide 1 derived from domain 1 of human beta-2 glycoprotein I.

XX KW Human beta-2 glycoprotein I; beta-2 GPI; toleragen; B cell anergy;
KW beta-2 GPI-dependent antiphospholipid antibody; thrombosis;
KW recurrent foetal loss; thrombocytopenia; autoimmune disease;
KW systemic lupus erythematosus; coagulation assay.

XX OS Homo sapiens.

XX PN WO9964595-A1.

XX PD 16-DEC-1999.

XX PF 09-JUN-1999; 99WO-US013194.

XX PR 09-JUN-1998; 98US-0088656P.

XX PR 05-OCT-1998; 98US-0103088P.

XX PR 08-JUN-1999; 99US-00328199.

XX PA (LJOL-) LA JOLLA PHARM CO.

XX PI Marquis DM, Iverson GM, Victoria EJ, Jones DS, Linnik MD;

XX DR WPI; 2000-116542/10.

XX PT New isolated domain 1 beta-2 GPI polypeptides, used for inhibiting

XX PT antiphospholipid antibodies for treating, e.g. thrombosis.

XX PS Claim 3; Page 19; 158pp; English.

XX CC The present sequence is a peptide fragment derived from domain 1 of human
CC beta-2 glycoprotein, a phospholipid binding serum protein. Isolated
CC domain 1 of beta-2 GPI protein binds to and inhibits beta-2 GPI-dependent
CC antiphospholipid antibodies. The fragments are useful as toleragens when
CC they bind to the antibodies at the surface of a B cell and triggers B
CC cell anergy. The polypeptides and mimetics can be used for treating
CC disorders associated with beta-2GPI-dependent aPL-associated pathologies,
CC e.g. thrombosis, recurrent foetal loss, thrombocytopenia or autoimmune
CC diseases such as systemic lupus erythematosus. The polypeptides can also
CC be used to detect and purify antibodies. They can also be used in
CC coagulation assays

XX SQ Sequence 6 AA;

Query Match 60.5%; Score 23; DB 3; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CVPLTC 6

DB 1 CTPRVC 6

RESULT 12

AAAR15772
ID AAR15772 standard; protein; 4 AA.

XX AC AAR15772;

XX DT 25-MAR-2003 (revised)

XX DT 09-JAN-2003 (revised)

XX DT 29-JAN-1992 (first entry)

XX DE Farnesyl-protein transferase inhibitor (25).

XX KW Farnesyl; transferase; FT; inhibitor; p21ras; rat.

XX OS Synthetic.

XX PN WO9116340-A.

XX PD 31-OCT-1991.

XX PF 18-APR-1990; 90US-00510706.

XX PR 18-APR-1990; 90US-00510706.

XX PR 20-NOV-1990; 90US-00615715.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Brown MS, Goldstein JL, Reiss Y;

XX DR WPI; 1991-339750/46.

XX PT Compn. comprising purified farnesyl-protein transferase - used to

XX PT inhibit attachment of farnesyl moiety to RAS protein in malignant cells

XX PS Claim 25; Page 68; 87pp; English.

XX CC This peptide or the peptides represented in AAR15751-81, AAR14723 and
XX AAR14711 inhibit the rat Fts represented in AAR14712-22. They show FT
XX inhibition at an IC50 of 0.01-10 microm. The most potent inhibitors are
XX ones in which phenylalanine occurs at the third position of a
XX tetrapeptide whose N-terminus is cysteine. The inhibitors have a farnesyl
XX acceptor or inhibitor sequence within its structure and are capable of
XX inhibiting the farnesylation of p21ras by FT. See also AAR14711-23 and
XX AAQ14541-47. (Updated on 09-JAN-2003 to add missing OS field.) (Updated
XX on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 4 AA;

Query Match 57.9%; Score 22; DB 2; Length 4;

Best Local Similarity 75.0%; Pred. No. 1.8e+06;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CVPL 4

DB 1 CVPM 4

RESULT 13

AAAR49769
ID AAR49769 standard; peptide; 4 AA.

XX AC AAR49769;

XX DT 25-MAR-2003 (revised)

XX DT 08-AUG-1994 (first entry)

XX DE Farnesyltransferase-inhibitor.

KW Farnesyltransferase-inhibitor; farnesyltransferase; FT; p21ras;
 KW ras protein; farnesylation; cancer therapy.
 XX Synthetic.

XX WO9404561-A1.
 XX PN
 XX 03-MAR-1994.

PD 24-AUG-1993; 93WO-US08062.
 XX PF
 XX 24-AUG-1992; 92US-00935087.

XX PR
 XX 24-AUG-1992; 92US-00935087.
 XX (TEXA) UNIV TEXAS SYSTEM.

PA (GETH) GENENTECH INC.
 XX PA
 XX PI Brown MS, Goldstein JL, Reiss Y, Marsters JC;

XX WPI; 1994-083105/10.

XX New farnesyl-transferase inhibitors - used for inhibiting attachment of a
 PT farnesyl moiety to a p21ras protein in malignant cells.

XX Disclosures; Page 33; 183pp; English.

XX Peptides given in AAR49741-75, AAR49777-78 and AAR49785-88, which include
 CC a family of tetrapeptides based on the recognition site (AAR49776) of
 CC farnesyltransferase (FT), are potential anticancer agents that inhibit
 CC FT, thereby preventing expression of p21ras. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX correct PN field.)

XX Sequence 4 AA;

Query Match 57.9%; Score 22; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CVPL 4
 DB 1 CVPM 4

RESULT 14

AAR77833
 ID AAR77833 standard; protein; 4 AA.

XX AC

XX AAR77833;

XX 25-MAR-2003 (revised)

DT 23-JAN-1996 (first entry)

XX Farnesyl transferase inhibitor tetrapeptide, CVPM.

XX Farnesyl transferase; inhibitor; cancer; ras; p21.

XX Synthetic.

XX US5420245-A.

XX 30-MAY-1995.

XX 03-APR-1992; 92US-00863169.

XX 18-APR-1990; 90US-00510706.

XX 20-NOV-1990; 90US-00615715.

XX 16-JAN-1992; 92US-00822011.

XX (TEXA) UNIV TEXAS.

XX Reiss Y, Goldstein JL, Brown MS;

XX WPI; 1995-206308/27.

XX

PT New farnesyl transferase inhibitor peptide(s) - based on farnesyl
 PT acceptor substrate carboxy terminal sequences, used for the treatment of
 PT cancer.
 XX

PS Claim 2; Col 62; 55pp; English.

XX AAR77800, AAR77805-R77838 are tetrapeptide inhibitors of farnesyl
 CC transferase. They all obey a generic formula for the C-terminal sequence
 CC of 4-10 amino acid inhibitory peptides; the formula is -CAAX, where C=
 CC cysteine, A= any aliphatic, aromatic or hydroxy amino acid and X= any
 CC normal amino acid. Farnesyl transferase is involved in the farnesylation
 CC of various cellular proteins including the cancer related ras proteins.
 CC The transforming activity of ras is dependent on the localisation of the
 CC protein to membranes, a property which is thought to be dependent upon
 CC the addition of farnesyl groups. The peptide inhibitors are useful for
 CC treating cancers and ras-related cancers in particular. (Updated on 25-
 CC MAR-2003 to correct PF field.)
 XX

XX Sequence 4 AA;

Query Match 57.9%; Score 22; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CVPL 4
 DB 1 CVPM 4

RESULT 15

AAW04459

ID AAW04459 standard; peptide; 4 AA.

XX AC

XX AAW04459;

XX 30-JUL-1997 (first entry)

XX Farnesyl transferase peptide inhibitor used in cancer treatment.

XX Farnesyl transferase; inhibitor; cancer; tumour; neoplasia; prenyl;

XX ras protein; K-ras B; malignant; detection; identification.

XX Synthetic.

XX WO9634113-A2.

XX 31-OCT-1996.

XX 29-APR-1996; 96WO-US005969.

XX 27-APR-1995; 95US-00429964.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Brown MS, Goldstein JL, James GL;

XX WPI; 1996-497642/49.

XX Assay for farnesyl transferase activity - by determining ability to
 PT transfer farnesyl moiety to K-Ras B protein, partic. useful for
 PT identifying inhibitors.

XX Disclosures; Page 34; 257pp; English.

XX AAW04433-W04465 are peptide inhibitors of farnesyl transferase (FT)
 CC activity. The peptides block the attachment of prenyl groups to ras
 CC proteins in malignant cells of patients suffering from cancer or a
 CC precancerous state and as such are used to treat cancer. The peptides
 CC were identified by determining the ability of candidate substances to
 CC inhibit a FT enzyme, by inhibiting the transfer of a farnesyl moiety to a
 CC K-RasB protein
 XX

XX Sequence 4 AA;

Query Match 57.9%; Score 22; DB 2; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CVPL 4
Db 1 CVPM 4

Search completed: April 1, 2005, 11:51:23
Job time : 118, secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 11:53:35 ; Search time 92 Seconds
(without alignments)
21.626 Million cell updates/sec

Title: US-09-761-636A-12

Perfect score: 38
Sequence: 1 CVPLTC 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 35400

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	38	100.0	6	9	US-09-761-636A-12
2	26	68.4	6	14	US-10-006-869-1374
3	26	68.4	6	15	US-10-395-032-1374
4	25	65.8	6	14	US-10-006-869-1798
5	25	65.8	6	14	US-10-006-869-3970
6	25	65.8	6	14	US-10-006-869-4046
7	25	65.8	6	15	US-10-395-032-1798
8	25	65.8	6	15	US-10-395-032-1798
9	25	65.8	6	15	US-10-395-032-1798
10	25	65.8	6	15	US-10-422-571-75
11	24	63.2	6	14	US-10-006-869-3573
12	24	63.2	6	15	US-10-395-032-3573
13	23	60.5	6	14	US-10-006-869-2154

14	23	60.5	6	14	US-10-006-869-4040	Sequence 4040, Ap
15	23	60.5	6	15	US-10-395-032-2154	Sequence 2154, Ap
16	23	60.5	6	15	US-10-395-032-4040	Sequence 4040, Ap
17	23	60.5	6	16	US-10-003-058-5	Sequence 5, Appl
18	22	57.9	4	14	US-10-083-894-35	Sequence 35, Appl
19	22	57.9	6	11	US-09-943-944E-103	Sequence 103, App
20	22	57.9	6	14	US-10-006-869-1737	Sequence 1737, Ap
21	22	57.9	6	14	US-10-006-869-2719	Sequence 2719, Ap
22	22	57.9	6	15	US-10-395-032-1737	Sequence 1737, Ap
23	22	57.9	6	15	US-10-395-032-2719	Sequence 2719, Ap
24	21	55.3	6	9	US-09-911-838-184	Sequence 184, App
25	21	55.3	6	9	US-09-911-838-186	Sequence 186, App
26	21	55.3	6	10	US-09-792-286-222	Sequence 222, App
27	21	55.3	6	10	US-09-792-286-226	Sequence 226, App
28	21	55.3	6	10	US-09-792-286-278	Sequence 278, App
29	21	55.3	6	14	US-10-006-869-1885	Sequence 1885, Ap
30	21	55.3	6	14	US-10-006-869-2747	Sequence 2747, Ap
31	21	55.3	6	14	US-10-058-513-9	Sequence 9, Appl
32	21	55.3	6	15	US-10-395-032-1885	Sequence 1885, Ap
33	21	55.3	6	15	US-10-395-032-2747	Sequence 2747, Ap
34	21	55.3	6	16	US-10-714-564A-1063	Sequence 1063, Ap
35	20	52.6	5	10	US-09-753-139C-8	Sequence 8, Appl
36	20	52.6	5	15	US-10-416-797-16	Sequence 16, Appl
37	20	52.6	5	15	US-10-327-598-239	Sequence 239, App
38	20	52.6	6	9	US-09-911-838-90	Sequence 90, Appl
39	20	52.6	6	9	US-09-911-838-92	Sequence 92, Appl
40	20	52.6	6	9	US-09-911-838-94	Sequence 94, Appl
41	20	52.6	6	9	US-09-911-838-96	Sequence 96, Appl
42	20	52.6	6	10	US-09-935-430-697	Sequence 697, App
43	20	52.6	6	14	US-10-006-869-1591	Sequence 1591, Ap
44	20	52.6	6	14	US-10-271-343-52	Sequence 52, Appl
45	20	52.6	6	14	US-10-436-826-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-09-761-636A-12
; Sequence 12, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR FILING DATE: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-12

Query Match 100.0%; Score 38; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 1 CVPLTC 6

RESULT 2
US-10-006-869-1374

; Sequence 1374, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1374
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
US-10-006-869-1374

Query Match 68.4%; Score 26; DB 14; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
| | | |
Db 1 CEPKTC 6

RESULT 3
US-10-395-032-1374
; Sequence 1374, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1374
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
US-10-395-032-1374

Query Match 68.4%; Score 26; DB 15; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
| | | |
Db 1 CEPKTC 6

RESULT 4
US-10-006-869-1798
; Sequence 1798, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1798
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence
US-10-006-869-1798

Query Match 65.8%; Score 25; DB 14; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
| | | |
Db 1 CDPKTC 6

RESULT 5
US-10-006-869-3970
; Sequence 3970, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3970
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-14 cell adhesion recognition sequence
US-10-006-869-3970

Query Match 65.8%; Score 25; DB 14; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
| | | |
Db 1 CDPKTC 6

RESULT 6
US-10-006-869-4046
; Sequence 4046, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4046


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; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-10-006-869-4046

Query Match          65.8%; Score 25; DB 14; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
   ||||
Db 1 CDPKTC 6

RESULT 7
US-10-395-032-1798
; Sequence 1798, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1798
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence
US-10-395-032-1798

Query Match          65.8%; Score 25; DB 15; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
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Db 1 CDPKTC 6

RESULT 8
US-10-395-032-3970
; Sequence 3970, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3970
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-14 cell adhesion recognition sequence
US-10-395-032-3970
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Query Match          65.8%; Score 25; DB 15; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
   ||||
Db 1 CDPKTC 6

RESULT 9
US-10-395-032-4046
; Sequence 4046, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4046
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-10-395-032-4046
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Query Match          65.8%; Score 25; DB 15; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTC 6
   ||||
Db 1 CDPKTC 6

RESULT 10
US-10-422-571-75
; Sequence 75, Application US/10422571
; Publication No. US20040083497A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Paris, Mary
; APPLICANT: Ge, Wangmao
; TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
; TITLE OF INVENTION: Entitled 191P4D12(b) Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20082.00
; CURRENT APPLICATION NUMBER: US/10/422,571
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US60/404,306
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US60/423,290
; PRIOR FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-422-571-75

Query Match          65.8%; Score 25; DB 15; Length 6;
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Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PLTC 6
Db 3 PLTC 6

RESULT 11
US-10-006-869-3573
; Sequence 3573, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3573
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-10-006-869-3573

Query Match 63.2%; Score 24; DB 14; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CVPLTC 6
Db 1 CDPVSC 6

RESULT 12
US-10-395-032-3573
; Sequence 3573, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3573
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-10-395-032-3573

Query Match 63.2%; Score 24; DB 15; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CVPLTC 6
Db 1 CDPVSC 6

us-09-761-636a-12.closed.rapb
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Db 1 CDPVSC 6

RESULT 13
US-10-006-869-2154
; Sequence 2154, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2154
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-15 cell adhesion recognition sequence
US-10-006-869-2154

Query Match 60.5%; Score 23; DB 14; Length 6;
Best Local Similarity 56.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CVPLTC 6
Db 1 CDELTC 6

RESULT 14
US-10-006-869-4040
; Sequence 4040, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4040
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-10-006-869-4040

Query Match 60.5%; Score 23; DB 14; Length 6;
Best Local Similarity 56.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CVPLTC 6
Db 1 CDELTC 6

RESULT 15
US-10-395-032-2154
; Sequence 2154, Application US/10395032
; Publication No. US20030229199A1
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; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2154
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-15 cell adhesion recognition sequence
US-10-395-032-2154

Query Match      60.5%; Score 23; DB 15; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CVPLTC 6
        |   |||
Db      1 CDELTG 6

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Job time : 92 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 11:13:06 ; Search time 17 Seconds
(without alignments)
39.520 Million cell updates/sec

Title: US-09-761-636A-10

Perfect score: 50

Sequence: 1 CSVPLTSVC 9

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 99282

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	52.0	9	4 US-09-760-599-34	Sequence 34, Appl
2	25	50.0	9	3 US-09-258-754-199	Sequence 199, App
3	25	50.0	9	3 US-09-042-107-199	Sequence 199, App
4	25	50.0	9	3 US-09-187-859-3614	Sequence 3614, Ap
5	25	50.0	9	4 US-09-839-542B-3614	Sequence 3614, Ap
6	25	50.0	9	4 US-09-722-250D-199	Sequence 199, App
7	25	50.0	9	4 US-09-760-599-25	Sequence 25, Appl
8	25	50.0	9	4 US-09-483-550B-25	Sequence 25, Appl
9	25	50.0	9	4 US-09-676-475A-199	Sequence 199, App
10	24	48.0	6	1 US-08-483-434A-21	Sequence 21, Appl
11	24	48.0	6	3 US-08-476-134A-30	Sequence 30, Appl
12	24	48.0	6	6 5190920-26	Patent No. 5190920
13	24	48.0	6	6 5506208-28	Patent No. 5506208
14	24	48.0	6	6 5190920-26	Patent No. 5190920
15	24	48.0	6	6 5506208-28	Patent No. 5506208
16	24	48.0	7	4 US-09-377-081-2	Sequence 2, Appl
17	24	48.0	9	1 US-07-958-903A-43	Sequence 43, Appl
18	24	48.0	9	1 US-08-462-018-43	Sequence 43, Appl
19	24	48.0	9	1 US-08-823-245-43	Sequence 43, Appl
20	24	48.0	9	2 US-08-598-873-49	Sequence 49, Appl
21	24	48.0	9	3 US-08-605-430-49	Sequence 49, Appl
22	24	48.0	9	3 US-07-963-329A-43	Sequence 43, Appl
23	24	48.0	9	4 US-09-760-599-9	Sequence 9, Appl
24	24	48.0	9	4 US-09-760-599-17	Sequence 17, Appl
25	24	48.0	9	4 US-09-760-599-36	Sequence 36, Appl
26	24	48.0	9	4 US-09-760-599-38	Sequence 38, Appl
27	24	48.0	9	4 US-09-760-599-48	Sequence 48, Appl

28	24	48.0	9	4 US-09-483-550B-9	Sequence 9, Appli
29	24	48.0	9	4 US-09-483-550B-17	Sequence 17, Appl
30	24	48.0	9	4 US-09-318-001-43	Sequence 43, Appl
31	24	48.0	9	4 US-09-064-159-43	Sequence 43, Appl
32	24	48.0	9	4 US-09-717-054-49	Sequence 49, Appl
33	24	48.0	9	4 US-09-747-802-6	Sequence 6, Appli
34	24	48.0	9	5 PCT-US92-09443A-43	Sequence 43, Appl
35	23	46.0	8	4 US-08-475-955-67	Sequence 67, Appl
36	23	46.0	9	1 US-08-195-075-4	Sequence 4, Appli
37	23	46.0	9	1 US-08-467-083-3	Sequence 3, Appli
38	23	46.0	9	1 US-08-414-417B-3	Sequence 3, Appli
39	23	46.0	9	2 US-08-486-348A-3	Sequence 3, Appli
40	23	46.0	9	2 US-08-468-545B-3	Sequence 3, Appli
41	23	46.0	9	2 US-08-986-234-80	Sequence 80, Appl
42	23	46.0	9	3 US-08-466-680B-3	Sequence 3, Appli
43	23	46.0	9	3 US-09-258-754-146	Sequence 146, App
44	23	46.0	9	3 US-09-258-754-308	Sequence 308, App
45	23	46.0	9	3 US-09-139-802-92	Sequence 92, Appl

ALIGNMENTS

RESULT 1
US-09-760-599-34
; Sequence 34, Application US/09760599
; Patent No. 6630447
; GENERAL INFORMATION:
; APPLICANT: Larson Mr., Richard S.
; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
; FILE REFERENCE: SCI200/4-1CIP
; CURRENT APPLICATION NUMBER: US/09/760,599
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-760-599-34

Query Match 52.0%; Score 26; DB 4; Length 9;
Best Local Similarity 33.3%; Pred. No. 4.1e+05;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
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Db 1 CALMRMSIC 9

RESULT 2
US-09-258-754-199
; Sequence 199, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-199

Query Match 50.0%; Score 25; DB 3; Length 9;
Best Local Similarity 55.8%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CSVPLTSVC 9

Db 1 CSAYTTSPC 9

RESULT 3

US-09-042-107-199
; Sequence 199, Application US/09042107
; Patent No. 6212287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-199

Query Match 50.0%; Score 25; DB 3; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CSVPLTSVC 9

Db 1 CSAYTTSPC 9

RESULT 4

US-09-187-859-3614
; Sequence 3614, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3614
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-09-187-859-3614

Query Match 50.0%; Score 25; DB 3; Length 9;
Best Local Similarity 44.4%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CSVPLTSVC 9

Db 1 CTFHIDSVC 9

RESULT 5

US-09-839-542B-3614
; Sequence 3614, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3614
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-09-839-542B-3614

Query Match 50.0%; Score 25; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CSVPLTSVC 9

Db 1 CTFHIDSVC 9

RESULT 6

US-09-722-250D-199
; Sequence 199, Application US/09722250D
; Patent No. 6610651
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250D
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-199

Query Match 50.0%; Score 25; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CSVPLTSVC 9

Db 1 CSAYTTSPC 9

RESULT 7

US-09-760-599-25

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; Sequence 25, Application US/09760599
; Patent No. 6630447
; GENERAL INFORMATION:
; APPLICANT: Larson Mr., Richard S.
; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
; FILE REFERENCE: SCI200/4-1CIP
; CURRENT APPLICATION NUMBER: US/09/760,599
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 25
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-760-599-25

Query Match          50.0%; Score 25; DB 4; Length 9;
Best Local Similarity 33.3%; Pred. No. 4.1e+05;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSVPLTVC 9
DB 1 CMLRMNSIC 9

RESULT 8
US-09-483-550B-25
; Sequence 25, Application US/09483550B
; Patent No. 6649592
; GENERAL INFORMATION:
; APPLICANT: Larson Mr., Richard S.
; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
; FILE REFERENCE: SCI200/4-001
; CURRENT APPLICATION NUMBER: US/09/483,550B
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 25
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-483-550B-25

Query Match          50.0%; Score 25; DB 4; Length 9;
Best Local Similarity 33.3%; Pred. No. 4.1e+05;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSVPLTVC 9
DB 1 CMLRMNSIC 9

RESULT 9
US-09-676-475A-199
; Sequence 199, Application US/09676475A
; Patent No. 6784153
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; FILE REFERENCE: P-LA 4377
; CURRENT APPLICATION NUMBER: US/09/676,475A
; CURRENT FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: Patentin Ver. 2.0

; Sequence 25, Application US/09760599
; Patent No. 6630447
; GENERAL INFORMATION:
; APPLICANT: Larson Mr., Richard S.
; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
; FILE REFERENCE: SCI200/4-1CIP
; CURRENT APPLICATION NUMBER: US/09/760,599
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 25
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-676-475A-199

Query Match          50.0%; Score 25; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CSVPLTVC 9
DB 1 CSAYTTSPC 9

RESULT 10
US-08-483-434A-21
; Sequence 21, Application US/08483434A
; Patent No. 5648461
; GENERAL INFORMATION:
; APPLICANT: EVAL, Jacob
; APPLICANT: HAMILTON, Bruce K.
; APPLICANT: TUSZYNSKI, George P.
; TITLE OF INVENTION: Synthetic Analogs of Thrombospondin and
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,434A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/450,738
; FILING DATE: 25-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/185,614
; FILING DATE: 24-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/024,436
; FILING DATE: 01-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/587,197
; FILING DATE: 24-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/483,527
; FILING DATE: 22-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary Ph.D., Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9598-306 (9049)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 567-2020
; TELEFAX: (215) 567-2991
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: peptide
US-08-483-434A-21

Query Match      48.0%; Score 24; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSVP 4
Db 1 CSVP 4

RESULT 13
5506208-28
;Patent No. 5506208
;APPLICANT: EYAL, JACOB;HAMILTON, BRUCE K.;TUSZYNASKI,
;GEORGE P.
; TITLE OF INVENTION: METHOD FOR USING SYNTHETIC ANALOGS OF
; THROMBOSPONDIN FOR INHIBITING ANGIOGENESIS ACTIVITY
; NUMBER OF SEQUENCES: 45
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,181
; FILING DATE: 22-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 131,565
; FILING DATE: 04-OCT-1993
; APPLICATION NUMBER: 895,764
; FILING DATE: 09-JUN-1992
; APPLICATION NUMBER: 587,197
; FILING DATE: 24-SEP-1990
; SEQ ID NO:28:
; LENGTH: 6
5506208-28

Query Match      48.0%; Score 24; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSVP 4
Db 1 CSVP 4

RESULT 14
5190920-26
;Patent No. 5190920
;APPLICANT: EYAL, JACOB;HAMILTON, BRUCE K.;TUSZYNASKI,
;GEORGE P.
; TITLE OF INVENTION: METHOD FOR USING SYNTHETIC ANALOGS
; OF THROMBOSPONDIN FOR INHIBITING METASTASIS ACTIVITY
; NUMBER OF SEQUENCES: 32
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/587,197
; FILING DATE: 24-SEP-1990
; SEQ ID NO:26:
; LENGTH: 6
5190920-26

Query Match      48.0%; Score 24; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSVP 4
Db 1 CSVP 4

RESULT 15
5506208-28
;Patent No. 5506208
;APPLICANT: EYAL, JACOB;HAMILTON, BRUCE K.;TUSZYNASKI,
;GEORGE P.
; TITLE OF INVENTION: METHOD FOR USING SYNTHETIC ANALOGS OF
; THROMBOSPONDIN FOR INHIBITING ANGIOGENESIS ACTIVITY
; NUMBER OF SEQUENCES: 45
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,181
; FILING DATE: 22-MAR-1995
; PRIOR APPLICATION DATA:
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; MOLECULE TYPE: peptide
US-08-476-134A-30

Query Match      48.0%; Score 24; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSVP 4
Db 1 CSVP 4

RESULT 11
US-08-476-134A-30
;Sequence 30, Application US/08476134A
;Patent No. 6239110
;GENERAL INFORMATION:
;APPLICANT: EYAL, JACOB
;APPLICANT: HAMILTON, BRUCE K.
;APPLICANT: TUSZYNASKI, GEORGE P.
; TITLE OF INVENTION: SYNTHETIC ANALOGS OF THROMBOSPONDIN AND THERAPEUTIC USE
; OF THROMBOSPONDIN FOR INHIBITING METASTASIS ACTIVITY
; FILE REFERENCE: 07206-0009
; CURRENT APPLICATION NUMBER: US/08/476,134A
; CURRENT FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/587,197
; PRIOR FILING DATE: 1990-09-24
; PRIOR APPLICATION NUMBER: 07/483,527
; PRIOR FILING DATE: 1990-02-22
; PRIOR APPLICATION NUMBER: 08/450,738
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: 08/185,614
; PRIOR FILING DATE: 1994-01-24
; PRIOR APPLICATION NUMBER: 08/024,436
; PRIOR FILING DATE: 1993-03-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: analog of thrombospondin
US-08-476-134A-30

Query Match      48.0%; Score 24; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSVP 4
Db 1 CSVP 4

RESULT 12
5190920-26
;Patent No. 5190920
;APPLICANT: EYAL, JACOB;HAMILTON, BRUCE K.;TUSZYNASKI,
;GEORGE P.
; TITLE OF INVENTION: METHOD FOR USING SYNTHETIC ANALOGS
; OF THROMBOSPONDIN FOR INHIBITING METASTASIS ACTIVITY
; NUMBER OF SEQUENCES: 32
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/587,197
; FILING DATE: 24-SEP-1990
; SEQ ID NO:26:
; LENGTH: 6
5190920-26

Query Match      48.0%; Score 24; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; APPLICATION NUMBER: 131,565
; FILING DATE: 04-OCT-1993
; APPLICATION NUMBER: 895,764
; FILING DATE: 09-JUN-1992
; APPLICATION NUMBER: 587,197
; FILING DATE: 24-SEP-1990
; SEQ ID NO: 28
; LENGTH: 6
5506208-28

Query Match      48.0%; Score 24; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CSVP 4
        |||
Db      1 CSVP 4
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Search completed: April 1, 2005, 11:24:41
Job time : 17 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 11:11:38 ; Search time 39 Seconds
(without alignments)
17.270 Million cell updates/sec

Title: US-09-761-636A-11

Perfect score: 42

Sequence: 1 CVPLTSC 7

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 457

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	47.6	5	2 B22565	R-phycoerythrin al
2	15	35.7	6	2 H48394	glycoprotein compo
3	15	35.7	6	2 I65546	MHC H2-L antigen -
4	15	35.7	7	2 B34818	vicilin 57K chain
5	15	35.7	7	2 A34026	acetylcholinestera
6	14	33.3	5	2 E60274	major protein anti
7	13	31.0	7	2 S42620	aggreccan - bovine
8	12	28.6	6	2 C22565	R-phycoerythrin be
9	12	28.6	6	2 I67345	MHC H2-K-k cell su
10	12	28.6	7	2 S08606	hypothetical prote
11	11	26.2	4	2 I54357	schwannomin - mous
12	11	26.2	4	2 A30339	tyrosine-melanocyt
13	11	26.2	5	2 A60521	glycogen phosphory
14	11	26.2	6	2 I49421	laminin B1 - weste
15	11	26.2	7	2 E61491	seed protein ws-5
16	11	26.2	7	2 I48105	dihydrofolate redu
17	11	26.2	7	2 I48086	DNA topoisomerase
18	10	23.8	5	2 F22565	R-phycoerythrin ga
19	10	23.8	6	2 I37263	y protein - human
20	10	23.8	7	2 S38516	ribulose-bisphosph
21	10	23.8	7	2 PT0087	myomodulin - Calif
22	10	23.8	7	2 E30608	Ig kappa chain V-L
23	10	23.8	7	2 A28340	trypsinogen
24	10	23.8	7	2 A61081	tryptophyllin, bas
25	10	23.8	7	2 ECMUCR	catch-relaxing pep
26	10	23.8	7	4 I56695	hypothetical I2 pr
27	10	23.8	7	4 A58725	virotaxin - destro
28	9	21.4	3	3 A22565	R-phycoerythrin al
29	9	21.4	4	2 I51049	metallothionein-A

30 9 21.4 4 2 S43959 Ig mu chain V regi
31 9 21.4 4 2 S55238 pallidipin - assas
32 9 21.4 5 2 A33882 cadmium-binding pe
33 9 21.4 5 2 B37988 acid proteinase 11
34 9 21.4 5 2 B45525 actin I - malaria
35 9 21.4 5 2 S65726 hemoglobin, extrac
36 9 21.4 5 2 S11127 phosphoprotein, bo
37 9 21.4 5 2 H44817 34.5K structural p
38 9 21.4 5 2 F44817 34.5K structural p
39 9 21.4 5 2 B44817 34.5K structural p
40 9 21.4 5 2 D44817 35K structural pro
41 9 21.4 6 2 A61049 halo-toxin - Pseud
42 9 21.4 6 2 JU0355 lipopeptide WS1279
43 9 21.4 6 2 PQ0008 angiotensin-conver
44 9 21.4 6 2 A31263 dihydrofolate redu
45 9 21.4 6 2 I37027 protamine P1 - gor

ALIGNMENTS

RESULT 1

B22565
R-phycoerythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri
C>Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: B22565
J.Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601; PMID:3886644
A:Accession: B22565
A:Molecule type: protein
A:Residues: 1-5 <KLO>

Query Match 47.6%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVP 3
|||
Db 2 CVP 4

RESULT 2

H48394
glycoprotein component 16/major fat-globule membrane protein/MFG-B8 homolog - bovine (fir
C:Species: Bos primigenius taurus (cattle)
C>Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C:Accession: H48394
R.Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A:Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
II-like sequences
A:Reference number: A48394; MUID:93250576; PMID:8485470
A:Accession: H48394
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-6 <MAT>
A:Experimental source: milk
A>Note: sequence extracted from NCBI backbone (NCBIP:131518)
C:Keywords: glycoprotein

Query Match 35.7%; Score 15; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 VPLTSC 7
|||
Db 1 VELLGC 6

RESULT 3

I65546
MHC H2-L antigen - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I65546
R:Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
Cell 44, 261-272, 1986
A:Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and their function
A:Reference number: I52778; MUID:86106202; PMID:3510743
A:Accession: I65546
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: GB:M12483; NID:G199565; PIDN:AAA39663.1; PID:G554234

Query Match 35.7%; Score 15; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VPLT 5
| |
| |
Db 2 VPCT 5

RESULT 4
B34818
vicilin 57K chain - pigeon pea (fragment)
C:Species: Cajanus cajan (pigeon pea)
C:Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 30-Sep-1993
C:Accession: B34818
R:Mawel, Y.R.; Mawal, M.R.; Ranjekar, P.K.
Biochem. Biophys. Res. Commun. 166, 1446-1452, 1990
A:Title: Unusual denaturation properties of vicilin from Cajanus cajan.
A:Reference number: A34818; MUID:90165956; PMID:2306256
A:Accession: B34818
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MAW>

Query Match 35.7%; Score 15; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 TSC 7
| |
| |
Db 1 TTC 3

RESULT 5
A34026
acetylcholinesterase (EC 3.1.1.7) 5.6S form - Pacific electric ray (fragment)
C:Species: Torpedo californica (Pacific electric ray)
C:Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 08-Nov-1996
C:Accession: A34026
R:Gibney, G.; MacPhee-Quigley, K.; Thompson, B.; Vedvick, T.; Low, M.G.; Taylor, S.S.; Taylor, J. Biol. Chem. 263, 1140-1145, 1988
A:Title: Divergence in primary structure between the molecular forms of acetylcholinesterase from Torpedo californica and Torpedo marmorata
A:Reference number: A34026; MUID:88087239; PMID:3335534
A:Accession: A34026
A:Molecule type: protein
A:Residues: 1-7 <GIB>
C:Keywords: alternative splicing; carboxylic ester hydrolase

Query Match 35.7%; Score 15; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 TSC 7
| |
| |
Db 5 TAC 7

RESULT 6
I67345
major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)
C:Species: Mycobacterium tuberculosis
C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C:Accession: E60274
R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A:Title: Isolation and partial characterization of major protein antigens in the culture supernatant of Mycobacterium tuberculosis
A:Reference number: A60274; MUID:9109989; PMID:1898899
A:Accession: E60274
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <NAG>

Query Match 33.3%; Score 14; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PLT 5
| |
| |
Db 3 PIT 5

RESULT 7
S42620
aggreccan - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
C:Accession: S42620
R:Voegel, K.G.; Sandy, J.D.; Pogany, G.; Robbins, J.R.
Matrix Biol. 14, 171-179, 1994
A:Title: Aggreccan in bovine tendon.
A:Reference number: S42620; MUID:94340214; PMID:7520336
A:Accession: S42620
A:Molecule type: protein
A:Residues: 1-7 <VOG>
A:Experimental source: flexor tendon
C:Keywords: cartilage

Query Match 31.0%; Score 13; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PLTS 6
| |
| |
Db 2 PIVS 5

RESULT 8
C22565
R-phycoerythrin beta-1 chain - red alga (Gastrocionium coulteri) (fragment)
C:Species: Gastrocionium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: C22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601; PMID:3886644
A:Accession: C22565
A:Molecule type: protein
A:Residues: 1-6 <KLO>

Query Match 28.6%; Score 12; DB 2; Length 6;
Best Local Similarity 25.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTSC 7
| |
| |
Db 1 MAAC 4

RESULT 9
167345

MHC H2-K-k cell surface glycoprotein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I67345
R:Archibald, A.L.; Thompson, N.A.; Kvist, S.
EMBO J. 5, 957-965, 1986
A:Title: A single nucleotide difference at the 3' end of an intron causes differential expression of the H2-K-k gene
A:Reference number: I53243; MUID:86247587; PMID:3013627
A:Accession: I67345
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: GB:M26859; NID:G199439; PIDN:AAA39612.1; PID:G387458
A:introns: 6/1
C:Keywords: glycoprotein

Query Match 28.6%; Score 12; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 LTSC 7
|
|
|
Db 1 LPDC 4

RESULT 10
S08606
hypothetical protein 2 estrogen receptor 5'-region - chicken
C:Species: Gallus gallus (chicken)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-2004
C:Accession: S08606
R:Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, P.
EMBO J. 5, 891-897, 1986
A:Title: The chicken oestrogen receptor sequence: homology with v-erbA and the human oestrogen receptor
A:Reference number: S07192; MUID:86247578; PMID:3755102
A:Accession: S08606
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-7 <KRU>
A:Cross-references: EMBL:X03805; NID:G63378; PIDN:CAA27432.1; PID:G584490

Query Match 28.6%; Score 12; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 LTSC 7
|
|
|
Db 3 LAHC 6

RESULT 11
I54357
schwannomin - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I54357
R:Huynh, D.P.; Nechiporuk, T.; Pulst, S.
Hum. Mol. Genet. 3, 1075-1079, 1994
A:Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are caused by alternative splicing
A:Reference number: I54357; MUID:95072570; PMID:7981675
A:Accession: I54357
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-4 <RES>
A:Cross-references: GB:I28838; NID:G454836; PIDN:AAA57150.1; PID:G601923
A:Genetic: NF2

Query Match 26.2%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VP 3
|
|
Db 1 VP 2

RESULT 12
A32039
tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
C:Accession: A32039
R:Horvath, A.; Kastin, A.J.
J. Biol. Chem. 264, 2175-2179, 1989
A:Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1
A:Reference number: A32039; MUID:89123285; PMID:2563371
A:Accession: A32039
A:Molecule type: protein
A:Residues: 1-4 <HOR>
A:Experimental source: brain
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end
F:4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 26.2%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PL 4
|
|
|
Db 2 PL 3

RESULT 13
A60521
glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
N:Alternate names: glycogen phosphorylase b
C:Species: Liza ramada
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Mar-2004
C:Accession: A60521
R:Bonamusa, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A:Title: Purification and characterization of glycogen phosphorylase B from skeletal muscle
A:Reference number: A60521; MUID:90227907; PMID:2109669
A:Accession: A60521
A:Molecule type: protein
A:Residues: 1-5 <BON>
C:Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F:3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experimental

Query Match 26.2%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VP 3
|
|
|
Db 4 VP 5

RESULT 14
I49421
laminin B1 - western wild mouse (fragment)
C:Species: Mus spretus (western wild mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I49421
R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A:Reference number: I48934; MUID:94319082; PMID:8043949
A:Accession: I49421
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: EMBL:U05736; NID:G497073; PIDN:AAB60477.1; PID:G642829

Query Match 26.2%; Score 11; DB 2; Length 6;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 TSC 7
Db 3 STC 5

RESULT 15
E61491
seed protein ws-5 - winged bean (fragment)
C;Species: Psophocarpus tetragonolobus (winged bean)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
C;Accession: E61491
R;Hirano, H.
J. Protein Chem. 8, 115-130, 1989
A;Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dimensional gel electrophoresis
A;Reference number: A61491; MUID:89351606; PMID:2765119
A;Accession: E61491
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <HR>
C;Keywords: glycoprotein; seed

Query Match 26.2%; Score 11; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VP 3
Db 3 VP 4

Search completed: April 1, 2005, 11:39:37
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 11:25:18 ; Search time 115 Seconds
(without alignments)
31.170 Million cell updates/sec

Title: US-09-761-636A-11
Perfect score: 42
Sequence: 1 CVPLTSC 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 174

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	40.5	7	Q66113	cherry leaf
2	15	35.7	7	Q42564	fugu rubrip
3	13	31.0	6	E101_LITRU	litoria rub
4	12	28.6	5	FARP_CHICK	gallus gall
5	12	28.6	7	Q67113	influenza a
6	11	26.2	6	VP19_HV1K	human herpe
7	11	26.2	7	MNPI_LBPDE	leptinotars
8	11	26.2	7	TPFY_PACDA	leptinotars
9	11	26.2	7	Q8NH7	pachymedusa
10	11	26.2	7	Q8MFY6	homo sapien
11	11	26.2	7	P93233	taraxacum (
12	10	23.8	5	AP21_EJSFO	lycopersico
13	10	23.8	7	CARP_MYTED	eisenia foe
14	10	23.8	7	TY51_LITRU	mytilus edu
15	10	23.8	7	Q9CSB3	litoria rub
16	10	23.8	7	P70804	arabidopsis
17	10	23.8	7	P72081	azotobacter
18	10	23.8	7	Q8GL12	nocardia la
19	10	23.8	7	Q07624	borrelia bu
20	9	21.4	5	E103_LITRU	rous sarcom
21	9	21.4	6	C1P1_MYTED	litoria rub
22	9	21.4	6	C1P2_MYTED	mytilus edu
23	9	21.4	6	SAPP_SEPOF	sepia offic
24	9	21.4	7	ASCL_ALLAS	allium asca
25	9	21.4	7	BRHE_CONIM	conus imper
26	9	21.4	7	O50556	actinobacil
27	9	21.4	7	O54248	streptomyce
28	9	21.4	7	O55184	rattus norv
29	9	21.4	7	O9Y1Q9	human adeno
30	9	21.4	7	O9Y1R0	human adeno
31	9	21.4	7	O9YVE3	human adeno

Q8JJ20 gallus gall
P13071 citrobacter.
P67857 carcinus ma
P67858 limulus pol
P67859 periplaneta
P36414 pseudomonas
P11932 enterococcu
P81675 pinus pinas
P62970 bombina ori
P62971 notophthalm
P62968 sus scrofa
P62969 ovis aries
P19916 pseudomonas
P01858 homo sapien

ALIGNMENTS

RESULT 1

Q66113 Q66113 PRELIMINARY; PRT; 7 AA.
AC Q66113;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE C-terminus of the viral replicase (Fragment).
OS Cherry leaf roll virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
OC Nepovirus; Subgroup C.
OX NCBI_TaxID=12615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Walnut;
RX MEDLINE=96124520; PubMed=8560786;
RA Borja M., Sanchez F., Rowhani A., Bruening G., Ponz F.;
RT "Long, nearly identical untranslated sequences at the 3' terminal
RT regions of the genomic RNAs of cherry leafroll virus (walnut
RT strain).";
RL Virus Genes 10:245-252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Walnut;
RA Borja M.;
RL Thesis (1992), Biologia Molecular y Virologia Vegetal, CIT-INIA.
DR EMBL; Z34265; CAA84019.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 800 MW; 7417672EBDC6D740 CRC64;

Query Match 40.5%; Score 17; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVP 3
Db |:-|
4 CLP 6

RESULT 2

Q42564 Q42564 PRELIMINARY; PRT; 7 AA.
AC Q42564;
DT 01-JAN-1998 (TREMELrel. 05, Created)
DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Truncated voltage-gated sodium channel alpha subunit (Fragment).
GN Names=Scn8a;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;

```

RN SEQUENCE FROM N.A.
RX MEDLINE=97442476; PubMed=9295353; DOI=10.1074/jbc.272.38.24008;
RA Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
RT two-domain protein in fetal brain and non-neuronal cells.";
RL J. Biol. Chem. 272:24008-24015(1997).
DR ENBL; U97673; AAB80916.1; -.
KW GO:0005216; F:ion channel activity; IEA.
FT IONIC CHANNEL.
FT NON TER 1
SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

Query Match 35.7%; Score 15; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VPL 4
Db 1 VPL 3

RESULT 3
EIO1_LITRU STANDARD; PRT; 6 AA.
AC P82096;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Electrin 1
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
FT MOD RES 6 Methionine amide.
FT SEQUENCE 6 AA; 792 MW; 5683704772C9A000 CRC64;

Query Match 31.0%; Score 13; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VPL 4
Db 2 VFI 4

RESULT 4
FARP_CHICK STANDARD; PRT; 5 AA.
AC P83308;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRamide-like neuropeptide (LFLRF-amide).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE, AND SYNTHESIS.

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RC TISSUE=Brain;
RX PubMed=6137771;
RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
RT "A novel active pentapeptide from chicken brain identified by
RT antibodies to FMRamide.";
RL Nature 305:328-330(1983).
CC -!- FUNCTION: May function as a neurotransmitter or modulator.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
DR GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 5 Phenylalanine amide.
FT SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 28.6%; Score 12; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VPL 4
Db 1 LPL 3

RESULT 5
Q67113 PRELIMINARY; PRT; 7 AA.
AC Q67113;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Influenza virus type A (Udorn/72) hemagglutinin (seg 4) cDNA, 3' end.
DE (Fragment).
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=11320;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81001892; PubMed=7407922; DOI=10.1016/0092-8674(80)90486-9;
RA Dhar R., Chanock R.M., Lai C.-J.;
RT "Nonviral oligonucleotides at the 5' terminus of cytoplasmic influenza
RT viral mRNA deduced from cloned complete genomic sequences.";
RL Cell 21:495-500(1980).
DR ENBL; M25045; AAA43202.1; -.
FT NON TER 1
FT SEQUENCE 7 AA; 834 MW; 605EB0544EA40030 CRC64;

Query Match 28.6%; Score 12; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CV 2
Db 6 CI 7

RESULT 6
VP19_HV1K STANDARD; PRT; 6 AA.
AC P23210;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Capsid assembly and DNA maturation protein (Virion protein UL38)
DE (Capsid protein VP19C) (Fragment).
GN Name=UL38;
OS Human herpesvirus 1 (strain KOS) (HHV-1) (Human herpes simplex virus
OS 1).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10306;
RN [1]

```


RP SEQUENCE FROM N.A.
 RX MEDLINE=91101287; PubMed=1846198;
 RA Flanagan W.M., Papavasiliou A.G., Rice M., Hecht L.B.,
 RA Silverstein S., Wagner E.K.;
 RT "Analysis of the herpes simplex virus type 1 promoter controlling the
 RT expression of UL38, a true late gene involved in capsid assembly.";
 RL J. Virol. 65:769-786(1991).
 CC -!- FUNCTION: Component of the basal layer in which the capsids are
 CC embedded. Binds DNA.
 CC -!- SIMILARITY: Belongs to the herpesviruses VP19C family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; M57646; AAA45830.1; -;
 KW Capsid assembly; Coat protein; DNA-binding.
 FT NON TER 6
 SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;
 Query Match 26.2%; Score 11; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PL 4
 Db ||
 5 PL 6
 RESULT 7
 MNPL LEPEDE STANDARD; PRT; 7 AA.
 AC P42984;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Myotropic neuropeptide 1 (Led-MNP-I).
 OS Leptinotarsa decemlineata (Colorado potato beetle).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Chrysomeloidea; Chrysomelidae; Chrysomelinae; Doryphorini;
 OC Leptinotarsa.
 OX NCBI_TaxID=7539;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 RX MEDLINE=95380343; PubMed=7651886; DOI=10.1016/0196-9781(94)00205-K;
 RA Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
 RA Grauwels L., van Leuven F., de Loof A.;
 RT "Identification, characterization, and immunological localization of a
 RT novel myotropic neuropeptide in the Colorado potato beetle,
 RT Leptinotarsa decemlineata.";
 RL Peptides 16:365-374(1995).
 CC -!- FUNCTION: Myotropic peptide. Stimulates the contractions of the
 CC oviduct.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;
 Query Match 26.2%; Score 11; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PL 4
 Db ||
 5 PL 6

RESULT 8

TPFY PACDA
 ID TPFY PACDA STANDARD; PRT; 7 AA.
 AC P83455;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Tryptophyllin-1 (pdt-1)
 OS Pachymedusa dactinolor (Giant mexican leaf frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
 OC Phyllomedusinae; Pachymedusa.
 OX NCBI_TaxID=75988;
 RN [1]
 RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
 RP PRO-7.
 RC TISSUE=Skin secretion;
 RA Chen T.B., Orr D.F., Shaw C.;
 RT "Pachymedusa dactinolor tryptophyllin-1 (pdt-1): structural
 RT characterization, pharmacological activity and cloning of precursor
 RT cDNA.";
 RL Submitted (SEP-2002) to Swiss-Prot.
 CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular
 CC smooth muscle.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=WALDI; RANGE=1-7; NOTE=Ref.1.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0045986; P:negative regulation of smooth muscle contra. .; NAS.
 KW Amidation; Amphibian defense peptide; Direct protein sequencing;
 KW Hydroxylation.
 FT MOD_RES 3 3 Hydroxyproline.
 FT MOD_RES 7 7 Proline amide.
 SQ SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;
 Query Match 26.2%; Score 11; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VP 3
 Db ||
 6 VP 7
 RESULT 9
 Q8NH7 PRELIMINARY; PRT; 7 AA.
 AC Q8NH7;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DE Mini-cistron.
 GN Name=NHE3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Malakooti J., Ramaswamy K.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF282824; AAM53436.1; -;
 SQ SEQUENCE 7 AA; 842 MW; 74072DC772D406F0 CRC64;
 Query Match 26.2%; Score 11; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VP 3
 Db ||
 3 VP 4
 RESULT 10

```
Q8MFY6
ID Q8MFY6 PRELIMINARY; PRT; 7 AA.
AC Q8MFY6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Paba (Fragment).
GN Namespsba;
OS Taraxacum (sect. Dioszegia) sp. 4310Hnew.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae;
OC Taraxacum; unclassified Taraxacum.
OX NCBI_TaxID=154248;
RN [1]
RP SEQUENCE FROM N.A.
RX Tissue=Leaf;
RA Mes T.H.M.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY015477; AAK21591.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 675 MW; 587451BSA76DB70 CRC64;

Query Match 26.2%; Score 11; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PLTS 6
Db 3 PSTN 6

RESULT 11
P93233 PRELIMINARY; PRT; 7 AA.
ID P93233
AC P93233;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
DE (Fragment).
GN NamesLE-ACS1B;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97351561; PubMed=9207843; DOI=10.1023/A:1005800511372;
RA Oetiker J.H., Olson D.C., Shiu O.Y., Yang S.F.;
RT "Differential induction of seven 1-aminocyclopropane-1-carboxylate
RT synthase genes by elicitor in suspension cultures of tomato
RT (Lycopersicon esculentum).";
RL Plant Mol. Biol. 34:275-286(1997).
DR GO; GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . .; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
KW Lyase.
FT NON TER
SQ SEQUENCE 7 AA; 828 MW; 71B412C7377415D0 CRC64;

Query Match 26.2%; Score 11; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PL 4
Db 3 PL 4
```

```
RESULT 12
AP21 EISFO STANDARD; PRT; 5 AA.
ID AP21 EISFO
AC P84182;
DT 25-JAN-2005 (Rel. 46, Created)
DT 25-JAN-2005 (Rel. 46, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Antimicrobial peptide ORP3121.
OS Eissenia foetida (Common brandling worm) (Common dung-worm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Eisenia.
OX NCBI_TaxID=63396;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RX PubMed=15253156;
RA Liu Y.-Q., Sun Z.-J., Wang C., Li S.-J., Liu Y.-Z.;
RT "Purification of a novel antibacterial short peptide in earthworm
RT Eisenia foetida.";
RL Acta Biochim. Biophys. Sin. 36:297-302(2004).
CC -!- FUNCTION: Displays antimicrobial activity against E.coli, S.aureus
CC and P.aeruginosa.
CC -!- MASS SPECTROMETRY: MW=510.8; METHOD=MALDI; RANGE=1-5; NOTE=Ref.1.
KW Antibiotic; Direct protein sequencing.
SQ SEQUENCE 5 AA; 407 MW; 687DC5BEBDB00000 CRC64;

Query Match 23.8%; Score 10; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SC 7
Db 1 AC 2
```

```
RESULT 13
CARP MYTED STANDARD; PRT; 7 AA.
ID CARP MYTED
AC P10420;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Catch-relaxing peptide (CARP).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RX MEDLINE=88052022; PubMed=3676797;
RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
RA Muneoka Y.;
RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia.";
RL Brain Res. 422:374-376(1987).
CC -!- FUNCTION: This peptide exhibits both potentiating (contraction)
CC and inhibitory (relaxation) effects on the anterior byssus
CC retractor muscle.
CC PIR; A29342; ECMUCR.
DR Amidation; Direct protein sequencing; Hormone.
KW MOD RES 7
FT MOD RES 7 Leucine amide.
SQ SEQUENCE 7 AA; 831 MW; 6734072687669D80 CRC64;

Query Match 23.8%; Score 10; DB 1; Length 7;
Best Local Similarity 33.3%; Pred. No. 1.6e+06;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VPL 4
Db 2 MPM 4
```

```
RESULT 14
TY51_LITRU
```

ITV51 LITRU STANDARD; PRT; 7 AA.
ID P82065;
AC 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tryptophyllin 5.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.F., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: May act as a neuromodulator or neurotransmitter.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=965; METHOD=PAB; RANGE=1-7; NOTE=Ref.1.
KW Amidation; Amphibian defense peptide; Direct protein sequencing;
KW Neuropeptide; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 Pyrrolidone carboxylic acid.
FT MOD RES 7 7 Arginine amide.
SQ SEQUENCE 7 AA; 983 MW; 7401E9D3676046B0 CRC64;

Query Match 23.8%; Score 10; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VP 3
DB 2 IP 3

RESULT 15
Q9C5B3
ID Q9C5B3 PRELIMINARY; PRT; 7 AA.
AC Q9C5B3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein DiDi 10A-2b (Fragment).
GN Name=DiDi 10A-2b;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Roots;
RX MEDLINE=21171025; PubMed=11277426;
RA Vercauteren I., Van Der Schueren E., Van Montagu M., Gheysen G.;
RT "Arabidopsis thaliana genes expressed in the early compatible
RT interaction with root-knot nematodes.";
RL Mol. Plant Microbe Interact. 14:288-299(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Roots;
RA Vercauteren I.J.R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286350; CAB71014.2; -
KW Hypothetical protein.
FT NON_TER 1 1
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 719 MW; 6732C7287EB325D0 CRC64;

Query Match 23.8%; Score 10; DB 2; Length 7;

Best Local Similarity 33.3%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 5 TSC 7
DB 1 SKC 3
Search completed: April 1, 2005, 11:38:47
Job time : 116 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 11:24:47 ; Search time 117 Seconds
(without alignments)
23.140 Million cell updates/sec

Title: US-09-761-636A-11
Perfect score: 42
Sequence: 1 CVPLTSC 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 121728

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	100.0	7	AAU04530	Aau04530 VEGF base
2	31	73.8	7	AAW13421	Aaw13421 Kidney ho
3	31	73.8	7	AAW12007	Aabi2007 Kidney ho
4	31	73.8	7	AAE11813	Aae11813 Phage pep
5	31	73.8	7	AAU10724	Aaul0724 Kidney ho
6	31	73.8	7	ABU59533	Abu59533 Kidney re
7	31	73.8	7	ADC33700	Adc33700 Kidney ce
8	31	73.8	7	ADC33699	Adc33699 Kidney ce
9	31	73.8	7	ADN03565	Adn03565 Phage pep
10	29	69.0	6	AAU04531	Aau04531 VEGF base
11	28	66.7	7	ABJ00550	Abj00550 B lymphoc
12	28	66.7	7	ABG33862	Abg33862 B lymphoc
13	26	61.9	7	AAy61489	Aay61489 Cadherin-
14	25	59.5	7	AAy62764	Aay62764 PB-cadher
15	25	59.5	7	AAy62007	Aay62007 Cadherin-
16	25	59.5	7	AAy62224	Aay62224 Cadherin-
17	24	57.1	7	AAy85374	Aay85374 IL-2 deri
18	24	57.1	7	AAy64260	Aay64260 Cadherin-
19	23	54.8	6	AAW51449	Aaw51449 IGF-1 ana
20	23	54.8	6	ADP30438	Adp30438 Human sec
21	23	54.8	7	AAy85404	Aay85404 IL-2 deri
22	23	54.8	7	AAy61930	Aay61930 Cadherin-
23	23	54.8	7	AAy62758	Aay62758 PB-cadher
24	23	54.8	7	AAy64322	Aay64322 Cadherin-
25	23	54.8	7	AAy61506	Aay61506 Cadherin-

26	23	54.8	7	3	AAy62489	AAy62489 Cadherin-
27	23	54.8	7	3	AAy63236	AAy63236 Protocadh
28	23	54.8	7	5	ABB47076	Abb47076 Desmocoll
29	22	52.4	4	2	AAr15772	AAr15772 Farnesyl-
30	22	52.4	4	2	AAr49769	AAr49769 Farnesyl-
31	22	52.4	4	2	AAr77833	AAr77833 Farnesyl-
32	22	52.4	4	2	AAW04459	AAW04459 Farnesyl-
33	22	52.4	5	2	AAW67428	AAW67428 HCV pepti
34	22	52.4	6	6	ABU37236	Abj37236 Rhodopsin
35	22	52.4	7	2	AAr36871	AAr36871 Insulin-1
36	22	52.4	7	2	AAr43615	AAr43615 Peptide d
37	22	52.4	7	2	AAW67430	AAW67430 HCV pepti
38	22	52.4	7	3	AAy64307	AAy64307 Cadherin-
39	22	52.4	7	3	AAy64292	AAy64292 Cadherin-
40	22	52.4	7	3	AAy62135	AAy62135 Cadherin-
41	22	52.4	7	3	AAy63266	AAy63266 Protocadh
42	22	52.4	7	5	ABB46174	Abb46174 Desmoglei
43	22	52.4	7	5	ABJ04536	Abj04536 Molt-4 le
44	22	52.4	7	8	ADP06887	Adp06887 Cell adhe
45	21	50.0	7	2	AAW60386	AAW60386 Tumour ho

ALIGNMENTS

RESULT 1
AAU04530
ID AAU04530 standard; peptide; 7 AA.
XX
AC AAU04530;
XX
DT 26-SEP-2001 (first entry)
XX
DE VEGF based monocyclic peptide 8.
XX
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..7 /note= "This bond cyclises the peptide"
XX
PN WO200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX
(LUDW-) LUDWIG INST CANCER RES.
XX
PI Achen MG, Hughes RA, Stackner S, Cendron A;
XX
DR WPI; 2001-442248/47.
XX
PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
XX residues.
XX
PS Claim 49; Page 32; 102pp; English.
XX
CC The sequence represents a monomeric monocyclic peptide of the invention,
CC whose 3-dimensional structure is modelled on the expose loop of human
CC VEGFD (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis.
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 42; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
 Db 1 CVPLTSC 7

RESULT 2
 AAW13421
 ID AAW13421 standard; peptide; 7 AA.
 AC AAW13421;

DT 15-JAN-1998 (first entry)

DE Kidney homing peptide.

XX Kidney homing peptide; in vivo panning; screening; phage display;
 KW drug delivery.

XX Synthetic.

XX WO9710507-A1.

XX 20-MAR-1997.

XX 10-SEP-1996; 96WO-US014600.

PR 11-SEP-1995; 95US-00526708.

PR 11-SEP-1995; 95US-00526710.

XX (LJOL-) LA JOLLA CANCER RES FOUND.

XX Ruoslahti E, Pasqualini R;

DR WPI; 1997-202359/18.

XX Obtaining compound that homes to selected organ or tissue - by in vivo
 PT panning method, specifically to identify brain, kidney, angiogenic
 PT vasculature or tumour tissue homing peptide(s).

XX Claim 16; Page 68; 75pp; English.

XX This synthetic peptide is a claimed example of a kidney-homing peptide
 CC that was identified using a novel method for obtaining molecules that
 CC home to a selected organ or tissue. This in vivo panning method typically

CC involves administering a phage display library to a subject, and
 CC identifying expressed peptides which home to the desired organ or tissue,
 CC e.g. brain, kidney, angiogenic vascular tissue or tumour tissue. The
 CC isolated peptides (see AAW13412-52, AAW1181-86) can be used to target
 CC e.g. drugs, toxins or labels to the selected organ/tissue (claimed) or to
 CC identify and/or isolate target molecules (claimed). The peptides can be
 CC directly identified in vivo, as compared to prior art in vitro screening
 CC methods, which require further examination to see if they maintain
 CC specificity in vivo

XX Sequence 7 AA;

Query Match 73.8%; Score 31; DB 2; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
 Db 1 CLPVASC 7

RESULT 3

AAB12007
 ID AAB12007 standard; peptide; 7 AA.

XX AAB12007;

XX 17-OCT-2000 (first entry)

XX Kidney homing peptide # 1.

XX Kidney; homing peptide; organ targeting; tissue targeting; mouse; cyclic.

XX Mus sp.

XX Key Location/Qualifiers

FT Disulfide-bond 1. .7
 FT /note= "Can optionally form a cyclic peptide"

XX US6068829-A.

XX 30-MAY-2000.

XX 23-JUN-1997; 97US-00862855.

XX 11-SEP-1995; 95US-00526710.

XX 10-MAR-1997; 97US-00813273.

XX (BURN-) BURNHAM INST.

XX Pasqualini R, Ruoslahti E;

XX WPI; 2000-410850/35.

XX Identifying and recovering organ homing molecules or peptides by in vivo
 PT panning comprises administering a library of diverse peptides linked to a
 PT tag which facilitates recovery of these peptides.

XX Example 2; Col 18; 20pp; English.

XX The present sequence is a mouse kidney homing peptide. This sequence was
 CC identified by using in vivo panning to screen a library of potential
 CC organ homing molecules. The present sequence can be used to direct a
 CC moiety to a kidney tissue, by linking the moiety to the present sequence.
 CC Examples of potential moieties are drugs, toxins or a detectable label

XX Sequence 7 AA;

Query Match 73.8%; Score 31; DB 3; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7

XX	Kidney homing peptide #1 useful for delivery of target molecules.
DE	
XX	
KW	Organ targeting; tissue targeting; cancer; tumour homing molecule;
KW	delivery of target molecule; kidney homing peptide.
XX	
OS	Synthetic.
XX	
PN	US6306365-B1.
XX	
PD	23-OCT-2001.
XX	
PF	08-JAN-1999; 99US-00227906.
XX	
PR	11-SEP-1995; 95US-00526710.
PR	10-MAR-1997; 97US-00813273.
PR	23-JUN-1997; 97US-00862855.
XX	
PA	(BURN-) BURNHAM INST.
XX	
PI	Ruoslahti E, Pasqualini R;
XX	
XX	WPI; 2002-040196/05.
XX	
PT	Recovering molecules that home to an organ or tissue, useful for
PT	identifying molecules that home to a specific organ or tissue, e.g.
PT	identifying a tumor homing molecule to identify the presence of cancer,
PT	by in vivo panning of a library.
XX	
PS	Example 2; Col 18; 21pp; English.
XX	
CC	The present invention relates to a method of recovering molecules that
CC	home to a selected organ or tissue. The method comprises administering to
CC	the subject the library of diverse molecules, collecting a sample of the
CC	selected organ or tissue (e.g. brain or kidney), and recovering from the
CC	sample several molecules that home to the selected organ or tissue. The
CC	method is useful for identifying molecules, particularly useful for
CC	screening large number of molecules (e.g. peptides), that home to a
CC	specific organ. The identified molecule is useful for e.g. raising an
CC	antibody specific for a target molecule, targeting a desired moiety (e.g.
CC	drug, toxin or detectable label) to the selected organ. Specifically, the
CC	method is useful for identifying the presence of cancer in a subject by
CC	linking an appropriate moiety to a tumour homing molecule. The present
CC	method provides a direct means for identifying molecules that
CC	specifically home to a selected organ and, therefore provides a
CC	significant advantage over previous methods, which require that a
CC	molecule identified using an in vitro screening method subsequently be
CC	examined to determine if it maintains its specificity in vivo. AAU10724-
CC	AAU10738 represent kidney homing peptides described in the present
CC	invention
XX	
SQ	Sequence 7 AA;
	Query Match 73.8%; Score 31; DB 5; Length 7;
	Best Local Similarity 57.1%; Pred. No. 1.8e+06;
	Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY	1 CVPILTSC 7
	: :
Db	1 CUPVASC 7
RESULT 6	
ABU59533	
ID	ABU59533 standard; peptide; 7 AA.
XX	
AC	ABU59533;
XX	
DT	22-APR-2003 (first entry)
XX	
DE	Kidney receptor targeting peptide #1.
XX	
KW	Targeting liqand; bioactive agent; polymer matrix; cancer; cytostatic;

KW cathepsin-D substrate; peptides; neuroreceptor; adrenal receptor;
KW fibronectin; vitronectin; integrin; RGD motif; angiogenic endothelium;
KW tumour; cationic cancer-targeting peptide.
XX Synthetic.
XX US2002041898-A1.
XX PD 11-APR-2002.
XX PF 25-JUL-2001; 2001US-00912609.
XX PR 05-JAN-2000; 2000US-00478124.
XX PR 31-OCT-2000; 2000US-00703474.
XX (UNGE/) UNGER E C.
XX PA (MATS/) MATSUNAGA T O.
XX PA (RAMA/) RAMASWAMI V.
XX PA (ROMA/) ROMANOWSKI M J.
XX Unger EC, Matsunaga TO, Ramaswami V, Romanowski MJ;
XX WPI; 2003-208921/20.
XX Targeted delivery system comprising a bioactive agent homogeneously
XX dispersed in a targeted matrix is especially useful in cancer therapy.
XX Claim 25; Page 38; 46pp; English.
XX The invention relates to a composition comprising a bioactive agent
XX homogeneously dispersed in a targeted matrix (polymer and targeting
XX ligand). Also included are a targeted matrix for use as a delivery
XX vehicle comprising a polymer associated with a targeting ligand,
XX enhancing the bioavailability of an agent comprising administration of
XX the composition and treating cancer comprising administration of the
XX novel composition. The method is useful for targeted delivery of a drug,
XX especially in cancer therapy. The targeting ligand may be a peptide.
XX Examples of targeting peptides are disclosed including cathepsin-D
XX substrate peptides, peptides targeting receptors in the brain and kidney,
XX peptides recognising fibronectin- and vitronectin-binding integrins,
XX peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g., antibodies,
XX peptides targeting the angiogenic endothelium of solid tumours, tissue
XX specific peptides (e.g. of lung, skin, pancreas, intestine, uterus,
XX adrenal gland and retina), and cationic cancer-targeting peptides. The
XX present sequence is a peptide targeting ligand disclosed in the invention
XX Sequence 7 AA;
Query Match 73.8%; Score 31; DB 6; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CVPLTSC 7
Db 1 CLPVASC 7
RESULT 7
ADC33700
ID ADC33700 standard; peptide; 7 AA.
XX ADC33700;
XX 18-DEC-2003 (first entry)
XX Kidney cell targeted peptide SEQ ID NO:4.
XX chimeric retrovirus envelope protein; ecotropic envelope protein;
XX cytosstatic; gene therapy; cancer.
XX Synthetic.
XX WO2003076596-A2.

XX cathepsin-D substrate; peptides; neuroreceptor; adrenal receptor;
XX fibronectin; vitronectin; integrin; RGD motif; angiogenic endothelium;
XX tumour; cationic cancer-targeting peptide.
XX Synthetic.
XX US2002041898-A1.
XX PD 11-APR-2002.
XX PF 25-JUL-2001; 2001US-00912609.
XX PR 05-JAN-2000; 2000US-00478124.
XX PR 31-OCT-2000; 2000US-00703474.
XX (UNGE/) UNGER E C.
XX PA (MATS/) MATSUNAGA T O.
XX PA (RAMA/) RAMASWAMI V.
XX PA (ROMA/) ROMANOWSKI M J.
XX Unger EC, Matsunaga TO, Ramaswami V, Romanowski MJ;
XX WPI; 2003-208921/20.
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XX Claim 25; Page 38; 46pp; English.
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XX the composition and treating cancer comprising administration of the
XX novel composition. The method is useful for targeted delivery of a drug,
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XX peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g., antibodies,
XX peptides targeting the angiogenic endothelium of solid tumours, tissue
XX specific peptides (e.g. of lung, skin, pancreas, intestine, uterus,
XX adrenal gland and retina), and cationic cancer-targeting peptides. The
XX present sequence is a peptide targeting ligand disclosed in the invention
XX Sequence 7 AA;
Query Match 73.8%; Score 31; DB 6; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CVPLTSC 7
Db 1 CLPVASC 7
RESULT 7
ADC33700
ID ADC33700 standard; peptide; 7 AA.
XX ADC33700;
XX 18-DEC-2003 (first entry)
XX Kidney cell targeted peptide SEQ ID NO:4.
XX chimeric retrovirus envelope protein; ecotropic envelope protein;
XX cytosstatic; gene therapy; cancer.
XX Synthetic.
XX WO2003076596-A2.

XX cathepsin-D substrate; peptides; neuroreceptor; adrenal receptor;
XX fibronectin; vitronectin; integrin; RGD motif; angiogenic endothelium;
XX tumour; cationic cancer-targeting peptide.
XX Synthetic.
XX US2002041898-A1.
XX PD 11-APR-2002.
XX PF 25-JUL-2001; 2001US-00912609.
XX PR 05-JAN-2000; 2000US-00478124.
XX PR 31-OCT-2000; 2000US-00703474.
XX (UNGE/) UNGER E C.
XX PA (MATS/) MATSUNAGA T O.
XX PA (RAMA/) RAMASWAMI V.
XX PA (ROMA/) ROMANOWSKI M J.
XX Unger EC, Matsunaga TO, Ramaswami V, Romanowski MJ;
XX WPI; 2003-208921/20.
XX Targeted delivery system comprising a bioactive agent homogeneously
XX dispersed in a targeted matrix is especially useful in cancer therapy.
XX Claim 25; Page 38; 46pp; English.
XX The invention relates to a composition comprising a bioactive agent
XX homogeneously dispersed in a targeted matrix (polymer and targeting
XX ligand). Also included are a targeted matrix for use as a delivery
XX vehicle comprising a polymer associated with a targeting ligand,
XX enhancing the bioavailability of an agent comprising administration of
XX the composition and treating cancer comprising administration of the
XX novel composition. The method is useful for targeted delivery of a drug,
XX especially in cancer therapy. The targeting ligand may be a peptide.
XX Examples of targeting peptides are disclosed including cathepsin-D
XX substrate peptides, peptides targeting receptors in the brain and kidney,
XX peptides recognising fibronectin- and vitronectin-binding integrins,
XX peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g., antibodies,
XX peptides targeting the angiogenic endothelium of solid tumours, tissue
XX specific peptides (e.g. of lung, skin, pancreas, intestine, uterus,
XX adrenal gland and retina), and cationic cancer-targeting peptides. The
XX present sequence is a peptide targeting ligand disclosed in the invention
XX Sequence 7 AA;
Query Match 73.8%; Score 31; DB 6; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CVPLTSC 7
Db 1 CLPVASC 7
RESULT 7
ADC33700
ID ADC33700 standard; peptide; 7 AA.
XX ADC33700;
XX 18-DEC-2003 (first entry)
XX Kidney cell targeted peptide SEQ ID NO:4.
XX chimeric retrovirus envelope protein; ecotropic envelope protein;
XX cytosstatic; gene therapy; cancer.
XX Synthetic.
XX WO2003076596-A2.

XX 18-SEP-2003.
XX 07-MAR-2003; 2003WO-US007323.
XX 08-MAR-2002; 2002US-0362655P.
XX (UYMA-) UNIV MASSACHUSETTS.
XX Green MR, Gollan TJ;
XX WPI; 2003-722332/68.
XX New chimeric retrovirus envelope protein comprising an ecotropic envelope
XX protein and a heterologous short peptide ligand inserted within the
XX ecotropic envelope protein useful for treating cancer.
XX Disclosure; SEQ ID NO 4; 42pp; English.
XX The present invention describes a chimeric retrovirus envelope protein
XX (I) comprising an ecotropic envelope protein and a heterologous short
XX peptide ligand inserted within the ecotropic envelope protein. Also
XX described: (1) a nucleic acid molecule comprising a sequence encoding the
XX recombinant chimeric envelope protein; (2) a vector comprising a nucleic
XX acid sequence encoding the chimeric envelope protein; (3) a recombinant
XX heteroviral particle comprising a chimeric envelope protein comprising a
XX heterologous short peptide ligand; (3) altering retroviral tropism; (4)
XX identifying a nucleic acid sequence encoding the chimeric envelope
XX protein that alters viral tropism; (5) delivering a nucleic acid sequence
XX to a cell; and (6) treating cancer. (I) has cytosstatic activity and can
XX be used in gene therapy. The chimeric retrovirus envelope protein is
XX useful for treating cancer, which comprises providing a cancer cell, e.g.
XX human cancer cell and infecting the cancer cell with a virus, e.g.
XX retrovirus comprising the chimeric envelope protein comprising a
XX heterologous short peptide ligand and a therapeutically useful gene, e.g.
XX encoding thymidine kinase. The present sequence represents a kidney cell
XX targeted peptide, which is given in the exemplification of the present
XX invention.
XX Sequence 7 AA;
Query Match 73.8%; Score 31; DB 7; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CVPLTSC 7
Db 1 CLPVASC 7
RESULT 8
ADC33699
ID ADC33699 standard; peptide; 7 AA.
XX ADC33699;
XX 18-DEC-2003 (first entry)
XX Kidney cell targeted peptide SEQ ID NO:3.
XX chimeric retrovirus envelope protein; ecotropic envelope protein;
XX cytosstatic; gene therapy; cancer.
XX Synthetic.
XX WO2003076596-A2.
XX 18-SEP-2003.
XX 07-MAR-2003; 2003WO-US007323.
XX 08-MAR-2002; 2002US-0362655P.
XX


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PA (UYMA-) UNIV MASSACHUSETTS.
XX
PI Green MR, Gollan TJ;
XX
DR WPI; 2003-722332/68.
XX
XX New chimeric retrovirus envelope protein comprising an ecotropic envelope
PT protein and a heterologous short peptide ligand inserted within the
PT ecotropic envelope protein useful for treating cancer.
XX
PS Disclosure; SEQ ID NO 3; 42pp; English.
XX
CC The present invention describes a chimeric retrovirus envelope protein
CC (1) comprising an ecotropic envelope protein and a heterologous short
CC peptide ligand inserted within the ecotropic envelope protein. Also
CC described: (1) a nucleic acid molecule comprising a sequence encoding the
CC recombinant chimeric envelope protein; (2) a vector comprising a nucleic
CC acid sequence encoding the chimeric envelope protein; (3) a recombinant
CC retroviral particle comprising a chimeric envelope protein comprising a
CC heterologous short peptide ligand; (3) altering retroviral tropism; (4)
CC identifying a nucleic acid sequence encoding the chimeric envelope
CC protein that alters viral tropism; (5) delivering a nucleic acid sequence
CC to a cell; and (6) treating cancer. (1) has cytostatic activity and can
CC be used in gene therapy. The chimeric retrovirus envelope protein is
CC useful for treating cancer, which comprises providing a cancer cell, e.g.
CC human cancer cell and infecting the cancer cell with a virus, e.g.
CC retrovirus comprising the chimeric envelope protein comprising a
CC heterologous short peptide ligand and a therapeutically useful gene, e.g.
CC encoding thymidine kinase. The present sequence represents a kidney cell
CC targeted peptide, which is given in the exemplification of the present
CC invention.
XX
SQ Sequence 7 AA;
    Query Match      73.8%; Score 31; DB 7; Length 7;
    Best Local Similarity 57.1%; Pred. No. 1.8e+06;
    Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
   |:|:|
Db 1 CLPVASC 7

RESULT 9
ADN03565
ID ADN03565 standard; peptide; 7 AA.
XX
AC ADN03565;
XX
DT 01-JUL-2004 (first entry)
XX
DE Phage peptide display library derived kidney homing peptide #1.
XX
KW In vivo panning; screening; phage peptide display library.
XX
OS unidentified bacteriophage.
XX
PN US2004071689-A1.
XX
PD 15-APR-2004.
XX
PF 02-AUG-2001; 2001US-00922227.
XX
PR 11-SEP-1995; 95US-00526710.
PR 10-MAR-1997; 97US-00813273.
PR 23-MAY-1997; 97US-00862855.
PR 08-JAN-1999; 99US-00227906.
XX
XX (RUOS/) RUOSLAHTI E.
PA (PASQ/) PASQUALINI R.
PI Ruoslahti E, Pasqualini R;
XX
XX

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DR WPI; 2004-328524/30.
XX
XX Obtaining molecule that homes to selected organ involves administering
PT library of diverse molecules to subject, collecting the sample of the
PT selected organ, and identifying the molecule.
XX
XX Example 2; SEQ ID NO 21; 21pp; English.
XX
CC The invention relates to a method for in vivo panning of a library to
CC identify molecules that specifically home to a selected organ. The method
CC is useful for screening large numbers of molecules, e.g. peptides to
CC identify those that can home to selected organs. It can facilitate
CC recovery or identification of the molecule. The present sequence is a
CC kidney homing peptide derived form phage peptide display library. This
CC sequence is used to illustrate the method of the invention.
XX
SQ Sequence 7 AA;
    Query Match      73.8%; Score 31; DB 8; Length 7;
    Best Local Similarity 57.1%; Pred. No. 1.8e+06;
    Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
   |:|:|
Db 1 CLPVASC 7

RESULT 10
AAU04531
ID AAU04531 standard; peptide; 6 AA.
XX
AC AAU04531;
XX
DT 26-SEP-2001 (first entry)
XX
DE VEGF based monocyclic peptide 9.
XX
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..6
FT /note= "This bond cyclises the peptide"
XX
XX WO200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
XX 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
XX Achen MG, Hughes RA, Stacker S, Cendron A;
XX
XX WPI; 2001-442248/47.
XX
XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.
XX
XX Claim 49; Page 32; 102pp; English.
XX
XX The sequence represents a monomeric monocyclic peptide of the invention,
CC whose 3-dimensional structure is modelled on the exposed loop of human
CC VEGFD (vascular endothelial growth factor). The invention relates to a

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CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis.
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 6 AA;

Query Match 69.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLT 5
 |||||
 Db 1 CVPLT 5

RESULT 11
 ABJ00550
 ID ABJ00550 standard; peptide; 7 AA.
 AC ABJ00550;
 DT 05-SEP-2002 (first entry)
 XX B lymphocyte stimulator protein binding peptide #1.
 DE
 XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritis;
 KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
 KW antiasthmatic; antiallergic; thyromimetic; antianaemic; haemostatic;
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 2 /label= Phe, Trp, Tyr
 FT
 FT Misc-difference 4 /label= Pro, Tyr
 FT
 XX WO200216411-A2.
 XX
 XX 28-FEB-2002.
 XX
 XX 17-AUG-2001; 2001WO-US025850.
 XX
 XX 18-AUG-2000; 2000US-0226700P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.

XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
 XX WPI; 2002-499775/53.
 XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
 PT administering B lymphocyte stimulator binding polypeptide.
 PS Claim 69; Page 233; 387pp; English.
 XX The present invention relates to the treatment, prevention or
 CC amelioration of a disease or disorder associated with: aberrant B
 CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
 CC of haematopoietic origin; or proliferative disease; and reducing,
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation
 CC and graft rejection involving administration of BlyS binding polypeptide.
 CC The BlyS binding polypeptides are used in the treatment, prevention or
 CC amelioration of diseases such as immune system diseases, proliferative
 CC diseases, diseases of cells of hematopoietic origin, graft rejection,
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
 CC neurodegenerative diseases. The present sequence is a B lymphocyte
 CC stimulator protein binding peptide
 XX
 SQ Sequence 7 AA;

Query Match 66.7%; Score 28; DB 5; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
 |||||
 Db 1 CXPXTGC 7

RESULT 12
 ABG33862
 ID ABG33862 standard; peptide; 7 AA.
 AC ABG33862;
 DT 15-JUL-2002 (first entry)
 XX B lymphocyte stimulator (BlyS) binding peptide #436.
 DE
 XX B lymphocyte stimulator protein; B lymphocyte stimulator binding peptide;
 KW BlyS; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
 KW synovial fluid; saliva; mucus.
 XX
 OS Synthetic.
 XX WO200216412-A2.
 XX
 XX 28-FEB-2002.
 PD
 XX 17-AUG-2001; 2001WO-US025891.
 PF
 XX 18-AUG-2000; 2000US-0226489P.
 PR
 XX (DYAX-) DYAX CORP.
 PA
 XX Beltzer JP, Potter DM, Fleming TJ, Ladner RC;
 PI WPI; 2002-351647/38.
 DR
 XX New B-lymphocyte stimulator binding polypeptide useful in detecting or
 PT isolating BlyS or BlyS-like polypeptide comprises a specified amino acid
 PT sequence.
 XX
 PS Disclosure; Page 132; 269pp; English.
 XX
 XX The invention relates to a B lymphocyte stimulator (BlyS) binding
 CC polypeptide. BlyS binding peptides bind BlyS or BlyS-like proteins

CC reversibly or irreversibly. The binding peptides are used in detection,
 CC isolation and/or purification of Blys in a solution such as water or a
 CC buffer solution, as well as any fluid and/or cell obtained from an
 CC individual biological fluid, body tissue, body cell, cell line, tissue
 CC culture or other source containing Blys or Blys-like polypeptides. The
 CC biological fluids include sera, plasma, lymph, blood, blood fraction,
 CC urine, synovial fluid, spinal fluid, saliva and mucous. Sequences
 CC ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and
 CC ABG33852-33862 represent Blys binding peptides of the invention
 XX
 SQ Sequence 7 AA;
 Query Match 66.7%; Score 28; DB 5; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CVPLTSC 7
 | | | | |
 Db 1 CXPXTGC 7
 RESULT 13
 AAY61489
 ID AAY61489 standard; peptide; 7 AA.
 XX
 AC AAY61489;
 DT 02-MAR-2000 (first entry)
 DE Cadherin-7 cell adhesion recognition cyclic peptide SEQ ID NO:1375.
 KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; Li-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 1..7
 FT WO9957149-A2.
 PN 11-NOV-1999.
 XX
 XX 05-MAY-1999; 99WO-CA000363.
 PF 05-MAY-1998; 98US-00073040.
 PR 06-NOV-1998; 98US-00187859.
 PR 20-JAN-1999; 99US-00234395.
 PR 08-MAR-1999; 99US-00264516.
 XX
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 XX Blaschuk OW, Gour BJ, Byers S;
 XX WPI; 2000-038791/03.
 XX
 XX New cadherin modulating agents, used for modulating nonclassical cadherin
 PT-mediated functions for treating e.g. cancers, obesity, rheumatoid
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX
 XX Claim 36; Page 172; 252pp; English.
 PS
 XX The present invention describes cadherin modulating agents (WA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MAS can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.

CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 CC -related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AAY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
 CC the exemplification of the present invention
 XX
 SQ Sequence 7 AA;
 Query Match 61.9%; Score 26; DB 3; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CVPLTSC 7
 | | | | |
 Db 1 CXPXTGC 7
 RESULT 14
 AAY62764
 ID AAY62764 standard; peptide; 7 AA.
 XX
 AC AAY62764;
 XX
 DT 02-MAR-2000 (first entry)
 DE PB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:4047.
 KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; Li-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 1..7
 FT WO9957149-A2.
 PN 11-NOV-1999.
 XX
 XX 05-MAY-1999; 99WO-CA000363.
 PF 05-MAY-1998; 98US-00073040.
 PR 06-NOV-1998; 98US-00187859.
 PR 20-JAN-1999; 99US-00234395.
 PR 08-MAR-1999; 99US-00264516.
 XX
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 XX Blaschuk OW, Gour BJ, Byers S;
 XX WPI; 2000-038791/03.
 XX

PT New cadherin modulating agents, used for modulating nonclassical cadherin
PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
PT arthritis, multiple sclerosis, diabetes or a neurological disease.
XX
PS Claim 72; Page 193; 252pp; English.
XX
XX The present invention describes cadherin modulating agents (MA)
CC comprising peptides which comprise a nonclassical cadherin cell adhesion
CC recognition (CAR) sequence. The MAs can be used for modulating
CC nonclassical cadherin-mediated functions. They can be used for e.g.
CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
CC mammal, enhancing delivery of a drug through the skin of a mammal,
CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
CC expressing cell, preventing or treating obesity in a mammal, stimulating
CC blood vessel regression in a mammal, enhancing drug delivery to the
CC central nervous system, treating a demyelinating neurological disease,
CC increasing vasopermeability in a mammal, enhancing adhesion of
CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
CC a mammal, or preventing pregnancy in a mammal. They can also be used for
CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
CC -related macular degeneration, multiple sclerosis and diabetes. The
CC products can also be used for detection and diagnosis and in bioreactors.
CC AAY60592 to AAY64572 represent specifically claimed peptides, and
CC AAY64573 to AAY64643 and AA233183 to AA233186 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 7 AA;
Query Match 59.5%; Score 25; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CVPLTSC 7
DB 1 CDPKTGC 7
RESULT 15
AAY62007
ID AAY62007 standard; peptide; 7 AA.
XX
AC AAY62007;
XX
DT 02-MAR-2000 (first entry)
XX
DE Cadherin-12 cell adhesion recognition cyclic peptide SEQ ID NO:1799.
XX
KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
KW inhibition; cadherin extracellular domain; cell adhesion recognition;
KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
KW cadherin-14; cadherin-15; 1-cadherin; PB-cadherin;
KW cadherin related neuronal receptor; 1f-cadherin; protocadherin;
KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
KW neurological disease; cyclic.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Disulfide-bond 1..7
FT
XX
PN WO957149-A2.
XX
XX 11-NOV-1999.
PD
XX
PF 05-MAY-1999; 99WO-CA000363.
XX
PR 05-MAY-1998; 98US-00073040.
XX

PR 06-NOV-1998; 98US-00187859.
PR 20-JAN-1999; 99US-00234395.
PR 08-MAR-1999; 99US-00264516.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuk OW, Gour BJ, Byers S;
XX WPI; 2000-038791/03.
XX
PT New cadherin modulating agents, used for modulating nonclassical cadherin
PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
PT arthritis, multiple sclerosis, diabetes or a neurological disease.
XX
PS Claim 48; Page 180; 252pp; English.
XX
XX The present invention describes cadherin modulating agents (MA)
CC comprising peptides which comprise a nonclassical cadherin cell adhesion
CC recognition (CAR) sequence. The MAs can be used for modulating
CC nonclassical cadherin-mediated functions. They can be used for e.g.
CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
CC mammal, enhancing delivery of a drug through the skin of a mammal,
CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
CC expressing cell, preventing or treating obesity in a mammal, stimulating
CC blood vessel regression in a mammal, enhancing drug delivery to the
CC central nervous system, treating a demyelinating neurological disease,
CC increasing vasopermeability in a mammal, enhancing adhesion of
CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
CC a mammal, or preventing pregnancy in a mammal. They can also be used for
CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
CC -related macular degeneration, multiple sclerosis and diabetes. The
CC products can also be used for detection and diagnosis and in bioreactors.
CC AAY60592 to AAY64572 represent specifically claimed peptides, and
CC AAY64573 to AAY64643 and AA233183 to AA233186 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 7 AA;
Query Match 59.5%; Score 25; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CVPLTSC 7
DB 1 CDPKTGC 7

Search completed: April 1, 2005, 11:36:40
Job time : 118 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 11:38:54 ; Search time 93 Seconds
(without alignments)
24.959 Million cell updates/sec

Title: US-09-761-636A-11

Perfect score: 42

Sequence: 1 CVPLTSC 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 58233

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	31	73.8	7	9	US-09-912-609-7
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4	31	73.8	7	17	US-10-943-372-21
5	31	73.8	7	17	US-10-838-289-19
6	29	69.0	6	9	US-09-761-636A-12
7	28	66.7	7	10	US-09-932-613-8
8	28	66.7	7	10	US-09-932-322-8
9	26	61.9	7	14	US-10-006-869-1375
10	26	61.9	7	15	US-10-395-032-1375
11	25	59.5	7	14	US-10-006-869-1799
12	25	59.5	7	14	US-10-006-869-3971
13	25	59.5	7	14	US-10-006-869-4047

14	25	59.5	7	15	US-10-395-032-1799	Sequence 1799, Ap
15	25	59.5	7	15	US-10-395-032-3971	Sequence 3971, Ap
16	25	59.5	7	15	US-10-395-032-4047	Sequence 4047, Ap
17	24	57.1	7	14	US-10-006-869-3574	Sequence 3574, Ap
18	24	57.1	7	15	US-10-395-032-3574	Sequence 3574, Ap
19	23	54.8	7	14	US-10-006-869-1392	Sequence 1392, Ap
20	23	54.8	7	14	US-10-006-869-1740	Sequence 1740, Ap
21	23	54.8	7	14	US-10-006-869-2155	Sequence 2155, Ap
22	23	54.8	7	14	US-10-006-869-2720	Sequence 2720, Ap
23	23	54.8	7	14	US-10-006-869-3637	Sequence 3637, Ap
24	23	54.8	7	14	US-10-006-869-4041	Sequence 4041, Ap
25	23	54.8	7	15	US-10-395-032-1392	Sequence 1392, Ap
26	23	54.8	7	15	US-10-395-032-1740	Sequence 1740, Ap
27	23	54.8	7	15	US-10-395-032-2155	Sequence 2155, Ap
28	23	54.8	7	15	US-10-395-032-2720	Sequence 2720, Ap
29	23	54.8	7	15	US-10-395-032-3637	Sequence 3637, Ap
30	23	54.8	7	15	US-10-395-032-4041	Sequence 4041, Ap
31	22	52.4	4	14	US-10-083-894-35	Sequence 35, Appl
32	22	52.4	7	10	US-09-792-286-221	Sequence 221, Appl
33	22	52.4	7	10	US-09-792-286-225	Sequence 225, Appl
34	22	52.4	7	14	US-10-006-869-1888	Sequence 1888, Ap
35	22	52.4	7	14	US-10-006-869-2750	Sequence 2750, Ap
36	22	52.4	7	14	US-10-006-869-3606	Sequence 3606, Ap
37	22	52.4	7	14	US-10-006-869-3621	Sequence 3621, Ap
38	22	52.4	7	15	US-10-395-032-1888	Sequence 1888, Ap
39	22	52.4	7	15	US-10-395-032-2750	Sequence 2750, Ap
40	22	52.4	7	15	US-10-395-032-3606	Sequence 3606, Ap
41	22	52.4	7	15	US-10-395-032-3621	Sequence 3621, Ap
42	22	52.4	7	16	US-10-714-564A-1064	Sequence 1064, Ap
43	21	50.0	6	9	US-09-911-838-184	Sequence 184, Appl
44	21	50.0	6	9	US-09-911-838-186	Sequence 186, Appl
45	21	50.0	7	9	US-09-765-086-103	Sequence 103, Appl

ALIGNMENTS

RESULT 1
US-09-761-636A-11
; Sequence 11, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-11

Query Match 100.0%; Score 42; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
|||
Db 1 CVPLTSC 7

RESULT 2
US-09-912-609-7

; Sequence 7, Application US/09912609
; Publication No. US20020041898A1
; GENERAL INFORMATION:
; APPLICANT: UNGER, EVAN C.
; APPLICANT: MATSUNAGA, TERRY ONICHI
; APPLICANT: RAMASWAMI, VARADARAJAN
; APPLICANT: ROMANOWSKI, MAREK J.
; TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 5030-0001.24
; CURRENT APPLICATION NUMBER: US/09/912,609
; CURRENT FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 09/703,474
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: 09/478,124
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-912-609-7

Query Match 73.8%; Score 31; DB 9; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.3e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
|:|:|
Db 1 CLPVASC 7

RESULT 3
US-09-922-227-21
; Sequence 21, Application US/09922227
; Publication No. US20040071689A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/922,227
; FILING DATE: 02-Aug-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; APPLICATION NUMBER: US 08/862,855
; FILING DATE: 23-MAY-1997
; APPLICATION NUMBER: US 09/227,906
; FILING DATE: 08-JAN-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-LJ 4859
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-922-227-21

Query Match 73.8%; Score 31; DB 11; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.3e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
|:|:|
Db 1 CLPVASC 7

RESULT 4
US-10-943-372-21
; Sequence 21, Application US/10943372
; Publication No. US20050037417A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home To A Selected Organ In Vivo
; FILE REFERENCE: 66821-313
; CURRENT APPLICATION NUMBER: US/10/943,372
; CURRENT FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 09/922,227
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/227,906
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/862,855
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/813,273
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 08/526,710
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-943-372-21

Query Match 73.8%; Score 31; DB 17; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.3e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
|:|:|
Db 1 CLPVASC 7

RESULT 5
US-10-838-289-19
; Sequence 19, Application US/10838289
; Publication No. US20050058603A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Jiming
; APPLICANT: Ai, Hua
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
; TITLE OF INVENTION: NANOSHELLS
; FILE REFERENCE: CWRU-P01-040

; CURRENT APPLICATION NUMBER: US/10/838,289
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 60/502,429
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/467,389
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Kidney homing peptide
US-10-838-289-19

Query Match 73.8%; Score 31; DB 17; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.3e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
|:|:|
Db 1 CLPVASC 7

RESULT 6

US-09-761-636A-12
; Sequence 12, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/476,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-12

Query Match 69.0%; Score 29; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLT 5
|:|:|
Db 1 CVPLT 5

RESULT 7

US-09-932-613-8
; Sequence 8, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT: DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17

; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
; NAME/KEY: MISC FEATURE
; LOCATION: (2)..(2)
; OTHER INFORMATION: X2 is Phe, Trp, or Tyr (preferably Tyr);
; NAME/KEY: MISC FEATURE
; LOCATION: (4)..(4)
; OTHER INFORMATION: X4 is Pro or Tyr (preferably Pro);
US-09-932-613-8

Query Match 66.7%; Score 28; DB 10; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
|:|:|
Db 1 CXPXTGC 7

RESULT 8

US-09-932-322-8
; Sequence 8, Application US/09932322
; Publication No. US20030194743A1
; GENERAL INFORMATION:
; APPLICANT: Dyax Corp.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Ladner, Robert Charles
; TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (Blys)
; FILE REFERENCE: Dyx-018.1 PCT: DYX-018.1 US
; CURRENT APPLICATION NUMBER: US/09/932,322
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
; NAME/KEY: MISC FEATURE
; LOCATION: (2)..(2)
; OTHER INFORMATION: X2 is Phe, Trp, or Tyr (preferably Tyr);
; NAME/KEY: MISC FEATURE
; LOCATION: (4)..(4)
; OTHER INFORMATION: X4 is Pro or Tyr (preferably Pro);
US-09-932-322-8

Query Match 66.7%; Score 28; DB 10; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
|:|:|
Db 1 CXPXTGC 7

RESULT 9

US-10-006-869-1375
; Sequence 1375, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gout, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1375
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
US-10-006-869-1375

Query Match 61.9%; Score 26; DB 14; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
| | | | |
Db 1 CEPKTGC 7

RESULT 10

US-10-395-032-1375
; Sequence 1375, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1375
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
US-10-395-032-1375

Query Match 61.9%; Score 26; DB 15; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
| | | | |
Db 1 CEPKTGC 7

RESULT 11

US-10-006-869-1799
; Sequence 1799, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1799

; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence
US-10-006-869-1799

Query Match 59.5%; Score 25; DB 14; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
| | | | |
Db 1 CDPKTGC 7

RESULT 12

US-10-006-869-3971
; Sequence 3971, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3971
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-14 cell adhesion recognition sequence
US-10-006-869-3971

Query Match 59.5%; Score 25; DB 14; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
| | | | |
Db 1 CDPKTGC 7

RESULT 13

US-10-006-869-4047
; Sequence 4047, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4047
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-10-006-869-4047

Db 1 CDPKTGC 7

Search completed: April 1, 2005, 11:49:14
Job time : 94 secs

Query Match 59.5%; Score 25; DB 14; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
Db 1 CDPKTGC 7

RESULT 14
US-10-395-032-1799
; Sequence 1799, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1799
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence
US-10-395-032-1799

Query Match 59.5%; Score 25; DB 15; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
Db 1 CDPKTGC 7

RESULT 15
US-10-395-032-3971
; Sequence 3971, Application US/10395032
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3971
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-14 cell adhesion recognition sequence
US-10-395-032-3971

Query Match 59.5%; Score 25; DB 15; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVPLTSC 7

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OM protein - protein search, using sw model

Run on: April 1, 2005, 11:12:11 ; Search time 46.5 Seconds
(without alignments)
99.112 Million cell updates/sec

Title: US-09-761-636A-10
Perfect score: 50
Sequence: 1 CSVPLTVC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1455

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_O3: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	20	40.0	8	2	Q7AUJ4	Q7auj4 acinetobact
2	19	38.0	9	1	MGMT_BOVIN	P29177 bos taurus
3	18	36.0	9	2	Q9FXL0	Q9fxl0 liliu long
4	17	34.0	7	2	O42564	O42564 fugu rubrip
5	17	34.0	7	2	Q8JJ20	Q8jj20 gallus gall
6	17	34.0	8	2	O85562	O85562 moloney mur
7	17	34.0	9	2	Q8CG13	Q8cg13 mus musculu
8	16	32.0	8	2	Q16468	Q16468 homo sapien
9	16	32.0	8	2	Q9Y4X6	Q9y4x6 homo sapien
10	16	32.0	8	2	Q8L802	Q8l802 zea mays (m
11	16	32.0	8	2	Q8KFX4	Q8kfx4 microcystis
12	16	32.0	8	2	Q849P4	Q849p4 salmonella
13	16	32.0	9	2	Q7W4R6	Q7w4r6 homo sapien
14	16	32.0	9	2	Q7TRU7	Q7tru7 bos taurus
15	16	32.0	9	2	O35953	O35953 mus musculu
16	15	30.0	8	2	Q70Y88	Q70y88 platostoma
17	15	30.0	8	2	Q7IMR4	Q7imr4 brassica na
18	15	30.0	8	2	Q9MD43	Q9md43 rattus norv
19	15	30.0	8	2	Q9TKES	Q9tkes leptospermu
20	15	30.0	8	2	Q9SAY7	Q9say7 dioscorea t
21	15	30.0	8	2	Q56140	Q56140 streptococc
22	15	30.0	9	2	Q9TKF2	Q9tkf2 asteromyritu
23	15	30.0	9	2	Q9TKG1	Q9tkg1 calothamnu
24	14	28.0	7	2	P70804	P70804 azotobacter
25	14	28.0	7	2	Q07624	Q07624 rous sarcom
26	14	28.0	8	1	ACT_CARMA	P80709 carcinus ma
27	14	28.0	8	2	Q7LIH2	Q7lih2 saccharomyc
28	14	28.0	8	2	Q7LIUR9	Q7liur9 homo sapien
29	14	28.0	8	2	Q7M039	Q7m039 rattus norv
30	14	28.0	9	1	YBFR_AZOVI	P25825 azotobacter
31	14	28.0	9	2	Q7M4D5	Q7m4d5 diadema set

RESULT 1

Q7AUJ4
ID Q7AUJ4 PRELIMINARY; PRT; 8 AA.
AC Q7AUJ4;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Transposase (Fragment).
GN Name=tnp17;
OS Acinetobacter sp. BW3.
OG Plasmid pKLH207.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=106395;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BW3;
RX PubMed15073307; DOI=10.1099/mic.0.26844-0;
RA Kholodii G., Mindlin S., Gorlenko Z., Petrova M., Hobman J.,
RA Nikiforov V.;
RT "Translocation of transposition-deficient [Tn(d)PKLH2-like]
RT transposons in the natural environment: mechanistic insights from the
RT study of adjacent DNA sequences.";
RL Microbiology 150:979-992(2004).
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BW3;
RA Kholodii G.Y.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, AJ486856; CAD31078.1; -.
KW Plasmid.
FT NON_TER
SQ SEQUENCE 8 AA; 911 MW; 2D71B2D6C1A73774 CRC64;

Query Match 40.0%; Score 20; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PLTSV 8
|||
Db 2 PLTQV 6

RESULT 2

MGMT_BOVIN
ID_MGMT_BOVIN STANDARD; PRT; 9 AA.
AC P29177;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-methylguanine-DNA methyltransferase) (MGMT) (O-6-methylguanine-DNA-alkyltransferase) (Fragment).
GN Name=MGMT;

OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=thymus;
 RX MEDLINE=90174912; PubMed=2308822;
 RA Rydberg B., Hall J., Karran P.;
 RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA
 methyltransferase.";
 RL Nucleic Acids Res. 18:17-21(1990).
 CC -!- FUNCTION: Involved in the cellular defense against the biological
 effects of O6-methylguanine (O6-MeG) in DNA. Repairs alkylated
 guanine in DNA by stoichiometrically transferring the alkyl group
 at the O-6 position to a cysteine residue in the enzyme. This is a
 suicide reaction; the enzyme is irreversibly inactivated.
 CC -!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) + protein
 L-cysteine = DNA (without 6-O-methylguanine) + protein S-methyl-L-
 cysteine.
 CC -!- SIMILARITY: Belongs to the MGMT family.
 DR InterPro: IPR001497; Methyltransf_1.
 DR PROSITE: PS00374; MGMT; PARTIAL.
 KW Direct protein sequencing; DNA repair; Methyltransferase; Transferase.
 FT NON_TER 1
 FT ACT_SITE 9 9 Alkyl group acceptor (By similarity).
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 38.0%; Score 19; DB 1; Length 9;
 Best Local Similarity 28.6%; Pred. No. 1.6e+06;
 Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 VPLTSVC 9
 Db 3 IPILTPC 9

RESULT 3
 Q9FXL0 PRELIMINARY; PRT; 9 AA.
 ID Q9FXL0
 AC Q9FXL0
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE LIM8 protein (Fragment).
 GN Name=LIM8;
 OS Lilium longiflorum (Trumpet Lily).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lilium.
 OX NCBI_TaxID=4690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Uefuji H., Takase H., Hiratsuka K.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; AB050987; BAB17856.1; -.
 FT NON_TER 9
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1021 MW; 6F8BD76685A6C2CB CRC64;

Query Match 36.0%; Score 18; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.6e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVPLT 6
 Db 5 SMPVT 9

RESULT 4
 O42564 PRELIMINARY; PRT; 7 AA.
 ID O42564
 AC O42564;

DT 01-JAN-1998 (TReMBLrel. 05, Created)
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Truncated voltage-gated sodium channel alpha subunit (Fragment).
 GN Name=Scn8a;
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97442476; PubMed=9295353; DOI=10.1074/jbc.272.38.24008;
 RA Plummer N.W., McBurney M.W., Meisler M.H.;
 RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
 two-domain protein in fetal brain and non-neuronal cells.";
 RL J. Biol. Chem. 272:24008-24015(1997).
 DR EMBL; U97673; AAB80916.1; -.
 DR GO; GO:0005216; F:ion channel activity; IEA.
 KW Ionic channel.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

Query Match 34.0%; Score 17; DB 2; Length 7;
 Best Local Similarity 71.4%; Pred. No. 1.6e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 3 VPLTSVC 9
 Db 1 VPL--VC 5

RESULT 5
 Q8JJ20 PRELIMINARY; PRT; 7 AA.
 ID Q8JJ20
 AC Q8JJ20
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE Extracellular fatty acid binding protein (Fragment).
 GN Name=EXFASP;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Wang Q., Li N., Li H.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; AF487519; AAL96665.1; -.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 780 MW; 72CB1AB2D5BBB70 CRC64;

Query Match 34.0%; Score 17; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSV 3
 Db 2 CSV 4

RESULT 6
 Q85562 PRELIMINARY; PRT; 8 AA.
 ID Q85562
 AC Q85562
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Truncated env protein (Fragment).

OS Moloney murine leukemia virus.
 OC Viruses; Retrod viruses; Retroviridae; Gammaretrovirus.
 OX NCBI_TaxID=11801;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82196891; PubMed=6281735;
 RA Donoghue D.J., Hunter T.;
 RT "A generalized method of subcloning DNA fragments by restriction site
 RT reconstruction: Application to sequencing the amino-terminal region of
 RT the transforming gene of Gazdar murine sarcoma virus."
 RL Nucleic Acids Res. 10:2549-2564(1982).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83164305; PubMed=6300424;
 RA Donoghue D.J., Hunter T.;
 RT "Recombination junctions of variants of Moloney murine sarcoma virus:
 RT Generation and divergence of a mammalian transforming gene."
 RL J. Virol. 45:607-617(1983).
 DR EMBL; K03105; AAA46490.1; -.
 FT NON_TER 1
 SQ SEQUENCE 8 AA; 732 MW; 98C2D5BEB44DC76D CRC64;
 Query Match 34.0%; Score 17; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSV 3
 Db |||
 5 CSV 7
 RESULT 7
 ID Q8CG13 PRELIMINARY; PRT; 9 AA.
 AC Q8CG13;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Glutamate receptor ionotropic N-methyl D-aspartate-like 1A
 DE (Fragment).
 GN Name=Grin1a;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA Wydner K.S., Mohan Raj B.K., Sciorra L.J., Roginski R.S.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF462417; AAO15648.1; -.
 DR EMBL; AF462416; AAO15648.1; JOINED.
 DR MGD; MGI:107282; Grin1a.
 DR GO; GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1091 MW; 6A91233EB059C33B CRC64;
 Query Match 34.0%; Score 17; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CSV 4
 Db | | |
 6 CKLP 9
 RESULT 8
 ID Q16468 PRELIMINARY; PRT; 8 AA.
 AC Q16468;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE H.sapiens DNA for cosmid CCL3-1134 PCR primer 1 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96435920; PubMed=8838806; DOI=10.1006/geno.1996.0137;
 RA James L.A., Ogilvie D.J., Yamakawa K., Nakamura Y., Stirling C.J.,
 RA Anand R.;
 RT "Walking, cloning and mapping with YACs in 3q27. Localisation of 5
 RT ESTs including 3 members of the Cystatin gene family and
 RT identification of CpG islands."
 RL Genomics 32:425-430(1996).
 DR EMBL; X88976; CAA61407.1; -.
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 925 MW; FD5411A7376871E6 CRC64;
 Query Match 32.0%; Score 16; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 PLT 6
 Db |||
 4 PLT 6
 RESULT 9
 ID Q9Y4X6 PRELIMINARY; PRT; 8 AA.
 AC Q9Y4X6;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Nuclear LIM interactor (Fragment).
 GN Name=NLI;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20108906; PubMed=10640831;
 RA Drechsler M., Schumacher V., Friedrich S., Wildhardt G., Giesler S.,
 RA Schroth A., Bodem J., Royer-Pokora B.;
 RT "Genomic structure, alternative transcripts and chromosome location of
 RT the human LIM domain binding protein gene LDB1."
 RL Cytogenet. Cell Genet. 87:119-124(1999).
 DR EMBL; AJ243097; CAB45408.1; -.
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 767 MW; EE6EBDBEB862D5B6 CRC64;
 Query Match 32.0%; Score 16; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CSV 4
 Db | | |
 5 CACP 8
 RESULT 10
 ID Q8L802 PRELIMINARY; PRT; 8 AA.
 AC Q8L802;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Pat (Fragment).
 GN Name=Pat; (Maize).
 OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA Ronning S.B., Berdal K.G., Vaitilingom M.M., Holst-Jensen A.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
FR EMBL; AY123624; AAM89275.1;
FT NON TER 1
SQ SEQUENCE 8 AA; 909 MW; 6046C1B2D77412D7 CRC64;

Query Match 32.0%; Score 16; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 PLTSV 8
Db [1];
4 PVIQI 8

RESULT 11
ID Q8KPY4 PRELIMINARY; PRT; 8 AA.
AC Q8KPY4;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Phycocyanin alpha subunit (Fragment).
GN Name:pcp;
OS Microcystis sp. T96-1.
OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.
OX NCBI_TaxID=198099;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22338268; PubMed=12450830;
RX DOI=10.1128/AEM.68.12.6070-6076.2002;
RA Baker J.A., Entsch B., Neilan B.A., McKay D.B.;
RT "Monitoring changing toxigenicity of a cyanobacterial bloom by
RT molecular methods."
RL Appl. Environ. Microbiol. 68:6070-6076(2002).
DR EMBL; AY117046; AAM54719.1;
FT NON TER 8
SQ SEQUENCE 8 AA; 890 MW; F4DB01A73771A336 CRC64;

Query Match 32.0%; Score 16; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PLT 6
Db [1];
4 PLT 6

RESULT 12
ID Q849P4 PRELIMINARY; PRT; 8 AA.
AC Q849P4;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE PipB (Fragment).
OS Salmonella derby.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=28144;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22660262; PubMed=12775700;
RX DOI=10.1128/JB.185.12.3624-3635.2003;
RA Amavisit P., Lightfoot D., Browning G.F., Markham P.F.;
RT "Variation between pathogenic serovars within salmonella pathogenicity
RT islands."

RL J. Bacteriol. 185:3624-3635(2003).
DR EMBL; AY144492; AAO49836.1;
FT NON TER 8
SQ SEQUENCE 8 AA; 861 MW; EFC5BDD451A04766 CRC64;

Query Match 32.0%; Score 16; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 VPLTS 7
Db [1];
1 MEITN 5

RESULT 13
ID Q7M4R6 PRELIMINARY; PRT; 9 AA.
AC Q7M4R6;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE 118K stomach cancer antigen (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=90216080; PubMed=2323853;
RA Shiraishi Y.;
RT "Western blotting analysis for malignant lymphoma and stomach cancer
RT antigens from carcinogen-transformed blood syndrome cells."
RL Int. J. Cancer 45:783-787(1990).
DR PIR; A60356; A60356.
FT NON TER 1
FT NON TER 9
SQ SEQUENCE 9 AA; 949 MW; 3D057042D7633737 CRC64;

Query Match 32.0%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VPLTSV 8
Db [1];
1 IPLKEV 6

RESULT 14
ID Q9TRU7 PRELIMINARY; PRT; 9 AA.
AC Q9TRU7;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE GAP-3, GTPase-activating protein (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=92112868; PubMed=1309786;
RA Nice E.C., Fabri L., Hammacher A., Holden J., Simpson R.J.,
RA Burgess A.W.;
RT "The purification of a Rap1 GTPase-activating protein from bovine
RT brain cytosol."
RL J. Biol. Chem. 267:1546-1553(1992).
FT NON TER 1
FT NON TER 9
SQ SEQUENCE 9 AA; 1063 MW; 89EDA77B47604B5A CRC64;

Query Match 32.0%; Score 16; DB 2; Length 9;

Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 VPLTSV 8
:|
Db 4 IPYPSV 9

RESULT 15

O35953 PRELIMINARY; PRT; 9 AA.
AC O35953;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Truncated voltage-gated sodium channel alpha subunit (Fragment).
GN Name=Scn8a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RII;
RX MEDLINE=97442476; PubMed=9295353; DOI=10.1074/jbc.272.38.24008;
RA Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
RL two-domain protein in fetal brain and non-neuronal cells.";
RL J. Biol. Chem. 272:24008-24015(1997).
DR EMBL; U97672; AAB80914.1; -
DR MGD; MGI:103169; Scn8a.
DR GO; GO:0007628; P:adult walking behavior; IMP.
DR GO; GO:0007626; P:locomotory behavior; IMP.
KW Ionic channel.
FT NON_TER 1
SQ SEQUENCE 9 AA; 898 MW; 22D92865B735B737 CRC64;

Query Match 32.0%; Score 16; DB 2; Length 9;

Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 VPLT 6
:|
Db 1 VPLS 4

Search completed: April 1, 2005, 11:23:56
Job time : 46.5 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 11:11:16 ; Search time 58.5 Seconds
(without alignments)
59.502 Million cell updates/sec

Title: US-09-761-636A-10

Perfect score: 50

Sequence: 1 CSVPITSV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 330156

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A. Genesep 16Dec04: *
1: genesep1980s: *
2: genesep1990s: *
3: genesep2000s: *
4: genesep2001s: *
5: genesep2002s: *
6: genesep2003as: *
7: genesep2003bs: *
8: genesep2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	9	AAU04529	AAU04529 VEGF base
2	37	74.0	9	ABJ04424	ABJ04424 Stem cell
3	32	64.0	9	ABG34948	ABG34948 Human bon
4	32	64.0	9	ADK65202	ADK65202 Human VEG
5	30	60.0	7	ABJ37356	ABJ37356 G-protein
6	30	60.0	7	ABJ37436	ABJ37436 G-protein
7	30	60.0	9	ABR05266	ABR05266 Vascular
8	29	58.0	9	ADK09526	ADK09526 Human pap
9	29	58.0	9	ADR42755	ADR42755 Modulator
10	28	56.0	8	ADR58247	ADR58247 Immunogen
11	28	56.0	8	ADO24736	ADO24736 Mouse lep
12	28	56.0	8	ADR11353	ADR11353 HLA-A2.1
13	28	56.0	9	ADC44660	ADC44660 Endotheli
14	28	56.0	9	ADK65204	ADK65204 Human VEG
15	28	56.0	9	ADO24737	ADO24737 Mouse lep
16	27	54.0	9	AAW45666	AAW45666 HBV X 69
17	27	54.0	9	AAV46691	AAV46691 Immunogen
18	27	54.0	9	ABP54842	ABP54842 Alpha-I1b
19	27	54.0	9	ABP533878	ABP533878 cMET-HGF
20	26	52.0	7	ADB79677	ADB79677 Parapoxvi
21	26	52.0	7	ADP75071	ADP75071 Parapoxvi
22	26	52.0	9	AAU03756	AAU03756 Cyclic pe
23	26	52.0	9	ABP54826	ABP54826 Alpha-I1b
24	26	52.0	9	ABP54835	ABP54835 Alpha-I1b
25	26	52.0	9	ABP54823	ABP54823 Alpha-I1b

26	26	52.0	9	ABR75294	ABR75294 Biologica
27	26	52.0	9	ADR42761	ADR42761 Modulator
28	25	50.0	7	AB51972	AB51972 Human sec
29	25	50.0	8	ABJ04484	ABJ04484 HUVEC cel
30	25	50.0	8	ADF83349	ADF83349 Aphis gos
31	25	50.0	8	ADG94501	ADG94501 Human JAM
32	25	50.0	8	ADI46899	ADI46899 Permeabil
33	25	50.0	8	ADP87076	ADP87076 Junctiona
34	25	50.0	9	AAV48844	AAV48844 Membrane
35	25	50.0	9	AAV64300	AAV64300 Cadherin-
36	25	50.0	9	AAU03747	AAU03747 Cyclic pe
37	25	50.0	9	ABJ04620	ABJ04620 Bone matr
38	25	50.0	9	ABJ04630	ABJ04630 Bone matr
39	25	50.0	9	ABJ04417	ABJ04417 Stem cell
40	25	50.0	9	ADC44658	ADC44658 Endotheli
41	25	50.0	9	ADE78117	ADE78117 Synthetic
42	25	50.0	9	ADE78037	ADE78037 Synthetic
43	25	50.0	9	ADE78097	ADE78097 Synthetic
44	25	50.0	9	ADE77841	ADE77841 Synthetic
45	25	50.0	9	ADP64586	ADP64586 Endotheli

ALIGNMENTS

RESULT 1
AAU04529
ID AAU04529 standard; peptide; 9 AA.
XX
AC AAU04529;
XX
DT 26-SEP-2001 (first entry)
XX
DE VEGF based monocyclic peptide 7.
XX
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..9 /note= "This bond cyclises the peptide"
FT
XX
PN WO200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR WPI; 2001-442248/47.
XX
PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.
XX
PS Claim 49; Page 32; 102pp; English.
XX
CC The sequence represents a monomeric monocyclic peptide of the invention,
CC whose 3-dimensional structure is modelled on the expose loop of human
CC VEGF (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
 |||||
 Db 1 CSVPLTSVC 9

RESULT 2
 ABJ04424
 ID ABJ04424 standard; peptide; 9 AA.

AC ABJ04424;

DT 24-OCT-2002 (first entry)

DE Stem cell (mesenchymal) targeting peptide 13.

XX
 KW BRASIL; targeting peptide; bacterial infection;

KW Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;
 KW inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;
 KW viral infection; cardiovascular disease; degenerative disease.

XX Unidentified.

XX WO200220822-A2.

XX 14-MAR-2002.

PF 07-SEP-2001; 2001WO-US028124.

PR 08-SEP-2000; 2000US-0231266P.

PR 17-JAN-2001; 2001US-00765101.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Arap W, Pasqualini R;

XX WPI; 2002-404697/43.

XX Identification of targeting peptides that can be used to treat diseases
 PT e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis
 PT of Selective Ligands) method comprises a single differential
 PT centrifugation step.

PS Example 5; Page 75; 167pp; English.

XX

CC The invention comprises a method (BRASIL - Biopanning and Rapid Analysis
 CC of Selective Interactive Ligands) to obtain a targeting peptide. The
 CC BRASIL method of the invention involves: exposing a target to a phage
 CC display library in a first phase; exposing the first phase to a second
 CC phase; and separating the phage bound to the target from unbound phage.
 CC The BRASIL method of the invention allows cell phages to be separated
 CC from the remaining unbound phage in a single differential centrifugation
 CC step. When compared to conventional cell panning methods, the BRASIL
 CC method shows a significant increase in recovery of specific phage and a
 CC substantial decrease in background. The BRASIL method is useful for
 CC identifying targeting peptides. The targeting peptides identified by the
 CC method of the invention are useful for treating disease states, such as:
 CC diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune
 CC disease; bacterial infection; viral infection; cardiovascular disease and
 CC degenerative disease. The present amino acid sequence represents a
 CC targeting peptide of the invention

SQ Sequence 9 AA;

Query Match 74.0%; Score 37; DB 5; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
 |||||

Db 1 CSVPVSSSC 9

RESULT 3

ABG34948

ID ABG34948 standard; peptide; 9 AA.

AC ABG34948;

DT 15-JUL-2002 (first entry)

DE Human bone marrow targeting peptide #20.

KW Targeting peptide; cancer; Hodgkin's disease; cytostatic;
 KW immunosuppressive; anti-inflammatory; antiarthritic; antiviral;
 KW antiatherosclerotic; antidiabetic; antibacterial; diabetes mellitus;
 KW inflammatory disease; arthritis; atherosclerosis; cancer;
 KW autoimmune disease; bacterial infection; viral infection.

XX Homo sapiens.

XX WO200220722-A2.

XX 14-MAR-2002.

PF 07-SEP-2001; 2001WO-US027702.

PR 08-SEP-2000; 2000US-0231266P.

PR 17-JAN-2001; 2001US-00765101.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Arap W, Pasqualini R;

XX WPI; 2002-383050/41.

XX Identifying targeting peptides useful for treating e.g. diabetes
 PT mellitus, inflammatory diseases, cancer, or autoimmune diseases,
 PT comprises exposing a sample to a phage display library and recovering
 PT phage bound to the sample.

PS Claim 56; Page 207; 298pp; English.

XX This invention relates to a novel method for identifying disease
 CC targeting peptides. The method comprises exposing a sample from an organ,
 CC tissue or cell type of interest, to a phage display library and
 CC recovering phage bound to the sample (the phage expresses targeting
 CC peptides). The peptides identified by the method of the invention may

CC have cytostatic, immunosuppressive, anti-inflammatory, antiarthritic,
 CC antiatherosclerotic, antidiabetic, antibacterial and antiviral
 CC activities. The methods and composition are useful for identifying
 CC targeting peptides and one or more receptors for a targeting peptide. The
 CC targeting peptides are used for selective delivery of therapeutic agents,
 CC including gene therapy vectors and fusion proteins, to specific organs,
 CC tissues, or cell types in subject. The targeting peptide may also be used
 CC for treating diseases such as diabetes mellitus, inflammatory diseases,
 CC arthritis, atherosclerosis, cancer, autoimmune diseases, bacterial and
 CC viral infections and Hodgkin's disease. The present sequence represents a
 CC targeting peptide of the invention

XX Sequence 9 AA;

Query Match 64.0%; Score 32; DB 5; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.8e+06;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSVPPLTVC 9

DB 1 CSPPPLTVC 9

RESULT 4

ID ADK65202 standard; peptide; 9 AA.

XX ADK65202;

06-MAY-2004 (first entry)

DE Human VEGF-D-derived peptide #18 for anti-angiogenesis treatment.

XX antiangiogenic; cytostatic; antiinflammatory; immunosuppressive;
 KW ophthalmological; gynecological; antiarteriosclerotic; virucide;
 KW hepatotropic; dermatological; anti-HIV; antidiabetic; antipsoriatic;
 KW antirheumatic; antiarthritic; antithyroid; immunization; angiogenesis;
 KW vascular endothelial growth factor; VEGF; neuropilin;
 KW placental growth factor; tumor; neoplasias; metastases; inflammation;
 KW autoimmunity; eye disease; arthritis; endometriosis; arteriosclerosis;
 KW edema; hepatitis; Kaposi sarcoma; diabetes; psoriasis;
 KW rheumatoid arthritis; thyroiditis; diabetic retinopathy;
 KW transplant rejection; macular degeneration; neovascular glaucoma;
 KW hemangioma; angiofibroma.

XX Homo sapiens.

XX WO2003086450-A1.

XX 23-OCT-2003.

XX 11-APR-2003; 2003WO-CU0000004.

XX 15-APR-2002; 2002CU-00000076.

XX (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.

XX Bequet Romero M, Acevedo Castro BE, Gavilondo Cowley JV;

XX Fernandez Molina LE, Lopez Ochoa O, Silva Rodriguez RDLC;

XX Musachio Lasa A, Galban Rodriguez E, Vazquez Blonquist DM;

XX WPI; 2003-833615/77.

XX Active immunization against angiogenic proteins, useful for treating e.g.
 PT tumors and inflammation, particularly contains vascular endothelial
 PT growth factor or its receptor.

PS Disclosure; Page 18; 53pp; Spanish.

XX The invention relates to an active immunization against angiogenic
 CC proteins comprising administration of a vaccination composition (A),
 CC optionally containing an adjuvant, that comprises polypeptides (I),
 CC directly associated with an increase in angiogenesis, their variants, or

CC their encoding polynucleotides (II). Angiogenesis-associated polypeptides
 CC are: members of the vascular endothelial growth factor (VEGF) family,
 CC especially the 121, 165 or 189 isoforms of VEGF-A, the 167 isoform of
 CC VEGF-B, or VEGF-C or -D; a (co-)receptor of VEGF, particularly VEGFR-1,
 CC 2 or -3; NRP-1 or -2 (members of the neuropilin family); or placental
 CC growth factor. (A) is used for treatment or prevention of tumors in
 CC mammals, particularly humans but also farm animals and pets, also many
 CC other conditions associated with excessive angiogenesis, specifically
 CC malignant or benign neoplasias (and their metastases), acute or chronic
 CC inflammation, autoimmunity and eye diseases (claimed). Among the diseases
 CC that may be treated are arthritis, endometriosis, arteriosclerosis,
 CC edema, infectious diseases (hepatitis and Kaposi sarcoma), diabetes,
 CC psoriasis, rheumatoid arthritis, thyroiditis, diabetic retinopathy,
 CC transplant rejection, macular degeneration, neovascular glaucoma, the
 CC hemangioma and angiofibroma. The method destroys cells that are the
 CC source of angiogenic proteins, rather than just neutralizing the activity
 CC of such proteins (as in passive immunization). This sequence represents
 CC an immunisation peptides of the invention derived from the VEGF proteins.

XX Sequence 9 AA;

Query Match 64.0%; Score 32; DB 7; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVPLTSV 8

DB 3 SVPLTSV 9

RESULT 5

ID ABJ37356 standard; peptide; 7 AA.

XX ABJ37356;

08-MAY-2003 (first entry)

DE G-protein coupled receptor peptide region #68.

XX Compound library; microenvironment; G-protein Coupled Receptor; GPCR.

XX Unidentified.

XX WO2003004147-A2.

XX 16-JAN-2003.

XX 05-JUL-2002; 2002WO-GB003094.

XX 06-JUL-2001; 2001GB-00016570.

XX (BIOF-) BIOFOCUS PLC.

XX Crossley R, Rose VS, Stevens AP;

XX WPI; 2003-221549/21.

XX Producing compound library, by generating biological target model using
 PT target sequence information, defining microenvironments interacting with
 PT ligand and motifs interacting with microenvironment, and assembling
 PT motifs.

PS Disclosure; Fig 3; 39pp; English.

XX The invention relates to a novel method for producing a compound library.
 CC The novel method involves reducing a biological target into a group of
 CC one or more amino acids required for interaction with a ligand, to
 CC generate a model of the biological target, using the model to define a
 CC microenvironment in the biological target, capable of interacting with the
 CC ligand, defining motifs which interact with the microenvironment, and
 CC assembling the motifs to generate a compound library for synthesis. The
 CC novel method is useful to produce compound libraries for screening

CC natural ligands such as peptides and proteins or for producing chemical
CC compounds based on drug motifs for screening. This sequence represents a
CC peptide of a G-protein Coupled Receptor (GPCR), which relates to the
CC novel compound library production method of the invention
XX
SQ Sequence 7 AA;

Query Match 60.0%; Score 30; DB 6; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSVPLT 6
DB 1 CSLPLT 6
||:||||

RESULT 6
ABJ37436
ID ABJ37436 standard; peptide; 7 AA.
XX
AC ABJ37436;
XX
DT 08-MAY-2003 (first entry)
XX
DE G-protein coupled receptor endothelin ET-A receptor peptide #68.
XX
DE Compound library; microenvironment; G-protein Coupled Receptor; GPCR.
XX
KW Unidentified.
XX
OS WO2003004147-A2.
XX
PN 16-JAN-2003.
XX
PD 05-JUL-2002; 2002WO-GB003094.
XX
PF 06-JUL-2001; 2001GB-00016570.
XX
PR (BIOF-) BIOFOCUS PLC.
XX
PA Crossley R, Rose VS, Stevens AP;
XX
PI WPI; 2003-221549/21.
XX
DR Producing compound library, by generating biological target model using
PT target sequence information, defining microenvironments interacting with
PT ligand and motifs interacting with microenvironment, and assembling
PT motifs.
XX
PS Disclosure; Fig 7; 39pp; English.
XX
CC The invention relates to a novel method for producing a compound library.
CC The novel method involves reducing a biological target into a group of
CC one or more amino acids required for interaction with a ligand, to
CC generate a model of the biological target, using the model to define a
CC microenvironment in the biological target capable of interacting with the
CC ligand, defining motifs which interact with the microenvironment, and
CC assembling the motifs to generate a compound library for synthesis. The
CC novel method is useful to produce compound libraries for screening
CC natural ligands such as peptides and proteins or for producing chemical
CC compounds based on drug motifs for screening. This sequence represents a
CC peptide of a G-protein Coupled Receptor (GPCR) including Endothelin Et-A
CC receptor, which relates to the novel compound library production method
CC of the invention
XX
SQ Sequence 7 AA;

Query Match 60.0%; Score 30; DB 6; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSVPLT 6
||:||||

Db 1 CSLPLT 6

RESULT 7
ABB05266
ID ABB05266 standard; peptide; 9 AA.
XX
AC ABB05266;
XX
DT 29-AUG-2003 (revised)
DT 04-APR-2002 (first entry)
XX
DE Vascular endothelial growth factor binding peptide V-20 SEQ ID NO:98.
XX
KW Human; tumour necrosis factor alpha; TNF-alpha; VEGF; detergent; stain;
KW bacteriophage; phage library; vascular endothelial growth factor;
KW collar soil; polyurethane; egg; tea; hair; skin; cleaning composition.
XX
OS Unidentified bacteriophage.
OS Unidentified.
XX
PN WO200179479-A2.
XX
PD 25-OCT-2001.
XX
PF 11-APR-2001; 2001WO-US011811.
XX
PR 14-APR-2000; 2000US-0197259P.
XX
PA (GEMV) GENENCOR INT INC.
XX
PI Estell DA, Murray CJ, Tijerina P, Chen Y;
XX
DR WPI; 2002-139323/18.
XX
PT Screening ligand library comprises allowing binding of ligand with anti-
PT target, contacting unbound ligands with selected target to form target-
PT bound ligand complex and identifying target bound ligands on the complex.
XX
PS Claim 22; Page 28; 51pp; English.
XX
CC The present invention describes a method for screening a ligand library
CC (LL). The method comprises: (a) contacting the LL with an anti-target
CC (AT) to allow the ligands to bind to the AT; (b) separating unbound
CC ligands; (c) contacting the unbound ligands with a selected target (T) to
CC allow binding of unbound ligands to (T) to form a (T)-bound ligand
CC complex (C); (d) separating (C) from ligands which do not bind (T); and
CC (e) identifying (T)-bound ligands on (C). The method can be used for
CC screening a ligand library, e.g., a library of peptides, polypeptides,
CC non-polypeptides or oligonucleotides. A ligand (I) identified by the
CC method can be used in a cleaning, therapeutic or personal care
CC application. The method is preferably useful for identifying peptide
CC useful in cleaning compositions, which involves contacting peptide
CC library with AT such as fabric, ceramic, glass, stainless steel or
CC plastic; separating unbound AT peptides; contacting unbound AT peptides
CC with a target which is a stain such as porphyrin derived stain, tannin
CC derived stain, carotenoid pigment derived stain, anthocyanin pigment
CC derived stain, soil-based derived stain, oil-based derived stain, and
CC human body stain, to allow unbound peptide to bind with the stain to form
CC the stain-bound peptide complex and identifying the stain-bound peptide on
CC the stain-bound peptide complex. A selective targeting method for
CC screening a library of ligands that bind to a target may be used to
CC identify ligands that bind to a target under harsh conditions. The
CC selective targeting method may be used to screen and identify a ligand
CC useful for therapeutic intervention, e.g., a library of ligands may be
CC screened to identify a tumour-bound ligand. The selective targeting
CC method may be used to identify cell type specific surface molecules.
CC Preferred anti-targets include one or more different cell types, cells in
CC different states, or cells that do not display the surface molecule.
CC ABB05232 to ABB05346 represent phage-peptides ligands which are used in
CC the exemplification of the present invention. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX

```

SQ      Sequence 9 AA;
Query Match      60.0%; Score 30; DB 5; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 CSVPLTSVC 9
Db      1 CRMPTSKVC 9

RESULT 8
ADK09526
ID      ADK09526 standard; peptide; 9 AA.
XX
AC      ADK09526;
XX
DT      06-MAY-2004 (first entry)
XX
DE      Human papillomavirus peptide #1581.
XX
KW      pathogenic virus; alternative reading frame; antigenic determinant;
KW      virucide; vaccine; therapeutic agent; infection; HPV.
XX
OS      Human papillomavirus.
XX
PN      WO2004011650-A2.
XX
PD      05-FEB-2004.
XX
PF      24-JUL-2003; 2003WO-EP008112.
XX
PR      24-JUL-2002; 2002AT-00001124.
PR      11-JUL-2003; 2003EP-00450171.
XX
PA      (INTE-) INTERCELL AG.
XX
PI      Mattner F, Schmidt W, Habel A;
XX
WPI; 2004-169243/16.
XX
PT      New polypeptide encoded by an alternative reading frame of a pathogenic
PT      virus comprising an antigenic determinant, useful for treating or
PT      preventing an infection with the pathogenic virus.
XX
PS      Claim 18; Page 190; 220pp; English.
XX
CC      This invention relates to a novel polypeptide encoded by an alternative
CC      reading frame of a pathogenic virus, where the polypeptide starts with a
CC      methionine amino acid residue, which comprises an antigenic determinant
CC      and more than 7 amino acid residues. The invention may be useful for the
CC      production of compounds with a virucide activity or the development of a
CC      vaccine. The polypeptide or its fragments may be useful as a therapeutic
CC      agent. It is also useful for the manufacture of a medicament for treating
CC      or preventing an infection with the pathogenic virus. The present
CC      sequence is that of a human papillomavirus (HPV) epitope peptide of the
CC      invention.
XX
SQ      Sequence 9 AA;
Query Match      58.0%; Score 29; DB 8; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 CSVPLTSV 8
Db      1 CQPLTNI 8

RESULT 9
ADR42755
ID      ADR42755 standard; peptide; 9 AA.
XX

```

```

AC      ADR42755;
XX
DT      18-NOV-2004 (first entry)
XX
DE      Modulatory chemokine-binding peptide BKT-P78.
XX
KW      Chemokine-binding peptide; MCP-1; SDF-1alpha; MIG; eotaxin;
KW      interleukin-8; abnormal cell migration; vaccine; inflammation; allergy;
KW      non-optimal immune response; autoimmune reaction; allograft rejection;
KW      diabetes; sepsis; cancer; malignant cell growth; bacterial infection;
KW      viral infection; arthritis; colitis; psoriasis; atherosclerosis;
KW      hypertension; reperfusion ischaemia.
XX
OS      Synthetic.
XX
PN      US2004171552-A1.
XX
PD      02-SEP-2004.
XX
PF      28-AUG-2003; 2003US-00649873.
XX
PR      27-FEB-2003; 2003WO-IL000155.
XX
PA      (BIOK-) BIOKINE THERAPEUTICS LTD.
XX
PI      Peled A, Eizenberg O, Vaizel-Ohayon D;
XX
WPI; 2004-625117/60.
XX
PT      New peptidic chemokine modulators for modulating a biological effect of a
PT      chemokine, useful for treating a condition involving abnormal cell
PT      migration in a subject, e.g. inflammatory condition, or cancer
PT      metastasis.
XX
PS      Claim 19; SEQ ID NO 29; 50pp; English.
XX
CC      The invention relates to peptidic chemokine modulators for modulating a
CC      biological effect of a chemokine comprising a molecule composed of the
CC      amino acids histidine (H), serine (S), alanine (A), leucine (L),
CC      isoleucine (I), lysine (K), arginine (R), threonine (T), and proline (P),
CC      and featuring at least 2 Histidines spread along said molecule, where the
CC      molecule features an overall positive charge (family 1) or a molecule
CC      composed of the amino acids H, P, T, L, R, Tryptophan (W), phenylalanine
CC      (F), and featuring at least two neighbouring histidines, where the
CC      molecule features an overall positive charge (family 2) and/or a molecule
CC      comprising a peptide having an amino acid sequence from a list, given in
CC      the specification. Also included are a composition for treating a
CC      condition involving abnormal cell migration in a subject comprising a
CC      therapeutic agent for administering to the subject, where therapeutic
CC      agent is any of the modulators cited above), a method for treating a
CC      disease modulated through and/or caused by binding of a chemokine to a
CC      chemokine receptor in a subject (by administering the therapeutic agent),
CC      an antibody for binding a chemokine-binding receptor (comprising the
CC      antibody capable of recognising at least a portion of a chemokine binding
CC      receptor, where the antibody also recognises a peptide of the sequence of
CC      the modulator), a vaccine formed with the antibody and a method for
CC      producing an antibody (by inducing formation of antibody against a
CC      peptide having the sequence of the chemokine modulator, where the
CC      antibody is also capable of recognising a chemokine binding receptor).
CC      The method, therapeutic agents and compositions are useful for treating a
CC      disease modulated through and/or caused by binding of a chemokine to a
CC      chemokine receptor, e.g. primary and secondary inflammation, allergy, non
CC      -optimal immune response, autoimmune reaction, allograft rejection,
CC      diabetes, sepsis, cancer, any type of malignant cell growth, acute and
CC      chronic bacterial and viral infections, arthritis, colitis, psoriasis,
CC      atherosclerosis, hypertension or reperfusion ischaemia. The present
CC      sequence is a modulatory chemokine-binding peptide of the invention
CC      binding chemokines MCP-1, SDF-1alpha, MIG, eotaxin and interleukin-8.
XX
SQ      Sequence 9 AA;
Query Match      58.0%; Score 29; DB 8; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.8e+06;

```

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
 Db 1 CSRPMNVC 9

RESULT 10
 ADE98247
 ID ADE98247 standard; peptide; 8 AA.
 XX AC ADE98247;
 XX DT 12-FEB-2004 (first entry)
 XX DE Immunogenic HLA-A2.1 binding peptide #729.
 XX KW cytostatic; anti-inflammatory; hepatotropic; virucide; anti-HIV;
 KW nephrotropic; neuroprotective; antiarthritic; antirheumatic;
 KW immunosuppressive; dermatological; muscular; nephrotropic; thyromimetic;
 KW haemostatic; antithyroid; antianaemic; anabolic; hypertensive;
 KW immunogenic peptide composition; immune response; prostate cancer;
 KW hepatitis B; hepatitis C; AIDS; renal carcinoma; cervical carcinoma;
 KW lymphoma; cytomegalovirus; CMV; condyloma acuminatum;
 KW autoimmune associated disorder; multiple sclerosis; rheumatoid arthritis;
 KW Sjogren syndrome; scleroderma; polymyositis; dermatomyositis;
 KW systemic lupus erythematosus; juvenile rheumatoid arthritis;
 KW ankylosing spondylitis; myasthenia gravis; MG; bullous pemphigoid;
 KW pemphigus; glomerulonephritis; Goodpasture's syndrome;
 KW autoimmune haemolytic anaemia; Hashimoto's disease; pernicious anaemia;
 KW idiopathic thrombocytopenic purpura; Grave's disease; Addison's disease;
 KW human leukocyte antigen A2.1; HLA A2.1;
 KW immunogenic HLA-A2.1 binding peptide.
 XX OS Synthetic.
 XX PN US2003185822-A1.
 XX PD 02-OCT-2003.
 XX PF 03-APR-2002; 2002US-00116557.
 XX PR 05-MAR-1993; 93US-00027146.
 XX PR 04-JUN-1993; 93US-00073205.
 XX PR 29-NOV-1993; 93US-00159184.
 XX PR 02-DEC-1994; 94US-00349177.
 XX PA (GREY/) GREY H M.
 XX PA (SETT/) SETTE A.
 XX PA (SIDN/) SIDNEY J.
 XX PI Grey HM, Sette A, Sidney J;
 XX DR WPI; 2004-041186/04.
 XX PT Immunogenic peptide composition for preventing, treating or diagnosing
 PT pathological states, e.g. prostate cancer, hepatitis B and C, Acquired
 PT immunodeficiency syndrome, and renal carcinoma, includes conserved
 PT residues at specified positions.
 XX PS Example 5; Page 12; 38pp; English.
 XX CC The invention describes an immunogenic peptide composition comprising 9
 CC residues including a first conserved residue at a second position from N-
 CC terminus, and a second conserved residue at C-terminal position. The
 CC inventive peptide composition is used to elicit an immune response
 CC against a desired antigen for preventing, treating or diagnosing
 CC pathological states, e.g. prostate cancer, hepatitis B, hepatitis C,
 CC AIDS, renal carcinoma, cervical carcinoma, lymphoma, cytomegalovirus
 CC (CMV), and condyloma acuminatum. It is also used to treat autoimmune
 CC associated disorders, e.g. multiple sclerosis, rheumatoid arthritis,
 CC Sjogren syndrome, scleroderma, polymyositis, dermatomyositis, systemic
 CC lupus erythematosus, juvenile rheumatoid arthritis, ankylosing

CC spondylitis, myasthenia gravis (MG), bullous pemphigoid, pemphigus,
 CC glomerulonephritis, Goodpasture's syndrome, autoimmune hemolytic anemia,
 CC Hashimoto's disease, pernicious anaemia, idiopathic thrombocytopenic
 CC purpura, Grave's disease, and Addison's disease. The invention defines
 CC positions within a motif enabling the selection of the peptides, which
 CC will bind efficiently to human leukocyte antigen (HLA) A2.1. This is the
 CC amino acid sequence of an immunogenic HLA-A2.1 binding peptide.

XX SQ Sequence 8 AA;

Query Match 56.0%; Score 28; DB 8; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPLTS 7
 Db 1 CEVPATS 7

RESULT 11
 ADO24736
 ID ADO24736 standard; peptide; 8 AA.
 XX AC ADO24736;
 XX DT 29-JUL-2004 (first entry)
 XX DE Mouse leptin protein peptide LEP (116-123).
 XX KW anorectic; antidiabetic; anabolic; body mass modulator;
 KW insulin release modulator; leptin; OB3 peptide; food intake reduction;
 KW blood glucose reduction; mouse.
 XX OS Mus sp.
 XX PN WO2004039832-A2.
 XX PD 13-MAY-2004.
 XX PF 31-OCT-2003; 2003WO-US034820.
 XX PR 31-OCT-2002; 2002US-0422723P.
 XX PA (CLPM-) CLF MEDICAL TECHNOLOGY ACCELERATION PROG.
 XX PI Grasso P, Lee DW, Leinung MC, Rozhavskaya-Arena M;
 XX DR WPI; 2004-400140/37.
 XX PT Novel isolated polypeptide comprising leptin-related OB3 peptide sequence
 PT capable of modulating body mass, useful for treating or preventing
 PT obesity, Type II diabetes mellitus or hyperglycemia.
 XX PS Example 11; Page 83; 143pp; English.
 XX CC The invention relates to an isolated polypeptide (I) comprising a leptin-
 CC related OB3 peptide sequence, where at least one of the amino acid is in
 CC the D-Isoform. The polypeptide reduces food intake and blood glucose.
 CC This sequence corresponds to amino acids 116-123 of the mouse leptin
 CC protein.
 XX SQ Sequence 8 AA;

Query Match 56.0%; Score 28; DB 8; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSVPLTS 7
 Db 2 CSLPQTS 8

RESULT 12

ADRI11353
 ID ADRI11353 standard; peptide; 8 AA.
 XX
 AC ADRI11353;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE HLA-A2.1 binding assay poly-A-binder peptide #4.
 XX
 KW cytostatic; virucide; immunosuppressive; anti-HIV; hepatotropic;
 KW antiinflammatory; neuroprotective; antirheumatic; antithyroidic;
 KW dermatological; muscular; nephrotropic; antianaemic; thyromimetic;
 KW haemostatic; anabolic; hypertensive; antithyroid; HLA-A2.1 binder;
 KW immune response stimulator; vaccine; HLA-A2.1; immunogenic;
 KW major histocompatibility complex; MHC; human viral disease;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW cervical carcinoma; lymphoma; cytomegalovirus; condyloma acuminatum;
 KW cancer; autoimmune disease; multiple sclerosis; rheumatoid arthritis;
 KW Sjogren syndrome; scleroderma; polymyositis; dermatomyositis;
 KW systemic lupus erythematosus; juvenile rheumatoid arthritis;
 KW ankylosing spondylitis; myasthenia gravis; bullous pemphigoid; pemphigus;
 KW glomerulonephritis; Goodpasture's syndrome;
 KW autoimmune haemolytic anaemia; Hashimoto's disease; pernicious anaemia;
 KW idiopathic thrombocytopenic purpura; Grave's disease; Addison's disease;
 KW T cell activation; poly-A-binder; HLA-A2.1 binding assay.
 XX
 OS Unidentified.
 XX
 PN US2004157780-A1.
 XX
 PD 12-AUG-2004.
 XX
 PF 04-FEB-2004; 2004US-00770493.
 XX
 PR 29-NOV-1993; 93US-00159184.
 PR 04-MAR-1994; 94US-00205713.
 XX
 PA (EPIM-) EPIMUNE INC.
 XX
 PI Grey HM, Sette A, Sidney J;
 XX
 WIPI; 2004-592793/57.
 DR
 XX
 PT Pharmaceutical composition useful for treating viral disease, autoimmune
 PT disease and cancer comprises a peptide capable of binding HLA-A2.1
 PT molecule and inducing an immune response.
 XX
 PS Example 5; Page 12; 36pp; English.
 XX
 CC The invention describes a pharmaceutical composition (P1) comprises a
 CC carrier and a peptide (A1) capable of binding an HLA-A2.1 molecule and
 CC inducing an immune response in a mammal. Also described are: a
 CC composition (C1) comprising an immunogenic peptide having an HLA-A2.1
 CC binding motif and 9 residues selected from either first conserved
 CC residues selected from I, V, A and T at the second position from the N-
 CC terminus and second conserved residues selected from V, L, I, A and M at
 CC the carbon-terminal position; or first conserved residue selected from L,
 CC M, I, V, A or T at the second position from the N-terminus; and a second
 CC conserved residue selected from A or M at the C-terminal position; and a
 CC composition (C2) comprising an immunogenic peptide having an HLA-A2.1
 CC binding motif and having 10 residues selected from a first conserved
 CC residue selected from L, M, I, V, A, or T at the second position from the
 CC N-terminus; and a second conserved residue selected from V, I, L, A or M
 CC at the C-terminal position. The first and second conserved residues are
 CC separated by 7 residues. Also disclosed are new peptides capable of
 CC binding selected major histocompatibility complex (MHC) molecules and
 CC inducing an immune response. The pharmaceutical compositions are useful
 CC for the treatment of human viral diseases (e.g. prostate cancer,
 CC hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical carcinoma,
 CC lymphoma, cytomegalovirus and condyloma acuminatum), cancers or
 CC autoimmune diseases, and to relieve the symptoms of, treat or prevent the
 CC occurrence or reoccurrence of autoimmune diseases e.g. multiple sclerosis
 CC (MS), rheumatoid arthritis, Sjogren syndrome, scleroderma, polymyositis,

CC dermatomyositis, systemic lupus erythematosus, juvenile rheumatoid
 CC arthritis, ankylosing spondylitis, myasthenia gravis, bullous pemphigoid,
 CC pemphigus, glomerulonephritis, Goodpasture's syndrome, autoimmune
 CC haemolytic anaemia, Hashimoto's disease, pernicious anaemia, idiopathic
 CC thrombocytopenic purpura, Grave's disease, and Addison's disease. The
 CC compositions are capable of specifically binding glycoproteins encoded by
 CC HLA-A2.1 allele and inducing T cell activation in T cells restricted by
 CC the A2.1 allele. This is the amino acid sequence of a poly-A-binder
 CC peptide used for HLA-A2.1 binding assays.
 XX
 SQ Sequence 8 AA;

Query Match 56.0%; Score 28; DB 8; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CSVPPLTS 7
 Db 1 CEVPATS 7

RESULT 13
 ADC44660

ID ADC44660 standard; peptide; 9 AA.

XX AC ADC44660;

XX DT 18-DEC-2003 (first entry)

XX DE Endothelial cell binding peptide SEQ ID NO:389.

XX KW endothelial cell binding protein; EGBP; anti-tumour; cytostatic;
 KW vasotropic; antipsoriatic; dermatological; ophthalmological;
 KW antidiabetic; antiarthritic; vulnery; antitumor; antiinflammatory;
 KW antibacterial; gynaecological; angiogenesis.

OS Synthetic.

XX PN WO2003037172-A2.

XX PD 08-MAY-2003.

XX PF 01-NOV-2002; 2002WO-US035258.

XX PR 01-NOV-2001; 2001US-0334822P.

XX PA (GPCB-) GPC BIOTECH INC.

XX PI Gyuris J, Lamphere L, Morris AJ, Tsaloun K;

XX WIPI; 2003-482072/45.

XX Novel synthetic or recombinant polypeptide useful for promoting, reducing
 PT proliferation and/or migration of endothelial cells, and for modulating
 PT angiogenesis, has endothelial cell binding protein sequences.

XX Claim 3; SEQ ID NO 389; 126pp; English.

XX The invention relates to a novel isolated, synthetic or recombinant
 CC peptide or polypeptide which includes one or more endothelial cell
 CC binding protein (EGBP) sequences. A peptide of the invention has anti-
 CC tumour, cytostatic, vasotropic, antipsoriatic, dermatological,
 CC ophthalmological, antidiabetic, antiarthritic, vulnery, antitumor,
 CC antiinflammatory, antibacterial, and gynaecological activity. The peptide
 CC is useful for promoting, reducing the proliferation and/or migration of
 CC endothelial cells, by treating the cells with an EGBP agonist, which is
 CC preferably the peptide, to promote proliferation and/or migration of the
 CC treated cells, and for reducing or promoting angiogenesis, by treating
 CC the cells with an EGBP antagonist, which is preferably the peptide of the
 CC invention. A peptide of the invention is also useful for manufacturing a
 CC medicament for promoting angiogenesis, by admixing an EGBP agonist or
 CC EGBP antagonist to promote or reduce angiogenesis at one or more sites in
 CC a treated mammal. The medicament is useful for promoting or reducing

CC angiogenesis. ECBP sequences are useful to alter the infectivity spectrum
CC of a viral particle. The present sequence represents an ECBP of the
CC invention.

XX
SQ Sequence 9 AA;

Query Match 56.0%; Score 28; DB 7; Length 9;
Best Local Similarity 33.3%; Pred. No. 1.8e+06;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSVPLTVC 9
| : : : :
Db 1 CDLPSTRIC 9

RESULT 14

ADK65204
ID ADK65204 standard; peptide; 9 AA.

XX
AC ADK65204;

XX
DT 06-MAY-2004 (first entry)

XX
DE Human VEGF-D-derived peptide #20 for anti-angiogenesis treatment.

XX
KW antiangiogenic; cytostatic; antiinflammatory; immunosuppressive;
KW ophthalmologic; gynecologic; antiarteriosclerotic; virucide;
KW hepatotropic; dermatologic; anti-HIV; antidiabetic; antipsoriatic;
KW antirheumatic; antiarthritic; antichyroid; immunization; angiogenesis;
KW vascular endothelial growth factor; VEGF; neuropilin;
KW placental growth factor; tumor; neoplasias; metastases; inflammation;
KW autoimmunity; eye disease; arthritis; endometriosis; arteriosclerosis;
KW edema; hepatitis; Kaposi sarcoma; diabetes; psoriasis;
KW rheumatoid arthritis; thyroiditis; diabetic retinopathy;
KW transplant rejection; macular degeneration; neovascular glaucoma;
KW hemangioma; angiofibroma.

XX
OS Homo sapiens.

XX
PN WO2003086450-A1.

XX
PD 23-OCT-2003.

XX
PF 11-APR-2003; 2003WO-CU000004.

XX
PR 15-APR-2002; 2002CU-00000076.

XX
PA (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.

XX
PI Bequet Romero M, Acevedo Castro BE, Gavilondo Cowley JV;
PI Fernandez Molina LE, Lopez Ochoa O, Silva Rodriguez RDLG;
PI Musachio Lasa A, Galban Rodriguez E, Vazquez Blomquist DM;
XX
XX WPI; 2003-833615/77.

XX
PT Active immunization against angiogenic proteins, useful for treating e.g.
PT tumors and inflammation, particularly contains vascular endothelial
PT growth factor or its receptor.

XX
PS Disclosure; Page 18; 53pp; Spanish.

XX
CC The invention relates to an active immunization against angiogenic
CC proteins comprising administration of a vaccination composition (A),
CC optionally containing an adjuvant, that comprises polypeptides (I)
CC directly associated with an increase in angiogenesis, their variants, or
CC their encoding polynucleotides (II). Angiogenesis-associated polypeptides
CC are: members of the vascular endothelial growth factor (VEGF) family,
CC especially the 121, 165 or 189 isoforms of VEGF-A, the 167 isoform of
CC VEGF-B, or VEGF-C or -D; a (co-)receptor of VEGF, particularly VEGFR-1, -
CC 2 or -3; NRP-1 or -2 (members of the neuropilin family); or placental
CC growth factor. (A) is used for treatment or prevention of tumors in
CC mammals, particularly humans but also farm animals and pets, also many
CC other conditions associated with excessive angiogenesis, specifically

CC malignant or benign neoplasias (and their metastases), acute or chronic
CC inflammation, autoimmunity and eye diseases (claimed). Among the diseases
CC that may be treated are arthritis, endometriosis, arteriosclerosis,
CC edema, infectious diseases (hepatitis and Kaposi sarcoma), diabetes,
CC psoriasis, rheumatoid arthritis, thyroiditis, diabetic retinopathy,
CC transplant rejection, macular degeneration, neovascular glaucoma,
CC hemangioma and angiofibroma. The method destroys cells that are the
CC source of angiogenic proteins, rather than just neutralizing the activity
CC of such proteins (as in passive immunization). This sequence represents
CC an immunisation peptides of the invention derived from the VEGF proteins.

XX
SQ Sequence 9 AA;

Query Match 56.0%; Score 28; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VPLTSV 8
| : : : :
Db 1 VPLTSV 6

RESULT 15

ADO24737
ID ADO24737 standard; peptide; 9 AA.

XX
AC ADO24737;

XX
DT 29-JUL-2004 (first entry)

XX
DE Mouse leptin protein peptide LEP(116-124).

XX
KW anorectic; antidiabetic; anabolic; body mass modulator;
KW insulin release modulator; leptin; OB3 peptide; food intake reduction;
KW blood glucose reduction; mouse.

XX
OS Mus sp.

XX
PN WO2004039832-A2.

XX
PD 13-MAY-2004.

XX
PF 31-OCT-2003; 2003WO-US034820.

XX
PR 31-OCT-2002; 2002US-0422723P.

XX
PA (CLFW-) CLF MEDICAL TECHNOLOGY ACCELERATION PROG.

XX
PI Grasso P, Lee DW, Leinung MC, Rozhavskaia-Arena M;

XX
DR WPI; 2004-400140/37.

XX
PT Novel isolated polypeptide comprising leptin-related OB3 peptide sequence
PT capable of modulating body mass, useful for treating or preventing
PT obesity, Type II diabetes mellitus or hyperglycemia.

XX
PS Example 11; Page 83; 143pp; English.

XX
CC The invention relates to an isolated polypeptide (I) comprising a leptin-
CC related OB3 peptide sequence, where at least one of the amino acid is in
CC the D-isoform. The polypeptide reduces food intake and blood glucose.
CC This sequence corresponds to amino acids 116-124 of the mouse leptin
CC protein.

XX
SQ Sequence 9 AA;

Query Match 56.0%; Score 28; DB 8; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSVPTS 7
| : : : :
Db 2 CSLPOTS 8

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Job time : 59.5 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 11:24:02 ; Search time 67 Seconds
(without alignments)
44,542 Million cell updates/sec

Title: US-09-761-636A-10

Perfect score: 50

Sequence: 1 CSVPLTSVC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 135600

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	50	100.0	9	9 US-09-761-636A-10	Sequence 10, Appl
2	32	64.0	9	15 US-10-363-208-24	Sequence 24, Appl
3	30	60.0	9	9 US-09-832-723-98	Sequence 98, Appl
4	30	60.0	9	14 US-10-303-331-98	Sequence 98, Appl
5	29	58.0	9	16 US-10-649-873-29	Sequence 29, Appl
6	28	56.0	8	17 US-10-698-510-41	Sequence 41, Appl
7	28	56.0	9	14 US-10-286-457-389	Sequence 389, Appl
8	28	56.0	9	17 US-10-698-510-42	Sequence 42, Appl
9	26	52.0	7	17 US-10-808-187-782	Sequence 782, Appl
10	26	52.0	9	9 US-09-760-599-34	Sequence 34, Appl
11	26	52.0	9	14 US-10-254-446A-147	Sequence 147, Appl
12	26	52.0	9	16 US-10-649-873-35	Sequence 35, Appl
13	25	50.0	7	17 US-10-808-187-1071	Sequence 1071, Ap

14	25	50.0	8	15	US-10-462-452-480	Sequence 480, App
15	25	50.0	8	15	US-10-601-953-609	Sequence 609, App
16	25	50.0	8	16	US-10-322-266-481	Sequence 481, App
17	25	50.0	9	9	US-09-760-599-25	Sequence 25, Appl
18	25	50.0	9	14	US-10-006-869-3614	Sequence 3614, Ap
19	25	50.0	9	14	US-10-286-457-387	Sequence 387, App
20	25	50.0	9	15	US-10-395-032-3614	Sequence 3614, Ap
21	25	50.0	9	17	US-10-838-289-254	Sequence 254, App
22	25	50.0	9	17	US-10-615-479B-25	Sequence 25, Appl
23	24	48.0	7	9	US-09-761-636A-11	Sequence 11, Appl
24	24	48.0	7	15	US-10-458-334-2	Sequence 2, Appl
25	24	48.0	7	17	US-10-698-510-2	Sequence 2, Appl
26	24	48.0	7	17	US-10-698-510-20	Sequence 20, Appl
27	24	48.0	7	17	US-10-698-510-21	Sequence 21, Appl
28	24	48.0	7	17	US-10-698-510-22	Sequence 22, Appl
29	24	48.0	7	17	US-10-698-510-23	Sequence 23, Appl
30	24	48.0	7	17	US-10-698-510-24	Sequence 24, Appl
31	24	48.0	7	17	US-10-698-510-25	Sequence 25, Appl
32	24	48.0	7	17	US-10-698-510-26	Sequence 26, Appl
33	24	48.0	7	17	US-10-698-510-27	Sequence 27, Appl
34	24	48.0	7	17	US-10-698-510-40	Sequence 40, Appl
35	24	48.0	9	8	US-08-344-824-293	Sequence 293, App
36	24	48.0	9	9	US-09-760-599-9	Sequence 9, Appl
37	24	48.0	9	9	US-09-760-599-17	Sequence 17, Appl
38	24	48.0	9	9	US-09-760-599-36	Sequence 36, Appl
39	24	48.0	9	9	US-09-760-599-38	Sequence 38, Appl
40	24	48.0	9	9	US-09-760-599-48	Sequence 48, Appl
41	24	48.0	9	10	US-09-935-430-249	Sequence 249, App
42	24	48.0	9	10	US-09-935-430-322	Sequence 322, App
43	24	48.0	9	10	US-09-935-430-349	Sequence 349, App
44	24	48.0	9	10	US-09-935-430-464	Sequence 464, App
45	24	48.0	9	10	US-09-747-802-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-761-636A-10
; Sequence 10, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-10

Query Match 100.0%; Score 50; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
Db 1 CSVPLTSVC 9

RESULT 2
US-10-363-208-24

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; Sequence 24, Application US/10363208
; Publication No. US20040048243A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774.P005PCT
; CURRENT APPLICATION NUMBER: US/10/363,208
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(9)
; OTHER INFORMATION: synthetic construct
US-10-363-208-24

Query Match          64.0%; Score 32; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
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Db 1 CSPPLTRWC 9

RESULT 3
US-09-832-723-98
; Sequence 98, Application US/09832723
; Patent No. US20020098524A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; APPLICANT: Chen, Yiyou
; APPLICANT: Murray, Christopher J.
; APPLICANT: Tijerina, Pilar
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-2
; CURRENT APPLICATION NUMBER: US/09/832,723
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,259
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptides screened from a phage display random
; peptide library
US-09-832-723-98

Query Match          60.0%; Score 30; DB 9; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.3e+06;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
   |||||
Db 1 CRMPTSKVC 9

RESULT 4
US-10-303-331-98
; Sequence 98, Application US/10303331
; Publication No. US20030152976A1
; GENERAL INFORMATION:
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Winetzkzy, Deborah S.
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-3
; CURRENT APPLICATION NUMBER: US/10/303,331
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: US 09/832,723
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,259
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptides screened from a phage display random
; peptide library
US-10-303-331-98

Query Match          60.0%; Score 30; DB 14; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.3e+06;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
   |||||
Db 1 CRMPTSKVC 9

RESULT 5
US-10-649-873-29
; Sequence 29, Application US/10649873
; Publication No. US20040171552A1
; GENERAL INFORMATION:
; APPLICANT: Biokine Therapeutics Ltd.
; APPLICANT: Peled, Amnon
; APPLICANT: Eizenberg, Orly
; APPLICANT: Vaizel-Onayon, Dalit
; TITLE OF INVENTION: NOVEL CHEMOKINE BINDING PEPTIDES CAPABLE OF MODULATING THE
; BIOLOGICAL ACTIVITY OF CHEMOKINES
; FILE REFERENCE: 26732
; CURRENT APPLICATION NUMBER: US/10/649,873
; CURRENT FILING DATE: 2003-08-28
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-649-873-29

Query Match          58.0%; Score 29; DB 16; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
   |||||
Db 1 CSRPAWVC 9

RESULT 6
US-10-698-510-41
; Sequence 41, Application US/10698510
; Publication No. US20050049193A1
; GENERAL INFORMATION:
; APPLICANT: Grasso, Patricia
; APPLICANT: Lee, Daniel
; APPLICANT: Leinung, Matthew
; TITLE OF INVENTION: Leptin Related Peptides
; FILE REFERENCE: 19705-001CIP
; CURRENT APPLICATION NUMBER: US/10/698,510
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/422,723
```

; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 09/377,081
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Truncated analog of mouse leptin
US-10-698-510-41

Query Match 56.0%; Score 28; DB 17; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSVPLTS 7
||:|
Db 2 CSLPQTS 8

RESULT 7
US-10-286-457-389
; Sequence 389, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 389
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based
US-10-286-457-389

Query Match 56.0%; Score 28; DB 14; Length 9;
Best Local Similarity 33.3%; Pred. No. 1.3e+06;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
||:|
Db 1 CDLPSTRIC 9

RESULT 8
US-10-698-510-42
; Sequence 42, Application US/10698510
; Publication No. US20050049193A1
; GENERAL INFORMATION:
; APPLICANT: Grasso, Patricia
; APPLICANT: Lee, Daniel
; APPLICANT: Leinung, Matthew
; TITLE OF INVENTION: Leptin Related Peptides
; FILE REFERENCE: 19705-001CIP
; CURRENT APPLICATION NUMBER: US/10/698,510
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/422,723
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 09/377,081
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42

; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Truncated analog of mouse leptin
US-10-698-510-42

Query Match 56.0%; Score 28; DB 17; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSVPLTS 7
||:|
Db 2 CSLPQTS 8

RESULT 9
US-10-808-187-782
; Sequence 782, Application US/10808187
; Publication No. US20050090909A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
; FILE REFERENCE: V9661-0078
; CURRENT APPLICATION NUMBER: US/10/808,187
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/468,139
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/471,200
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 782
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-808-187-782

Query Match 52.0%; Score 26; DB 17; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPLTS 7
||:|
Db 1 CSKPLNS 7

RESULT 10
US-09-760-599-34
; Sequence 34, Application US/09760599
; Patent No. US20010034326A1
; GENERAL INFORMATION:
; APPLICANT: Larson Mr., Richard S.

; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
; FILE REFERENCE: SC1200/4-1C1P
; CURRENT APPLICATION NUMBER: US/09/760,599
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-760-599-34

Query Match 52.0%; Score 26; DB 9; Length 9;
Best Local Similarity 33.3%; Pred. No. 1.3e+06;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
| : | : | : |
Db 1 CALRMSIC 9

RESULT 11
US-10-254-446A-147
; Sequence 147, Application US/10254446A
; Publication No. US20030113714A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela M
; APPLICANT: Smalley, Richard E.
; APPLICANT: Ryan, Esther
; APPLICANT: Lee, Seung-Wuk
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES
; FILE REFERENCE: 119927-1066
; CURRENT APPLICATION NUMBER: US/10/254,446A
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/325,664
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 147
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage biopan
US-10-254-446A-147

Query Match 52.0%; Score 26; DB 14; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.3e+06;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
| : | : | : |
Db 1 CKLQLTNQC 9

RESULT 12
US-10-649-873-35
; Sequence 35, Application US/10649873
; Publication No. US2004017152A1
; GENERAL INFORMATION:
; APPLICANT: Biokine Therapeutics Ltd.
; APPLICANT: Peled, Amnon
; APPLICANT: Eizenberg, Orly
; APPLICANT: Vaizel-Ohayon, Dalit
; TITLE OF INVENTION: NOVEL CHEMOKINE BINDING PEPTIDES CAPABLE OF MODULATING THE
; TITLE OF INVENTION: BIOLOGICAL ACTIVITY OF CHEMOKINES
; FILE REFERENCE: 26732
; CURRENT APPLICATION NUMBER: US/10/649,873
; CURRENT FILING DATE: 2003-08-28
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-649-873-35

Query Match 52.0%; Score 26; DB 16; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.3e+06;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
| : | : | : |
Db 1 CTHPKASMC 9

RESULT 13
US-10-808-187-1071
; Sequence 1071, Application US/10808187
; Publication No. US20050009009A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
; TITLE OF INVENTION: RESPIRATORY SYNDROME (SARS)
; FILE REFERENCE: V9661-0078
; CURRENT APPLICATION NUMBER: US/10/808,187
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/468,139
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/471,200
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 1071
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-808-187-1071

Query Match 50.0%; Score 25; DB 17; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LTSVC 9
| : | : | : |
Db 1 LTSIC 5

RESULT 14
US-10-462-452-480
; Sequence 480, Application US/10462452
; Publication No. US20040037809A1
; GENERAL INFORMATION:

```
; APPLICANT: Quay, Steven
; APPLICANT: El Shafy, Mohammed Abd
; APPLICANT: Gupta, Malini
; APPLICANT: de Meireles, Jorge
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
; FILE REFERENCE: 02-02US
; CURRENT APPLICATION NUMBER: US/10/462,452
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/393,066
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 480
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-452-480

Query Match          50.0%; Score 25; DB 15; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4  PLTSVC 9
Db      1  PVTVC 6

RESULT 15
US-10-601-953-609
; Sequence 609, Application US/10601953
; Publication No. US2004007540A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
; TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
; TITLE OF INVENTION: Therapeutic Compounds
; FILE REFERENCE: 02-03US
; CURRENT APPLICATION NUMBER: US/10/601,953
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/392,512
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 609
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-601-953-609

Query Match          50.0%; Score 25; DB 15; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4  PLTSVC 9
Db      1  PVTVC 6

Search completed: April 1, 2005, 11:34:31
Job time : 67 secs
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OM protein - protein search, using sw model

Run on: April 1, 2005, 11:06:10 ; Search time 43 Seconds
(without alignments)
19.096 Million cell updates/sec

Title: US-09-761-636A-7

Perfect score: 61

Sequence: 1 CISVPLTSVPC 11

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 125705

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	49.2	8	1	US-08-189-331-150
2	30	49.2	8	2	US-08-471-068-150
3	27	44.3	10	1	US-08-212-190A-5
4	27	44.3	10	2	US-08-900-321-5
5	27	44.3	10	4	US-09-436-469-5
6	27	44.3	10	5	PCT-US95-03610-5
7	26	42.6	6	2	US-08-769-745-15
8	26	42.6	8	1	US-08-189-331-149
9	26	42.6	8	2	US-08-471-068-149
10	25.5	41.8	9	1	US-08-331-383-33
11	25.5	41.8	9	3	US-08-549-008-43
12	25.5	41.8	9	3	US-08-802-981-143
13	25	41.0	8	1	US-08-360-239B-1
14	25	41.0	10	2	US-08-483-077C-26
15	25	41.0	10	2	US-08-519-109B-26
16	25	41.0	10	2	US-08-482-228-108
17	25	41.0	10	3	US-08-482-528-108
18	25	41.0	10	5	PCT-US95-10811-38
19	25	41.0	11	4	US-09-671-089-12
20	24	39.3	5	4	US-09-886-135A-5
21	24	39.3	6	1	US-08-483-434A-21
22	24	39.3	6	3	US-08-476-134A-30
23	24	39.3	6	6	5190920-26
24	24	39.3	6	6	5506208-28
25	24	39.3	6	6	5190920-26
26	24	39.3	6	6	5506208-28
27	24	39.3	7	3	US-09-438-150-1

28	24	39.3	9	2	US-08-340-283-154	Sequence 154, App
29	24	39.3	9	4	US-09-601-729-204	Sequence 204, App
30	24	39.3	10	3	US-08-836-075A-187	Sequence 187, App
31	23.5	38.5	9	1	US-08-331-383-31	Sequence 31, Appl
32	23.5	38.5	9	1	US-08-549-008-42	Sequence 42, Appl
33	23.5	38.5	9	3	US-08-802-981-142	Sequence 142, App
34	23.5	38.5	10	4	US-09-671-089-13	Sequence 13, Appl
35	23.5	38.5	11	3	US-08-802-981-144	Sequence 144, App
36	23	37.7	8	1	US-08-189-331-147	Sequence 147, App
37	23	37.7	8	1	US-08-189-331-148	Sequence 148, App
38	23	37.7	8	2	US-08-340-283-61	Sequence 61, Appl
39	23	37.7	8	2	US-08-471-068-147	Sequence 147, App
40	23	37.7	8	2	US-08-471-068-148	Sequence 148, App
41	23	37.7	9	1	US-08-195-075-4	Sequence 4, Appli
42	23	37.7	9	1	US-08-467-083-3	Sequence 3, Appli
43	23	37.7	9	1	US-08-414-417B-3	Sequence 3, Appli
44	23	37.7	9	2	US-08-486-348A-3	Sequence 3, Appli
45	23	37.7	9	2	US-08-468-545B-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-08-189-331-150
; Sequence 150, Application US/08189331
; Patent No. 5747334
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; APPLICANT: Fowlkes, D. M.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189,331
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-189-331-150

Query Match 49.2%; Score 30; DB 1; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CISVPLTS 8

Db 1 CUSAPQTS 8

RESULT 2
US-08-471-068-150
; Sequence 150, Application US/08471068
; Patent No. 5948635
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; APPLICANT: Fowkes, D. M.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,068
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/189,331
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Miarock, S. Leslie
; REGISTRATION NUMBER: 18,972
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEX: 212 869-8864/9741
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-471-068-150
Query Match 49.2%; Score 30; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.1e-05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 CTSVPLTS 8
Db 1 CVSAPQTS 8

RESULT 3
US-08-212-190A-5
; Sequence 5, Application US/08212190A
; Patent No. 5652223
; GENERAL INFORMATION:
; APPLICANT: KOHN, Elise C.
; APPLICANT: LIOTTA, Lance A.
; TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: Stuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,190A
; FILING DATE: 14-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 15280-204US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-212-190A-5
Query Match 44.3%; Score 27; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 VPLTSVPC 11
Db 1 VPPAPVPC 8

RESULT 4
US-08-900-321-5
; Sequence 5, Application US/08900321
; Patent No. 5981712
; GENERAL INFORMATION:
; APPLICANT: Kohn, Elise C.
; APPLICANT: Liotta, Lance A.
; APPLICANT: Kim, Young S.
; TITLE OF INVENTION: DNA Encoding CAI Resistance Proteins and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/900,321
; FILING DATE: 25-JUL-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,190
; FILING DATE: 14-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-204100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-900-321-5

Query Match 44.3%; Score 27; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 VPLTSVPC 11
|||
Db 1 VPPAPVPC 8

RESULT 5

US-09-436-469-5
; Sequence 5, Application US/09436469
; Patent No. 6790936
; GENERAL INFORMATION:
; APPLICANT: Kohn, Elise C.
; Liotta, Lance A.
; Kim, Young S.
; TITLE OF INVENTION: DNA Encoding CAI Resistance Proteins and
; Uses thereof

; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/436,469
; FILING DATE: 08-NO. 6790936-1999
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/900,321
; FILING DATE: 25-JUL-1997
; APPLICATION NUMBER: US 08/212,190
; FILING DATE: 14-MAR-1994

ATTORNEY/AGENT INFORMATION:

; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-204100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-436-469-5

Query Match 44.3%; Score 27; DB 4; Length 10;
Best Local Similarity 62.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 VPLTSVPC 11
|||
Db 1 VPPAPVPC 8

RESULT 6

PCT-US95-03610-5
; Sequence 5, Application PC/TUS9503610
; GENERAL INFORMATION:
; APPLICANT:

; TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND
; USES THEREOF
; NUMBER OF SEQUENCES: 10
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03610
; FILING DATE: 14-MAR-1995

CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,190
; FILING DATE: 14-MAR-1994

ATTORNEY/AGENT INFORMATION:

; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 15280-204000PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-03610-5

Query Match 44.3%; Score 27; DB 5; Length 10;

Best Local Similarity 62.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 VPLTSVPC 11
|||
Db 1 VPPAPVPC 8

RESULT 7

US-08-769-745-15
; Sequence 15, Application US/08769745
; Patent No. 5955259
; GENERAL INFORMATION:

; APPLICANT: Holmes, Todd C.
; APPLICANT: Levitan, Irwin B.
; APPLICANT: Brandeis University
; TITLE OF INVENTION: Mechanism for the Regulation of Ion
; CHANNEL ACTIVITY
; FILE REFERENCE: BRU96-02
; CURRENT APPLICATION NUMBER: US/08/769,745
; CURRENT FILING DATE: 1996-12-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Rat
US-08-769-745-15

Query Match 42.6%; Score 26; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 PLTSVP 10
| | | | |
Db 1 PLTPVP 6

RESULT 8
US-08-189-331-149
; Sequence 149, Application US/08189331
; Patent No. 5747334
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189,331
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 149:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-189-331-149

Query Match 42.6%; Score 26; DB 1; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 C1SVPLT 7
| : | | |
Db 2 CVSAFQT 8

RESULT 9
US-08-471-068-149
; Sequence 149, Application US/08471068
; Patent No. 5948635
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:

Query Match 42.6%; Score 26; DB 1; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 C1SVPLT 7
| : | | |
Db 2 CVSAFQT 8

RESULT 10
US-08-331-383-33
; Sequence 33, Application US/08331383
; Patent No. 5605809
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of
; TITLE OF INVENTION: Proteases in Biological Samples and Methods and Use
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,383
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 16865-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,068
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/189,331
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 149:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-471-068-149

Query Match 42.6%; Score 26; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 C1SVPLT 7
| : | | |
Db 2 CVSAFQT 8

RESULT 10
US-08-331-383-33
; Sequence 33, Application US/08331383
; Patent No. 5605809
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of
; TITLE OF INVENTION: Proteases in Biological Samples and Methods and Use
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,383
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 16865-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-331-383-33
Query Match 41.8%; Score 25.5; DB 1; Length 9;
Best Local Similarity 44.4%; Pred. No. 4.1e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 3 SVPLTSVPC 11
Db 2 AIPM-SIPC 9

RESULT 11
US-08-549-008-43
; Sequence 43, Application US/08549008
; Patent No. 5714342
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; TITLE OF INVENTION: Compositions for the Detection of
; TITLE OF INVENTION: Protease in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/549,008
; FILING DATE: 27-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,383
; FILING DATE: 28-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 016865-0001100S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-549-008-43
Query Match 41.8%; Score 25.5; DB 1; Length 9;
Best Local Similarity 44.4%; Pred. No. 4.1e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 3 SVPLTSVPC 11
Db 2 AIPM-SIPC 9

RESULT 12
US-08-802-981-143
; Sequence 143, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-0003000S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 143:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-802-981-143
Query Match 41.8%; Score 25.5; DB 3; Length 9;
Best Local Similarity 44.4%; Pred. No. 4.1e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 3 SVPLTSVPC 11
Db 2 AIPM-SIPC 9

RESULT 13
US-08-360-239B-1
; Sequence 1, Application US/08360239B
; Patent No. 5801222
; GENERAL INFORMATION:
; APPLICANT: Pettit, George R.
; APPLICANT: Tan, Rui
; TITLE OF INVENTION: Isolation and Structure of
; TITLE OF INVENTION: the Human Cancer Cell Growth Inhibitory Cyclic
; TITLE OF INVENTION: Octapeptides Phakellistatin 10 and 11
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Mybeck
; STREET: 8010 East Morgan Trail, #10
; CITY: Scottsdale
; STATE: Arizona
; COUNTRY: USA
; ZIP: 85258-1234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: DOS 5
; SOFTWARE: Microsoft Word for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,239B
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;; FILING DATE: 12/20/94
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Richard R. Mybeck
;; REGISTRATION NUMBER: 17,886
;; REFERENCE/DOCKET NUMBER: 4997
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (602)-483-1285
;; TELEFAX: (602)-483-7452
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acid residues
;; TYPE: amino acid
;; TOPOLOGY: Cyclic
;; MOLECULE TYPE: Cyclooctapeptide
;; DESCRIPTION: Cyclooctapeptide
;; DEVELOPMENTAL STAGE: whole organism
;; ORGANISM: Phakellia sp.
;; FEATURE:
;; NAME/KEY: Phakellistatin 10
;; NAME/KEY: amino acid analysis, high resolution
;; NAME/KEY: nuclear magnetic resonance and mass
;; NAME/KEY: spectral MS/MS techniques
;; OTHER INFORMATION: Phakellistatin 10 is a
;; OTHER INFORMATION: cell growth inhibitory peptide with
;; OTHER INFORMATION: activity in murine lymphocytic leukemia
;; OTHER INFORMATION: cell line of 2.1 mg/ml.
US-08-360-239B-1

Query Match 41.0%; Score 25; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 5 PLTSPV 10
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Db 1 PLTPip 6

RESULT 14
US-08-483-077C-26
; Sequence 26, Application US/08483077C
; Patent No. 5811391
; GENERAL INFORMATION:
; APPLICANT: Arrhenius, Thomas S.
; APPLICANT: Tempczyk, Anna
; APPLICANT: Ellices, Mariano J.
; APPLICANT: Zheng, Zhong-Li
; TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
; TITLE OF INVENTION: Compositions and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,077C
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-CY 1795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 10
; OTHER INFORMATION: /note= "The carboxy-terminus is a
; OTHER INFORMATION: carboxamide."

;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-CY 1647
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949
;; INFORMATION FOR SEQ ID NO: 26:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 10
;; OTHER INFORMATION: /note= "The carboxy-terminus is a
;; OTHER INFORMATION: carboxamide."
US-08-483-077C-26

Query Match 41.0%; Score 25; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 4.7e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 2 ISVPLTSPV 10
: ||| :|
Db 2 LDVFILDVP 10

RESULT 15
US-08-519-109B-26
; Sequence 26, Application US/08519109B
; Patent No. 5869448
; GENERAL INFORMATION:
; APPLICANT: Arrhenius, Thomas S.
; APPLICANT: Tempczyk, Anna
; APPLICANT: Ellices, Mariano J.
; APPLICANT: Zheng, Zhong-Li
; TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
; TITLE OF INVENTION: Compositions and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/519,109B
; FILING DATE: 25-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-CY 1795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 10
; OTHER INFORMATION: /note= "The carboxy-terminus is a
; OTHER INFORMATION: carboxamide."

US-08-519-109B-26

Query Match 41.0%; Score 25; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 4.7e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ISVPLTSVP 10
Db 2 LDVPILDVP 10

Search completed: April 1, 2005, 11:13:03
Job time : 43 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 11:19:07 ; Search time 11.5 Seconds
(without alignments)
75.300 Million cell updates/sec

Title: US-09-761-636A-10
Perfect score: 50
Sequence: 1 CSVPLTSVC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 791

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: piri:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	34.0	8	G33098	205K exoantigen -
2	16	32.0	9	PT0247	Ig heavy chain CRD
3	16	32.0	9	A60356	118K stomach cancer
4	15	30.0	5	A60521	glycogen phosphory
5	15	30.0	6	I63546	MHC H2-L antigen -
6	15	30.0	7	PH0932	T-cell receptor al
7	15	30.0	8	PH0803	T-cell receptor al
8	14	28.0	5	E60274	major protein anti
9	14	28.0	6	F41946	T-cell receptor ga
10	14	28.0	8	A42057	fibroblast growth
11	14	28.0	8	A35180	neutral proteinase
12	14	28.0	9	I52974	seminal vesicle pr
13	14	28.0	9	B41983	orf downstream to b
14	14	28.0	9	A60522	sperm-activating p
15	13	26.0	6	I49421	laminin B1 - weste
16	13	26.0	6	S23881	Na+/K+-exchanging
17	13	26.0	7	A12016	formylglycinamide
18	13	26.0	7	S42620	aggreccan - bovine
19	13	26.0	8	S59622	metallothionein is
20	13	26.0	8	P00701	unidentified 6.5/3
21	13	26.0	9	PT0268	Ig heavy chain CRD
22	12	24.0	6	A35039	hypothetical colla
23	12	24.0	7	E61491	seed protein ws-5
24	12	24.0	8	S10783	enamelin f - bovin
25	12	24.0	8	S71919	alcohol dehydrogen
26	12	24.0	9	S13636	coat protein beta
27	12	24.0	9	S70334	endosperm protein,
28	12	24.0	9	G58502	kidney and bladder
29	11	22.0	4	I54357	schwannomin - mous

30	11	22.0	4	2	A32039	tyrosine-melanocyt
31	11	22.0	5	2	B22565	R-phycoerythrin al
32	11	22.0	6	2	B34835	dnaA protein - Pae
33	11	22.0	6	2	PT0280	Ig heavy chain CRD
34	11	22.0	7	2	I48105	dihydrofolate redu
35	11	22.0	7	2	I48086	DNA topoisomerase
36	11	22.0	7	2	PH1602	Ig H chain V-D-J r
37	11	22.0	7	2	ECMUCR	catch-relaxing pop
38	11	22.0	8	2	B39745	endoglycosylcerami
39	11	22.0	8	2	S68802	nitrate reductase
40	11	22.0	8	2	PT0530	T-cell receptor be
41	11	22.0	8	2	S19288	acylase - Kluyvera
42	11	22.0	8	2	S21288	lectin - potato (f
43	11	22.0	8	2	I57018	gene Cfr protein
44	11	22.0	8	2	A42689	major postsynaptic
45	11	22.0	8	4	I54017	granulocyte-colony

ALIGNMENTS

RESULT 1

G33098
205K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C:Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C:Accession: G33098
R.Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A:Reference number: A33098
A:Accession: G33098
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <NIC>

Query Match 34.0%; Score 17; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VPLTSV 8
|||
DB 2 VPLXLV 7

RESULT 2

PT0247
Ig heavy chain CRD3 region (clone 2-106A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0247
R.Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0247
A:Molecule type: DNA
A:Residues: 1-9 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 32.0%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 SVPLTS 7
|||
DB 2 SAPIDS 7

RESULT 3

A60356
118K stomach cancer antigen - human (fragment)
C:Species: Homo sapiens (man)

C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C/Accession: A60356
R/Shiraishi, Y.

A/Title: J. Cancer 45, 783-787, 1990
A/Title: Western blotting analysis for malignant lymphoma and stomach cancer antigens fr
A/Reference number: A60356; MUID:90216080; PMID:2323853
A/Accession: A60356
A/Molecule type: protein
A/Residues: 1-9 <SHI>
A/Cross-references: UNIPROT:Q7M4R6
C/Keywords: glycoprotein

Query Match 32.0%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VPLTSV 8
| | |
Db 1 IFLKPV 6

RESULT 4

A60521
glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
N/Alternate names: glycogen phosphorylase b
C/Species: Liza ramada
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Mar-2004
C/Accession: A60521

R/Bonamusa, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A/Title: Purification and characterization of glycogen phosphorylase B from skeletal mus
A/Reference number: A60521; MUID:90227907; PMID:2109669
A/Accession: A60521
A/Molecule type: protein
A/Residues: 1-5 <BON>
C/Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F/3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experim

Query Match 30.0%; Score 15; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVP 4
| | |
Db 3 SVP 5

RESULT 5

I65546
MHC H2-L antigen - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C/Accession: I65546
R/Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
Cell 44, 261-272, 1986
A/Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and thei
A/Reference number: I52778; MUID:86106202; PMID:3510743
A/Accession: I65546
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-6 <RES>
A/Cross-references: GB:MI2483; NID:g199565; PIDN:AAA39663.1; PID:g554234

Query Match 30.0%; Score 15; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 VPLT 6
| | |
Db 2 VPCT 5

RESULT 6

PH0932

T-cell receptor beta chain V-D-J region (clone 3) - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C/Accession: PH0932
R/Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A/Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A/Reference number: PH0891; MUID:92078857; PMID:1836012
A/Accession: PH0932
A/Molecule type: mRNA
A/Residues: 1-7 <GOL>
A/Experimental source: complete Freund's adjuvant-immunized lymph node
C/Keywords: T-cell receptor

Query Match 30.0%; Score 15; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSVP 4
| | |
Db 1 CASP 4

RESULT 7

PH0803
T-cell receptor alpha chain (J2) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PH0803
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-r
allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; MUID:92078846; PMID:1836010
A/Accession: PH0803
A/Molecule type: mRNA
A/Residues: 1-8 <CAS>
A/Cross-references: EMBL:X60912
A/Experimental source: T lymphocyte
C/Keywords: T-cell receptor

Query Match 30.0%; Score 15; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVP 6
| | |
Db 1 CAAGIT 6

RESULT 8

E60274
major protein antigen MP763 - Mycobacterium tuberculosis (fragment)
C/Species: Mycobacterium tuberculosis
C/Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C/Accession: E60274
R/Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A/Title: Isolation and partial characterization of major protein antigens in the culture
A/Reference number: A60274; MUID:91099899; PMID:1898899
A/Accession: E60274
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-5 <NAG>

Query Match 28.0%; Score 14; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 PLT 6
| | |
Db 3 PIT 5

RESULT 9
F41946
T-cell receptor gamma chain (1a.27) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: F41946
R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and functional-site sequence analyses of T-cell receptor gamma gene
A:Reference number: A41946; MUID:92049316; PMID:1658619
A:Accession: F41946
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <WHE>
C:Keywords: T-cell receptor

Query Match 28.0%; Score 14; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSV 3
| | |
Db 2 CAV 4

RESULT 10
A42057
fibroblast growth factor receptor 1, secreted - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
R:Werner, S.; Duan, D.S.R.; de Vries, C.; Peters, K.G.; Johnson, D.E.; Williams, L.T.
Mol. Cell. Biol. 12, 82-88, 1992
A:Title: Differential splicing in the extracellular region of fibroblast growth factor X
A:Reference number: A42057; MUID:92107200; PMID:1309595
A:Accession: A42057
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 <WER>
A:Cross-references: GB:M80363
C:Keywords: growth factor receptor

Query Match 28.0%; Score 14; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 VPLTS 7
| | | |
Db 1 VLLTS 5

RESULT 11
A35180
neutral proteinase (EC 3.4.-.-), calcium-activated - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 09-Jul-2004
C:Accession: A35180
R:Yoshihara, Y.; Ueda, H.; Fujii, N.; Shide, A.; Yajima, H.; Satoh, M.
J. Biol. Chem. 265, 5809-5815, 1990
A:Title: Purification of a novel type of calcium-activated neutral protease from rat brain
A:Reference number: A35180; MUID:90202830; PMID:2318836
A:Accession: A35180
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <YOS>
A:Cross-references: UNIPROT:Q7M039
C:Keywords: hydrolase

Query Match 28.0%; Score 14; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PLTS 7
| | |
Db 1 PLTS 4

RESULT 12

IS2974

seminal vesicle protein IV - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999

C:Accession: IS2974

R:Teng, C.T.; Harris, S.E.

DNA 2, 105-111, 1993

A:Title: The seminal vesicle secretion IV gene: detection of S1 nuclease-sensitive sites

A:Reference number: IS2974; MUID:83261204; PMID:6307619

A:Accession: IS2974

A:Molecule type: DNA

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-9 <RES>

A:Cross-references: GB:M27324; MUID:9207124; PIDN:AAA63501.1; PID:9207125

C:Genetics:

A:Gene: SVSIV

Query Match 28.0%; Score 14; DB 2; Length 9;

Best Local Similarity 75.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LTSV 8

| | |

Db 3 LTSL 6

RESULT 13

B41983

orf downstream to bacterioferritin - Azotobacter vinelandii (fragment)

C:Species: Azotobacter vinelandii

C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: B41983

R:Grossman, M.J.; Hinton, S.M.; Minak-Bernero, V.; Slaughtter, C.; Stiefel, E.I.

Proc. Natl. Acad. Sci. U.S.A. 89, 2419-2423, 1992

A:Title: Unification of the ferritin family of proteins.

A:Reference number: A41983; MUID:92196129; PMID:1549605

A:Accession: B41983

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid; protein

A:Residues: 1-9 <GRO>

A:Cross-references: UNIPROT:P25825; GB:M83692; NID:G142297; PIDN:AAA22122.1; PID:G142299

A:Note: sequence extracted from NCBI backbone (NCBIP:88442)

Query Match 28.0%; Score 14; DB 2; Length 9;

Best Local Similarity 75.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PLTS 7

| | |

Db 4 PRTS 7

RESULT 14

A60522

sperm-activating peptide SAP-IV - sea urchin (Diadema setosum)

C:Species: Diadema setosum

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

C:Accession: A60522

R:Yoshino, K.I.; Kurita, M.; Yamaguchi, M.; Nomura, K.; Takao, T.; Shimonishi, Y.; Suzuki

Comp. Biochem. Physiol. B 95, 423-429, 1990

A:Title: A species-specific sperm-activating peptide from the egg jelly of the sea urchin

A:Reference number: A60522; MUID:90227916; PMID:2158412

A:Accession: A60522

A:Molecule type: protein

A:Residues: 1-9 <YOS>

A:Cross-references: UNIPROT:Q7M4D5

C:Superfamily: unassigned animal peptides
F:2-9/Disulfide bonds: #status experimental

Query Match 28.0%; Score 14; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 SVC 9
Db :|||
7 AVC 9

RESULT 15

I49421
laminin B1 - western wild mouse (fragment)
C:Species: Mus spretus (western wild mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C/Accession: I49421
R/Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
A>Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A/Reference number: I48934; MUID:94319082; PMID:8043949
A/Accession: I49421
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-6 <RES>
A/Cross-references: EMBL:U05736; NID:9497073; PIDN:AAB60477.1; PID:9642829

Query Match 26.0%; Score 13; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 SVC 9
Db :|||
3 STC 5

Search completed: April 1, 2005, 11:25:15
Job time : 12.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 10:49:44 ; Search time 43 Seconds
(without alignments)
13.888 Million cell updates/sec

Title: US-09-761-636A-6

Perfect score: 46

Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 77247

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCITUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	65.2	8	3	US-09-100-409A-27
2	26	56.5	8	4	US-09-089-878-3
3	25	54.3	8	1	US-08-397-633A-100
4	25	54.3	8	3	US-09-258-754-49
5	25	54.3	8	3	US-09-042-107-49
6	25	54.3	8	4	US-09-722-250D-49
7	25	54.3	8	4	US-09-676-475A-49
8	23	50.0	7	3	US-08-973-551-14
9	23	50.0	8	2	US-08-520-535-3
10	23	50.0	8	2	US-09-079-432-3
11	23	50.0	8	3	US-09-258-754-33
12	23	50.0	8	3	US-09-258-754-42
13	23	50.0	8	3	US-09-258-754-214
14	23	50.0	8	3	US-09-042-107-33
15	23	50.0	8	3	US-09-042-107-42
16	23	50.0	8	3	US-08-160-604-79
17	23	50.0	8	3	US-08-160-604-80
18	23	50.0	8	3	US-09-722-250D-33
19	23	50.0	8	4	US-09-722-250D-42
20	23	50.0	8	4	US-09-722-250D-214
21	23	50.0	8	4	US-09-428-082B-457
22	23	50.0	8	4	US-09-282-029A-115
23	23	50.0	8	4	US-09-185-908-115
24	23	50.0	8	4	US-09-676-475A-33
25	23	50.0	8	4	US-09-676-475A-42
26	23	50.0	8	4	US-09-676-475A-214
27	23	50.0	8	4	US-09-676-475A-214

28 23 50.0 8 4 US-09-434-355A-115 Sequence 115, Appl
29 22 47.8 6 3 US-09-187-859-3664 Sequence 3664, Ap
30 22 47.8 6 4 US-09-839-542B-3664 Sequence 3664, Ap
31 22 47.8 7 3 US-09-187-859-3665 Sequence 3665, Ap
32 22 47.8 7 4 US-09-839-542B-3665 Sequence 3665, Ap
33 22 47.8 8 3 US-09-258-754-36 Sequence 36, Appl
34 22 47.8 8 3 US-09-258-754-48 Sequence 48, Appl
35 22 47.8 8 3 US-09-258-754-256 Sequence 256, Appl
36 22 47.8 8 3 US-09-042-107-36 Sequence 36, Appl
37 22 47.8 8 3 US-09-042-107-48 Sequence 48, Appl
38 22 47.8 8 3 US-09-042-107-256 Sequence 256, Appl
39 22 47.8 8 3 US-09-187-859-1071 Sequence 1071, Ap
40 22 47.8 8 3 US-09-187-859-3624 Sequence 3624, Ap
41 22 47.8 8 4 US-09-839-542B-1071 Sequence 1071, Ap
42 22 47.8 8 4 US-09-839-542B-3624 Sequence 3624, Ap
43 22 47.8 8 4 US-09-722-250D-36 Sequence 36, Appl
44 22 47.8 8 4 US-09-722-250D-48 Sequence 48, Appl
45 22 47.8 8 4 US-09-722-250D-256 Sequence 256, Appl

ALIGNMENTS

RESULT 1

US-09-100-409A-27
; Sequence 27, Application US/09100409A
; Patent No. 6090388
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION FOR PREVENTION AND TREATMENT OF HIV INFECTION AND
; TITLE OF INVENTION: IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,409A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 1151-4154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-409A-27

Query Match 65.2%; Score 30; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CNEESLIC 8

DB 1 CNOGSFLC 8

```
RESULT 2
US-09-089-878-3
; Sequence 3, Application US/09089878
; Patent No. 6458528
; GENERAL INFORMATION:
; APPLICANT: Groat, Randall G.
; APPLICANT: O'Connor, Thomas P.
; APPLICANT: Mermet, Brian
; TITLE OF INVENTION: DIAGNOSIS OF FELINE IMMUNODEFICIENCY VIRUS INFECTION
; FILE OF INVENTION: USING ENV/GAG POLYPEPTIDE MARKERS
; FILE REFERENCE: 00088/111001
; CURRENT APPLICATION NUMBER: US/09/089,878
; CURRENT FILING DATE: 1998-06-03
; EARLIER APPLICATION NUMBER: US 60/085,615
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Feline immunodeficiency virus
US-09-089-878-3

Query Match          56.5%; Score 26; DB 4; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db 1 CQNQFFC 8

RESULT 3
US-08-397-633A-100
; Sequence 100, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; FILE OF INVENTION: OF ENZYMAIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,633A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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US-08-397-633A-100

Query Match          54.3%; Score 25; DB 1; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.1e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db 1 CGQSKVIC 8

RESULT 4
US-09-258-754-49
; Sequence 49, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; FILE OF INVENTION: Membrane Diptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-49

Query Match          54.3%; Score 25; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db 1 CGNETLRC 8

RESULT 5
US-09-042-107-49
; Sequence 49, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; FILE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-49

Query Match          54.3%; Score 25; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db 1 CGNETLRC 8
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Db 1 CGNETLRC 8

RESULT 6

US-09-722-250D-49

Sequence 49, Application US/09722250D

Patent No. 6610651

GENERAL INFORMATION:

APPLICANT: Ruoslahti, Erkki

APPLICANT: Pasqualini, Renata

TITLE OF INVENTION: Molecules that Home to Various Selected Organs or

TITLE OF INVENTION: Tissues

FILE REFERENCE: P-LJ 4514

CURRENT APPLICATION NUMBER: US/09/722,250D

CURRENT FILING DATE: 2000-11-22

PRIOR APPLICATION NUMBER: US 09/042,107

PRIOR FILING DATE: 1998-03-13

NUMBER OF SEQ ID NOS: 437

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 49

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-722-250D-49

Query Match 54.3%; Score 25; DB 4; Length 8;

Best Local Similarity 50.0%; Pred. No. 4.1e+05;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8

Db 1 CGNETLRC 8

RESULT 7

US-09-676-475A-49

Sequence 49, Application US/09676475A

Patent No. 6784153

GENERAL INFORMATION:

APPLICANT: Ruoslahti, Erkki

APPLICANT: Pasqualini, Renata

APPLICANT: Rajotte, Daniel

TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using

TITLE OF INVENTION: Membrane Dipeptidase

FILE REFERENCE: P-LA 4377

CURRENT APPLICATION NUMBER: US/09/676,475A

CURRENT FILING DATE: 1998-03-13

PRIOR APPLICATION NUMBER: 09/042,107

PRIOR FILING DATE: 1998-03-13

NUMBER OF SEQ ID NOS: 452

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 49

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-676-475A-49

Query Match 54.3%; Score 25; DB 4; Length 8;

Best Local Similarity 50.0%; Pred. No. 4.1e+05;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8

Db 1 CGNETLRC 8

RESULT 8

US-08-973-551-14

Sequence 14, Application US/08973551

Patent No. 6113902

GENERAL INFORMATION:

APPLICANT: Chermann, Jean-Claude

APPLICANT: Le Contel, Carole

APPLICANT: Galea, Pascale

TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING

TITLE OF INVENTION: AN INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND

TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF

TITLE OF INVENTION: DIAGNOSIS

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/973,551

FILING DATE: 30-DEC-1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR96/01006

FILING DATE: 28-JUN-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 9507914

FILING DATE: 30-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Granados, Patricia D.

REGISTRATION NUMBER: 33,683

REFERENCE/DOCKET NUMBER: 65691/130

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-973-551-14

Query Match 50.0%; Score 23; DB 3; Length 7;

Best Local Similarity 80.0%; Pred. No. 4.1e+05;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEES 5

Db 2 CNPES 6

RESULT 9

US-08-520-535-3

Sequence 3, Application US/08520535

Patent No. 5817750

GENERAL INFORMATION:

APPLICANT: Ruoslahti, Erkki

APPLICANT: Pasqualini, Renata

TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

```
/
/
/  ZIP: 92122
/  COMPUTER READABLE FORM:
/  MEDIUM TYPE: Floppy disk
/  COMPUTER: IBM PC compatible
/  OPERATING SYSTEM: PC-DOS/MS-DOS
/  SOFTWARE: PatentIn Release #1.0, Version #1.25
/  CURRENT APPLICATION DATA:
/  APPLICATION NUMBER: US/08/520,535
/  FILING DATE: 28-AUG-1995
/  CLASSIFICATION: 530
/  ATTORNEY/AGENT INFORMATION:
/  NAME: Campbell, Cathryn A.
/  REGISTRATION NUMBER: 31,815
/  REFERENCE/DOCKET NUMBER: P-LA 1794
/  TELECOMMUNICATION INFORMATION:
/  TELEPHONE: (619) 535-9001
/  TELEFAX: (619) 535-8949
/  INFORMATION FOR SEQ ID NO: 3:
/  SEQUENCE CHARACTERISTICS:
/  LENGTH: 8 amino acids
/  TYPE: amino acid
/  TOPOLOGY: circular
/  US-08-520-535-3
/
/  Query Match 50.0%; Score 23; DB 2; Length 8;
/  Best Local Similarity 37.5%; Pred. No. 4.1e+05;
/  Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
/
/  QY 1 CNEESLIC 8
/  Db 1 CWDDGLMC 8
/
/  RESULT 10
/  US-09-761-636a-6
/  Sequence 3, Application US/09079432
/  Patent No. 595572
/  GENERAL INFORMATION:
/  APPLICANT: Ruoslahti, Erkki
/  APPLICANT: Pasqualini, Renata
/  TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
/  NUMBER OF SEQUENCES: 28
/  CORRESPONDENCE ADDRESS:
/  ADDRESSEE: Campbell & Flores LLP
/  STREET: 4370 La Jolla Village Drive, Suite 700
/  CITY: San Diego
/  STATE: California
/  COUNTRY: USA
/  ZIP: 92122
/  COMPUTER READABLE FORM:
/  MEDIUM TYPE: Floppy disk
/  COMPUTER: IBM PC compatible
/  OPERATING SYSTEM: PC-DOS/MS-DOS
/  SOFTWARE: PatentIn Release #1.0, Version #1.25
/  CURRENT APPLICATION DATA:
/  APPLICATION NUMBER: US/09/079,432
/  FILING DATE:
/  CLASSIFICATION:
/  PRIOR APPLICATION DATA:
/  APPLICATION NUMBER: US 08/520,535
/  FILING DATE: 28-AUG-1995
/  ATTORNEY/AGENT INFORMATION:
/  NAME: Campbell, Cathryn A.
/  REGISTRATION NUMBER: 31,815
/  REFERENCE/DOCKET NUMBER: P-LA 1794
/  TELECOMMUNICATION INFORMATION:
/  TELEPHONE: (619) 535-9001
/  TELEFAX: (619) 535-8949
/  INFORMATION FOR SEQ ID NO: 3:
/  SEQUENCE CHARACTERISTICS:
/  LENGTH: 8 amino acids
/  TYPE: amino acid
/  TOPOLOGY: circular
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US-09-079-432-3
/
/  Query Match 50.0%; Score 23; DB 2; Length 8;
/  Best Local Similarity 37.5%; Pred. No. 4.1e+05;
/  Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
/
/  QY 1 CNEESLIC 8
/  Db 1 CWDDGLMC 8
/
/  RESULT 11
/  US-09-258-754-33
/  Sequence 33, Application US/09258754
/  Patent No. 6174687
/  GENERAL INFORMATION:
/  APPLICANT: Ruoslahti, Erkki
/  APPLICANT: Pasqualini, Renata
/  APPLICANT: Rajotte, Daniel
/  TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
/  FILE REFERENCE: P-LJ 3443
/  CURRENT APPLICATION NUMBER: US/09/258,754
/  CURRENT FILING DATE: 1999-02-26
/  EARLIER APPLICATION NUMBER: 09/042,107
/  EARLIER FILING DATE: 1998-03-13
/  NUMBER OF SEQ ID NOS: 452
/  SOFTWARE: PatentIn Ver. 2.0
/  SEQ ID NO 33
/  LENGTH: 8
/  TYPE: PRT
/  ORGANISM: Artificial Sequence
/  FEATURE:
/  OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/  US-09-258-754-33
/
/  Query Match 50.0%; Score 23; DB 3; Length 8;
/  Best Local Similarity 50.0%; Pred. No. 4.1e+05;
/  Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
/
/  QY 1 CNEESLIC 8
/  Db 1 CRHSSSC 8
/
/  RESULT 12
/  US-09-258-754-42
/  Sequence 42, Application US/09258754
/  Patent No. 6174687
/  GENERAL INFORMATION:
/  APPLICANT: Ruoslahti, Erkki
/  APPLICANT: Pasqualini, Renata
/  APPLICANT: Rajotte, Daniel
/  TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
/  FILE REFERENCE: P-LJ 3443
/  CURRENT APPLICATION NUMBER: US/09/258,754
/  CURRENT FILING DATE: 1999-02-26
/  EARLIER APPLICATION NUMBER: 09/042,107
/  EARLIER FILING DATE: 1998-03-13
/  NUMBER OF SEQ ID NOS: 452
/  SOFTWARE: PatentIn Ver. 2.0
/  SEQ ID NO 42
/  LENGTH: 8
/  TYPE: PRT
/  ORGANISM: Artificial Sequence
/  FEATURE:
/  OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/  US-09-258-754-42
/
/  Query Match 50.0%; Score 23; DB 3; Length 8;
/  Best Local Similarity 50.0%; Pred. No. 4.1e+05;
/  Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY 1 CNEESLIC 8
|:|:|
Db 1 CHEGYLTC 8

RESULT 13

US-09-258-754-214
; Sequence 214, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptides
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 214
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-214

Query Match 50.0%; Score 23; DB 3; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.1e+05;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
|:|:|
Db 1 CFXSTLLC 8

RESULT 14

US-09-042-107-33
; Sequence 33, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-33

Query Match 50.0%; Score 23; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
|:|:|
Db 1 CRHSSSC 8

RESULT 15

US-09-042-107-42

; Sequence 42, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-42

Query Match 50.0%; Score 23; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
|:|:|
Db 1 CHEGYLTC 8

Search completed: April 1, 2005, 10:57:21
Job time : 43 secs

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2005, 11:03:25 ; Search time 38 Seconds

(without alignments)
27.852 Million cell updates/sec

Title: US-09-761-636A-7

Perfect score: 61

Sequence: 1 CISVPLTSVPC 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1328

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	36.1	11	2 D57789	gallbladder stone
2	20	32.8	6	2 I65546	MHC H2-L antigen -
3	19	31.1	5	2 A60521	glycogen phosphory
4	18	29.5	10	2 C3191	hypothetical prote
5	17	27.9	8	2 G33098	205K exoantigen -
6	17	27.9	10	2 C39111	Ig heavy chain C r
7	17	27.9	10	2 PH0944	T-cell receptor be
8	17	27.9	11	2 PH0929	T-cell receptor be
9	17	27.9	11	2 S21727	gamma-interferon-i
10	16	26.2	4	2 I51049	metallothionein-A
11	16	26.2	9	2 PT0247	Ig heavy chain CRD
12	16	26.2	9	2 A60356	118K stomach cance
13	16	26.2	10	2 A61622	vitellinogenin, 190k
14	16	26.2	10	2 PH0926	T-cell receptor be
15	16	26.2	10	2 A32195	Na+/K+-exchanging
16	16	26.2	10	2 S62880	polygalacturonase
17	16	26.2	11	1 ECUQ2M	tachykinin II - ml
18	16	26.2	11	2 S00616	paraspinal crystal
19	15	24.6	10	2 B59272	peptide-N4-(N-acet
20	15	24.6	11	2 PH1584	Ig H chain V-D-J r
21	15	24.6	11	2 PH0941	T-cell receptor be
22	15	24.6	11	2 PH0042	stathmin - mouse (
23	14	23.0	5	2 E60274	major protein anti
24	14	23.0	6	4 A35039	hypothetical colla
25	14	23.0	7	2 PC1316	large granule L3 c
26	14	23.0	8	2 A33995	adipokinetic hormo
27	14	23.0	8	2 B4960	neuropeptide Led-C
28	14	23.0	8	2 S08996	hypertrehalosemic
29	14	23.0	8	2 B49823	adipokinetic hormo

30 14 23.0 8 2 PL0184 capsid protein VP-
31 14 23.0 8 2 A42057 fibroblast growth
32 14 23.0 8 2 A35180 neutral proteinase
33 14 23.0 9 2 I52974 seminal vesicle pr
34 14 23.0 9 2 B41983 orf dowstream to b
35 14 23.0 9 2 A29477 diuretic neurosept
36 14 23.0 10 1 XAVI6B angiotensin-conver
37 14 23.0 10 2 B33995 hypertrehalosemic
38 14 23.0 10 2 JCL416 hypertrehalosemic
39 14 23.0 10 2 S09138 hypertrehalosemic
40 14 23.0 10 2 PC2171 triacylglycerol 11
41 14 23.0 10 2 PA0050 protein QA100052 -
42 14 23.0 10 2 B61218 alpha-gliadin 6Ha
43 14 23.0 10 2 E86128 hypothetical prote
44 14 23.0 11 1 XASNEA bradykinin-potenti
45 14 23.0 11 2 S58244 pyrroloquinoline q

ALIGNMENTS

RESULT 1

D57789 gallbladder stone matrix protein, 14.5K - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 23-Feb-1996

C:Accession: D57789

R:Binette, J.P.; Binette, M.B.

A:Description: The proteins of gallbladder stones.

A:Reference number: A57789

A:Accession: D57789

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-11 <BIN>

Query Match 36.1%; Score 22; DB 2; Length 11;

Best Local Similarity 66.7%; Pred. No. 8.8e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 5 PLTSVP 10

Db 1 PATSAP 6

RESULT 2

I65546 MHC H2-L antigen - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999

C:Accession: I65546

R:Kimura, A.; Israel, A.; Le Bail, O.; Kourilesky, P.

Cell 44, 261-272, 1986

A>Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and their

A:Reference number: I52778; PMID:86106202; PMID:3510743

A:Accession: I65546

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-6 <RES>

A:Cross-references: GB:M12483; NID:G199565; PIDN:AAA39663.1; PID:G554234

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 6;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 9 VPC 11

Db 2 VPC 4

RESULT 3

A60521 Glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)

N:Alternate names: glycogen phosphorylase b

C:Species: Liza ramada

C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Mar-2004

C:Accession: A60521

R:Bonamusa, L.; Baanante, I.V.

Comp. Biochem. Physiol. B 95, 295-301, 1990

A>Title: Purification and characterization of glycogen phosphorylase B from skeletal muscle

A:Reference number: A60521; MUID:90227907; PMID:2109669

A:Accession: A60521

A:Molecule type: protein

A:Residues: 1-5 <BON>

C:Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein

F3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experiment

Query Match 31.1%; Score 19; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVP 5
| | | |
Db 2 ISVP 5

RESULT 4

C39191

Hypothetical protein 1 (Tetx 5' region) - Bacteroides fragilis

C:Species: Bacteroides fragilis

C>Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 30-Sep-1993

C:Accession: C39191

R:Speer, B.S.; Bedzyk, L.; Salyers, A.A.

J. Bacteriol. 173, 176-183, 1991

A>Title: Evidence that a novel tetracycline resistance gene found on two Bacteroides tra

A:Reference number: A39191; MUID:91100280; PMID:1846135

A:Accession: C39191

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-10 <SPE>

A:Cross-references: GB:M37699

Query Match 29.5%; Score 18; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 4e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SVPLTSV 9
| | | |
Db 4 SRPWTSI 10

RESULT 5

G33098

205K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)

C:Species: Plasmodium falciparum

C>Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000

C:Accession: G33098

R:Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A:Reference number: A33098

A:Accession: G33098

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <NIC>

Query Match 27.9%; Score 17; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 VPLTSV 9
| | | |
Db 2 VPLXLV 7

RESULT 6

C39111

Ig heavy chain C region - Pacific hagfish (fragment)

C:Species: Eptatretus stoutii (Pacific hagfish)

C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996

C:Accession: C39111

R:Varner, J.; Neame, P.; Litman, G.W.

Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991

A>Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural similarity

A:Reference number: A39111; MUID:91156684; PMID:2000382

A:Accession: C39111

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <VAR>

C:Keywords: heterotetramer; immunoglobulin

Query Match 27.9%; Score 17; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISVPL 6
| | | |
Db 4 ISSPL 8

RESULT 7

PH0944

T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C:Accession: PH0944

R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A>Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic

A:Reference number: PH0891; MUID:92078857; PMID:1836012

A:Accession: PH0944

A:Molecule type: mRNA

A:Residues: 1-10 <GOL>

A:Experimental source: complete Freund's adjuvant-immunized lymph node

A>Note: the authors translated the codon GAC for residue 9 as Glu

C:Keywords: T-cell receptor

Query Match 27.9%; Score 17; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 6e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVP 5
| | | |
Db 1 CASSP 5

RESULT 8

PH0929

T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C:Accession: PH0929

R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A>Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic

A:Reference number: PH0891; MUID:92078857; PMID:1836012

A:Accession: PH0929

A:Molecule type: mRNA

A:Residues: 1-11 <GOL>

A:Experimental source: concanavalin A-activated lymphoblast

C:Keywords: T-cell receptor

Query Match 27.9%; Score 17; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 6.6e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CISVPLT 7
| | | |
Db 1 CASRPGT 7

RESULT 9
S21727
gamma-interferon-induced protein: IP-30 precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S21727
R:Wei, M.L.; Cresswell, P.
Nature 356, 443-446, 1992
A:Title: HLA-A2 molecules in an antigen-processing mutant cell contain signal sequence-d
A:Reference number: S21727; MUID:92212461; PMID:1557127
A:Accession: S21727
A:Molecule type: protein
A:Status: preliminary
A:Residues: 1-11 <WEI>
A:Cross-references: UNIPROT:Q8NEI4; UNIPROT:Q9UPH8; UNIPROT:Q8WU77

Query Match 27.9%; Score 17; DB 2; Length 11;
Best Local Similarity 37.5%; Pred. No. 6.6e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISVPLTSV 9
: ||| :
Db 3 LDVPTAAV 10

RESULT 10
I51049
metallothionein-A - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I51049
R:Olsson, P.E.; Kling, P.; Ekell, L.J.; Kille, P.
Eur. J. Biochem. 230, 344-349, 1995
A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) me
A:Reference number: I51049; MUID:95324545; PMID:7601121
A:Accession: I51049
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <OLS>
A:Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328

Query Match 26.2%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PC 11
|||
Db 3 PC 4

RESULT 11
PT0247
Ig heavy chain CRD3 region (clone 2-106A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0247
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0247
A:Molecule type: DNA
A:Residues: 1-9 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 26.2%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SVPLTS 8
|||:

Db 2 SAPIDS 7

RESULT 12
A60356
118K stomach cancer antigen - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: A60356
R:Shiraishi, Y.
Int. J. Cancer 45, 783-787, 1990
A:Title: Western blotting analysis for malignant lymphoma and stomach cancer antigens fr
A:Reference number: A60356; MUID:90216080; PMID:2323853
A:Accession: A60356
A:Molecule type: protein
A:Residues: 1-9 <SHI>
A:Cross-references: UNIPROT:Q7M4R6
C:Keywords: glycoprotein

Query Match 26.2%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 VPLTSV 9
: ||| :
Db 1 IPLXPV 6

RESULT 13
A61622
vitellogenin, 190k chain - gypsy moth (fragment)
N:Contains: vitellin
C:Species: Lymantria dispar (gypsy moth)
C:Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 15-Oct-1999
C:Accession: A61622
R:Hiremath, S.; Eshita, S.
Insect Biochem. Mol. Biol. 22, 605-611, 1992
A:Title: Purification and characterization of vitellogenin from the gypsy moth, Lymantria
A:Reference number: A61622
A:Accession: A61622
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <HIR>
C:Keywords: egg yolk; hemolymph

Query Match 26.2%; Score 16; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLT 7
|||
Db 2 PLT 4

RESULT 14
PH0926
T-cell receptor beta chain V-D-J region (isolate 12) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0926
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi
A:Reference number: PH0926; MUID:92078857; PMID:1836012
A:Accession: PH0926
A:Molecule type: mRNA
A:Residues: 1-10 <GOL>
A:Experimental source: concanavalin A-activated lymphoblast
A:Note: the authors translated the codon AGA for residue 4 as Thr
C:Keywords: T-cell receptor

Query Match 26.2%; Score 16; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 9e+03;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVP 5
| | |
Db 1 CASRP 5

RESULT 15

A32195
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 20-Oct-1989 #sequence_revision 20-Oct-1989 #text_change 19-Apr-2002
C:Accession: A32195
R:Tyson, P.A.; Steinberg, M.; Wallick, E.T.; Kirley, T.L.
J. Biol. Chem. 264, 726-734, 1989
A:Title: Identification of the 5-iodoacetamidofluorescein reporter site on the Na,K-ATPase
A:Reference number: A32195; MUID:89093137; PMID:2536022
A:Accession: A32195
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <TYS>
C:Keywords: hydrolase

Query Match 26.2%; Score 16; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 9e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CISVPLTSV 9
| | |
Db 1 CIELCXGSV 9

Search completed: April 1, 2005, 11:11:12
Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 10:57:25 ; Search time 115 Seconds
(without alignments)
48.981 Million cell updates/sec

Title: US-09-761-636A-7
Perfect score: 61
Sequence: 1 CISVPLTSVPC 11

Scoring table: BLOSUMP2
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3223

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	37.7	11	1	TIN4_HOPTI
2	21	34.4	11	2	Q9TQSO
3	20	32.8	8	2	Q7AUJ4
4	20	32.8	10	2	Q85563
5	20	32.8	10	2	Q85598
6	20	32.8	10	2	Q85619
7	20	32.8	11	2	Q712U0
8	20	32.8	11	2	Q712U1
9	19	31.1	8	2	Q56140
10	19	31.1	10	2	Q9THM6
11	19	31.1	10	2	Q9THM7
12	19	31.1	10	2	Q9TKS0
13	19	31.1	10	2	Q9TKS1
14	19	31.1	10	2	Q9TKS2
15	19	31.1	10	2	Q9TKS3
16	19	31.1	10	2	Q9TKS4
17	19	31.1	10	2	Q9TKS6
18	19	31.1	10	2	Q9TKS7
19	19	31.1	10	2	Q9TKS8
20	19	31.1	10	2	Q9TKS9
21	19	31.1	10	2	Q9TKF0
22	19	31.1	10	2	Q9TKF1
23	19	31.1	10	2	Q9TKF3
24	19	31.1	10	2	Q9TKF4
25	19	31.1	10	2	Q9TKF6
26	19	31.1	10	2	Q9TKF7
27	19	31.1	10	2	Q9TKF8
28	19	31.1	10	2	Q9TKF9
29	19	31.1	10	2	Q9TKG0
30	19	31.1	10	2	Q9TKG2
31	19	31.1	11	1	TIN1_HOPTI

32 19 31.1 11 2 P83092 spinacia ol
33 18 29.5 8 1 COW2 CONPU P58785 conus purpu
34 18 29.5 9 2 Q9FXL0 Q9FX10 liliu long
35 18 29.5 11 2 Q9NY38 Q9NY38 homo sapien
36 18 29.5 11 2 Q99N81 Q99N81 mus musculu
37 17.5 28.7 9 1 MGMT BOVIN P29177 bos taurus
38 17 27.9 8 2 Q8KPX4 Q8KPX4 microcystis
39 17 27.9 9 2 Q7X6A3 Q7X6A3 zea mays (m
40 17 27.9 9 2 Q9K4M6 Q9K4M6 staphylococ
41 17 27.9 10 1 UPA4 HUMAN P30090 homo sapien
42 17 27.9 10 2 Q96041 Q96041 oenothera b
43 17 27.9 10 2 Q7Y0I8 Q7Y0I8 zea mays (m
44 17 27.9 10 2 Q39957 Q39957 gb virus c/
45 17 27.9 11 2 O77871 O77871 oreochromis

ALIGNMENTS

RESULT 1
TIN4_HOPTI
ID TIN4_HOPTI STANDARD; PRT; 11 AA.
AC P82654;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tigerlin-4.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RX TISSUE=Skin secretion;
RC PubMed=11031261; DOI=10.1074/jbc.M006615200;
RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P., Devi A.S.,
RA Nagaraj R., Sitaram N.;
RT "Tigerlins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,
CC S.aureus, M.luteus and P.putida. Antifungal activity against
CC S.cerevisiae.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1247; METHOD=WALDI; RANGE=1-11; NOTE=Ref.1.
KW Amphibian defense peptide; Antibiotic; Direct protein sequencing;
KW Fungicide.
FT DISULFID 3 11
SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 37.7%; Score 23; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 2,3e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CISVPL 6
| : | |
| : | |
Db 3 CVAIPL 8

RESULT 2
Q9TQSO
ID Q9TQSO PRELIMINARY; PRT; 11 AA.
AC Q9TQSO;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE C-kit (fragment).
GN Name=kit;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

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OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20154958; PubMed=10690368;
RA Olsen H.G., Vøge D.I., Lien S., Klungland H.;
RT "A polymorphism in the bovine c-kit gene.";
RL Anim. Genet. 31:71-71(2000).
DR EMBL; AJ243424; CAB60775.1; -.
DR EMBL; AJ243060; CAB60774.1; -.
FT NON_TER 1 11
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1126 MW; DD785FF8A2D2D772 CRC64;

Query Match 34.4%; Score 21; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 5.2e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SVPLTSV 9
Db :||: ||
3 AVPVSV 9

RESULT 3
Q7AUJ4 PRELIMINARY; PRT; 8 AA.
AC Q7AUJ4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transposase (Fragment).
GN Name=tnp17;
OS Acinetobacter sp. BW3.
OG Plasmid pKLH207.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=106395;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15073307; DOI=10.1099/mic.0.26844-0;
RA Kholodii G., Mindlin S., Gorlenko Z., Petrova M., Hobman J.,
RA Nikiforov V.;
RT Translocation of transposition-deficient [Tn(d)PKLH2-like]
RT transposons in the natural environment: mechanistic insights from the
RT study of adjacent DNA sequences.";
RL Microbiology 150:979-992(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BW3;
RX PubMed=15073307; DOI=10.1099/mic.0.26844-0;
RA Kholodii G., Mindlin S., Gorlenko Z., Petrova M., Hobman J.,
RA Nikiforov V.;
RT Translocation of transposition-deficient [Tn(d)PKLH2-like]
RT transposons in the natural environment: mechanistic insights from the
RT study of adjacent DNA sequences.";
RL Microbiology 150:979-992(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BW3;
RA Kholodii G.Y.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ486856; CAD31078.1; -.
KW Plasmid.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 911 MW; 2D71B2D6C1A73774 CRC64;

Query Match 32.8%; Score 20; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLTSV 9
Db :||: ||
2 PLTV 6

RESULT 4
Q85563 PRELIMINARY; PRT; 10 AA.
AC Q85563;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Moloney murine sarcoma virus (strain ml) env/mos 5' junction.

```

```

DE Env-mos fusion protein (Fragment).
OS Moloney murine leukemia virus.
OC Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11801;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82196891; PubMed=6281735;
RA Donoghue D.J., Hunter T.;
RT "A generalized method of subcloning DNA fragments by restriction site
RT reconstruction: Application to sequencing the amino-terminal region of
RT the transforming gene of Gazdar murine sarcoma virus.";
RL Nucleic Acids Res. 10:2549-2564(1982).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83164305; PubMed=6300424;
RA Donoghue D.J., Hunter T.;
RT "Recombination junctions of variants of Moloney murine sarcoma virus:
RT Generation and divergence of a mammalian transforming gene.";
RL J. Virol. 45:607-617(1983).
DR EMBL; K03105; AAA46491.1; -.
FT NON_TER 10 10
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1062 MW; F9ECFCBEA771B5B1 CRC64;

Query Match 32.8%; Score 20; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 7.2e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 SVPC 11
Db :||: ||
4 STPC 7

RESULT 5
Q85598 PRELIMINARY; PRT; 10 AA.
AC Q85598;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Moloney murine sarcoma virus (strain HTI) env/mos 5' junction.
DE (Fragment).
OS Moloney murine leukemia virus.
OC Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11801;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83164305; PubMed=6300424;
RA Donoghue D.J., Hunter T.;
RT "Recombination junctions of variants of Moloney murine sarcoma virus:
RT Generation and divergence of a mammalian transforming gene.";
RL J. Virol. 45:607-617(1983).
DR EMBL; K03106; AAA46492.1; -.
FT NON_TER 10 10
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1081 MW; 7BECFCBEA771B5A4 CRC64;

Query Match 32.8%; Score 20; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 7.2e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 SVPC 11
Db :||: ||
4 STPC 7

RESULT 6
Q85619 PRELIMINARY; PRT; 10 AA.
AC Q85619;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Moloney murine sarcoma virus (strain ml) env/mos 5' junction.
DE (Fragment).

```



```
OS Moloney murine leukemia virus.
OC Viruses; Retroviral viruses; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11801;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83164305; PubMed=6300424;
RA Donoghue D.J., Hunter T.;
RT "Recombination junctions of variants of Moloney murine sarcoma virus:
RT Generation and divergence of a mammalian transforming gene.";
RL J. Virol. 45:607-617(1983).
DR EMBL; K03108; AAA46494.1; -.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1081 MW; 7BECFCBEA771B5A4 CRC64;

Query Match 32.8%; Score 20; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 7.2e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 SVPC 11
DB 4 STPC 7

RESULT 7
Q712U0 PRELIMINARY; PRT; 11 AA.
AC Q712U0;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE M1 muscarinic acetylcholine receptor protein (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99267322; PubMed=10333492; DOI=10.1042/0264-6021.3400475;
RA Wood I.C., Garriga Canut M., Pepitoni S., Buckley N.J.;
RT "Neuronal expression of the rat M1 muscarinic acetylcholine receptor
RT gene is regulated by elements in the first exon.";
RL Biochem. J. 340:475-483(1999).
DR EMBL; AJ006522; CAA07083.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1099 MW; 982D0BF4C77772D5 CRC64;

Query Match 32.8%; Score 20; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TSVP 10
DB 3 TSVP 6

RESULT 8
Q712U1 PRELIMINARY; PRT; 11 AA.
AC Q712U1;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE M1 muscarinic acetylcholine receptor protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57B6a/129SV;
RX MEDLINE=99267322; PubMed=10333492; DOI=10.1042/0264-6021.3400475;

RA Wood I.C., Garriga Canut M., Pepitoni S., Buckley N.J.;
RT "Neuronal expression of the rat M1 muscarinic acetylcholine receptor
RT gene is regulated by elements in the first exon.";
RL Biochem. J. 340:475-483(1999).
DR EMBL; AJ006521; CAA07082.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1099 MW; 982D0BF4C77772D5 CRC64;

Query Match 32.8%; Score 20; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TSVP 10
DB 3 TSVP 6

RESULT 9
Q56140 PRELIMINARY; PRT; 8 AA.
AC Q56140;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE STP6 protein (Fragment).
GN Name=STP6;
OS Streptococcus thermophilus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1308;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ST11;
RX MEDLINE=95047254; PubMed=7958782;
RA Constable A., Mollet B.;
RT "Isolation and characterisation of promoter regions from Streptococcus
RT thermophilus.";
RL FEMS Microbiol. Lett. 122:85-90(1994).
DR EMBL; X78210; CAA55045.1; -.
FT NON TER 8 8
SQ SEQUENCE 8 AA; 846 MW; ED086772D5B045B6 CRC64;

Query Match 31.1%; Score 19; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TSVP 5
DB 3 TSVP 6

RESULT 10
Q9THM6 PRELIMINARY; PRT; 10 AA.
AC Q9THM6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE AtpB (Fragment).
GN Name=atpB;
OS Leptospermum polygalifolium subsp. tropicum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Myrtaceae; Leptospermum.
OX NCBI_TaxID=106056;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien M.M., Quinn C.J., Wilson P.G.;
RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
RL Aust. J. Bot. 48:621-628(2000).
```

```
RN [2]
RP SEQUENCE FROM N.A.
RA Heslewood M., Quinn C.J.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF184695; AAF03862.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;

Query Match 31.1%; Score 19; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10
Db 5 PTTSRP 10

RESULT 11
Q9THM7
ID Q9THM7 PRELIMINARY; PRT; 10 AA.
AC Q9THM7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE AtPB (Fragment).
GN Name=atPB;
OS Leptospermum madidum subsp. sativum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Myrtaceae; Leptospermum.
OC NCBI_TaxID=106052;
OX NCBI_TaxID=106052;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien M.M., Quinn C.J., Wilson P.G.;
RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
RL Aust. J. Bot. 48:621-628(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Heslewood M., Quinn C.J.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF184692; AAF03862.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;

Query Match 31.1%; Score 19; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10
Db 5 PTTSRP 10

RESULT 12
Q9TKE0
ID Q9TKE0 PRELIMINARY; PRT; 10 AA.
AC Q9TKE0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE AtPB (Fragment).
GN Name=atPB;
OS Neofabricia sericisepala.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Myrtaceae; Neofabricia.
OC NCBI_TaxID=106065;
OX NCBI_TaxID=106065;
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RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien M.M., Quinn C.J., Wilson P.G.;
RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
RL Aust. J. Bot. 48:621-628(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Heslewood M., Quinn C.J.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF184700; AAF03869.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;

Query Match 31.1%; Score 19; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10
Db 5 PTTSRP 10

RESULT 13
Q9TKE1
ID Q9TKE1 PRELIMINARY; PRT; 10 AA.
AC Q9TKE1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE AtPB (Fragment).
GN Name=atPB;
OS Neofabricia mjobergii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Myrtaceae; Neofabricia.
OC NCBI_TaxID=106064;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien M.M., Quinn C.J., Wilson P.G.;
RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
RL Aust. J. Bot. 48:621-628(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Heslewood M., Quinn C.J.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF184699; AAF03868.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;

Query Match 31.1%; Score 19; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10
Db 5 PTTSRP 10

RESULT 14
Q9TKE2
ID Q9TKE2 PRELIMINARY; PRT; 10 AA.
AC Q9TKE2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE AtPB (Fragment).
GN Name=atPB;
OS Leptospermum woornooran.
```

OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Myrtaceae; Leptospermum.
 OX NCBI_TaxID=106059;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA O'Brien M.M., Quinn C.J., Wilson P.G.;
 RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
 RL Aust. J. Bot. 48:621-628(2000).
 RN [2]

RP SEQUENCE FROM N.A.
 RA Heslewood M., Quinn C.J.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF184698; AAF03867.1; -;
 DR GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;

Query Match 31.1%; Score 19; DB 2; Length 10;
 Best Local Similarity 66.7%; Pred. No. 1.1e+04;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10
 | | | | |
 Db 5 PTTSRP 10

RESULT 15
 OSTKE3
 ID Q9TKE3 PRELIMINARY; PRT; 10 AA.
 AC Q9TKE3;
 DT 01-MAY-2000 (TREMELrel. 13, Created)
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE AtpB (Fragment).
 GN Name=atpB;
 OS Leptospermum parvifolium.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Myrtales; Myrtaceae; Leptospermum.
 OX NCBI_TaxID=106054;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA O'Brien M.M., Quinn C.J., Wilson P.G.;
 RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
 RL Aust. J. Bot. 48:621-628(2000).
 RN [2]

RP SEQUENCE FROM N.A.
 RA Heslewood M., Quinn C.J.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF184694; AAF03863.1; -;
 DR GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;

Query Match 31.1%; Score 19; DB 2; Length 10;
 Best Local Similarity 66.7%; Pred. No. 1.1e+04;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10
 | | | | |
 Db 5 PTTSRP 10

Search completed: April 1, 2005, 11:10:22
 Job time : 116 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 10:56:34 ; Search time 118 Seconds
(without alignments)
36.054 Million cell updates/sec

Title: US-09-761-636A-7

Perfect score: 61

Sequence: 1 CISVPLTSVPC 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 494136

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq16Dec04:*

1: Genesep1980a:*

2: Genesep1990a:*

3: Genesep2000a:*

4: Genesep2001a:*

5: Genesep2002a:*

6: Genesep2003a:*

7: Genesep2003bs:*

8: Genesep2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	11	AAU04526	Aau04526 VEGF base
2	59	96.7	11	AAU04542	Aau04542 VEGF base
3	57	93.4	11	AAU04545	Aau04545 VEGF base
4	54	88.5	11	AAU04543	Aau04543 VEGF base
5	52	85.2	11	AAU04544	Aau04544 VEGF base
6	45.5	74.6	10	AAU04532	Aau04532 VEGF base
7	41	67.2	9	AAU04533	Aau04533 VEGF base
8	36	59.0	9	ADR65202	Adk65202 Human VEG
9	35	57.4	9	ADR65204	Adk65204 Human VEG
10	32	52.5	9	AAU04529	Aau04529 VEGF base
11	30	49.2	8	AAR58418	Aar58418 Partial p
12	30	49.2	9	AAR54703	Aar54703 CA125/MUC
13	30	49.2	10	AAW12561	Aaw12561 SH2 bindi
14	30	49.2	11	AAW12615	Aaw12615 SH2 bindi
15	29	47.5	9	ADK06442	Adk06442 Hepatitis
16	29	47.5	9	ADM12370	Adm12370 MHC class
17	29	47.5	9	ADO38592	Ado38592 Ovarian c
18	29	47.5	9	ADR42764	Adr42764 Modulator
19	29	47.5	11	ABP47579	Abp47579 N. mening
20	29	47.5	11	ABP47580	Abp47580 N. mening
21	28	45.9	9	ADM35397	Adm35397 Human LY1
22	28	45.9	10	AD100781	Adi00781 Human up-
23	27	44.3	9	ADM35404	Adm35404 Human LY1
24	27	44.3	9	ADM35430	Adm35430 Human LY1
25	27	44.3	9	ADM35441	Adm35441 Human LY1

26	27	44.3	9	ADM35456	Adm35456 Human LY1
27	27	44.3	9	ADM35435	Adm35435 Human LY1
28	27	44.3	9	ADM35451	Adm35451 Human LY1
29	27	44.3	9	ADM35434	Adm35434 Human LY1
30	27	44.3	9	ADM35426	Adm35426 Human LY1
31	27	44.3	10	AAR77368	Aar77368 SH3 bindi
32	27	44.3	11	ABP47596	Abp47596 N. mening
33	27	44.3	11	ADI82595	Adi82595 C3 exoenz
34	26	42.6	6	AAV41619	Aav41619 Mammalian
35	26	42.6	8	AAR58417	Aar58417 Partial p
36	26	42.6	9	AAV26265	Aay26265 Isolated
37	26	42.6	9	ABR56927	Abt56927 Mouse pla
38	26	42.6	9	ADR28717	Adr28717 Immunosp
39	26	42.6	10	AAG73418	Aag73418 Human gen
40	26	42.6	10	ABG64264	Abg64264 Human alb
41	26	42.6	10	ADK06214	Adk06214 Hepatitis
42	26	42.6	10	ADL77529	Adl77529 Albumin f
43	25.5	41.8	9	AAR96138	Aar96138 Protease
44	25.5	41.8	9	AAW82212	Aaw82212 D-NorFES-
45	25.5	41.8	9	AAW46562	Aaw46562 Peptide b

ALIGNMENTS

RESULT 1

AAU04526

ID AAU04526 standard; peptide; 11 AA.

XX

AC AAU04526;

XX

DT 26-SEP-2001 (first entry)

XX

DE VEGF based monocyclic peptide 3.

XX

KW Human; VEGF; vascular endothelial growth factor; angiogenesis;

KW neovascularisation; lymphangiogenesis; psoriasis; tumour;

KW diabetes induced neovascular sequelae; rheumatoid arthritis;

KW diabetic retinopathy; chronic inflammation; cyclic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Disulfide-bond 1..11 /note= "This bond cyclises the peptide"

XX

PN WO200152875-A1.

XX

PD 26-JUL-2001.

 XX || PF | 18-JAN-2001; 2001WO-US001533. |
XX	
PR	18-JAN-2000; 2000US-0176293P.
PR	16-MAY-2000; 2000US-0204590P.
XX	
PA	(LUDW-) LUDWIG INST CANCER RES.
XX	
PI	Achen MG, Hughes RA, Stackner S, Cendron A;
XX	
DR	WPI; 2001-442248/47.
XX	
PT	Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.
XX	
PS	Claim 49; Page 32; 102pp; English.
XX	
CC	The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTSVPLTSVPC 11
 DB 1 CTSVPLTSVPC 11
 |||||

RESULT 2
 AAU04542
 ID AAU04542 standard; peptide; 11 AA.
 XX
 AC AAU04542;
 DT 26-SEP-2001 (first entry)
 DE VEGF based monocyclic peptide 20.
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..11
 FT /note= "This bond cyclises the peptide"
 XX
 PN WO200152875-A1.
 XX 26-JUL-2001.
 XX
 PF 18-JAN-2001; 2001WO-US001533.
 XX
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA Achen MG, Hughes RA, Stacker S, Cendron A;
 XX WPI; 2001-442248/47.
 DR Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 FT or lymphangiogenesis, is produced by cyclising a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine

PT residues.
 XX Example 25; Page 47; 102pp; English.
 XX The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 11 AA;

Query Match 96.7%; Score 59; DB 4; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.0045;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTSVPLTSVPC 11
 DB 1 CTSVPLTSVPC 11
 |||||
 RESULT 3
 AAU04545
 ID AAU04545 standard; peptide; 11 AA.
 XX
 AC AAU04545;
 XX
 DT 26-SEP-2001 (first entry)
 XX VEGF based monocyclic peptide 23.
 DE
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..11
 FT /note= "This bond cyclises the peptide"
 XX
 PN WO200152875-A1.
 XX 26-JUL-2001.
 XX
 PF 18-JAN-2001; 2001WO-US001533.
 XX
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX

PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Achen MG, Hughes RA, Stacker S, Cendron A;
 XX
 DR WPI; 2001-442248/47.
 XX
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX
 XX Example 25; Page 47; 102pp; English.
 PS
 XX The sequence represents a monomeric monocyclic peptide of the invention,
 XX whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain). The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 XX Sequence 11 AA;
 SQ
 Query Match 93.4%; Score 57; DB 4; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.0095;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CISVPLTSPVC 11
 Db |::|||::|||
 1 CVSPLTTPVC 11
 RESULT 4
 AAU04543
 ID AAU04543 standard; peptide; 11 AA.
 XX
 AC AAU04543;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE VEGF based monocyclic peptide 21.
 XX
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 1..11
 FT /note= "This bond cyclises the peptide"
 XX

PN WO200152875-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 18-JAN-2001; 2001WO-US001533.
 XX
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Achen MG, Hughes RA, Stacker S, Cendron A;
 XX
 DR WPI; 2001-442248/47.
 XX
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX
 XX Example 25; Page 47; 102pp; English.
 PS
 XX The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain). The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 XX Sequence 11 AA;
 SQ
 Query Match 88.5%; Score 54; DB 4; Length 11;
 Best Local Similarity 72.7%; Pred. No. 0.03;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CISVPLTSPVC 11
 Db |::|||::|||
 1 CITPLTSLPC 11
 RESULT 5
 AAU04544
 ID AAU04544 standard; peptide; 11 AA.
 XX
 AC AAU04544;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE VEGF based monocyclic peptide 22.
 XX
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;

KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 XX diabetic retinopathy; chronic inflammation; cyclic.

OS Synthetic.

XX Key Location/Qualifiers

FH Disulfide-bond 1..11 /note= "This bond cyclises the peptide"

FT WO200152875-A1.

PN 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

PR 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

PA Achen MG, Hughes RA, Stacker S, Cendron A;

XX WPI; 2001-442248/47.

DR Novel monomeric monocyclic peptide, used to interfere with angiogenesis,

XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment

PT from an exposed loop of a growth factor protein by oxidizing the cysteine

PT residues.

PT Example 25; Page 47; 102pp; English.

PS The sequence represents a monomeric monocyclic peptide of the invention,

XX whose 3-dimensional structure is modelled on the expose loop of human

CC VEGF (vascular endothelial growth factor). The invention relates to a

CC method of producing a monomeric monocyclic peptide by a measuring beta-

CC beta carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and

CC cyclising the peptide by oxidising the cysteine residues. The monocyclic

CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic

CC peptides) and a cyclic peptide with at least one amino acid deleted prior

CC to cyclisation are used to interfere with angiogenesis,

CC neovascularisation or lymphangiogenesis in a mammal with a condition

CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.

CC The condition is diabetic retinopathy, psoriasis, arthropathy,

CC hemangioma, vascularised malignant or benign tumour, post-recovery

CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold

CC trauma, substance-induced neovascularisation of the liver, excessive

CC hormone-related angiogenic dysfunction, diabetes induced neovascular

CC sequelae, hypertension induced neovascular sequelae, or chronic liver

CC infection. The peptides are also used to modulate vascular permeability

CC in a mammal (the mammal has a condition characterised by fluid

CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,

CC or brain. The peptides are used to image blood vessels and lymphatic

CC vasculature. The monomeric and bicyclic peptides are used to interfere

CC with at least one biological activity induced by VEGF, VEGF-C or -D and

CC are also used in combination with an anti-inflammatory agent, to treat a

CC chronic inflammation, especially rheumatoid arthritis, psoriasis and

CC diabetic retinopathy

XX Sequence 11 AA;

SQ Query Match 85.2%; Score 52; DB 4; Length 11;

Best Local Similarity 72.7%; Pred. No. 0.064;

Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QV 1 CTSVPLTSVPC 11

DB 1 CTSPLISSVPC 11

RESULT 6

AAU04532

ID AAU04532 standard; peptide; 10 AA.

XX

AC AAU04532;

XX

DT 26-SEP-2001 (first entry)

XX

DE VEGF based monocyclic peptide 10.

XX

KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Disulfide-bond 1..10

FT /note= "This bond cyclises the peptide"

XX

PN WO200152875-A1.

XX

PD 26-JUL-2001.

XX

PF 18-JAN-2001; 2001WO-US001533.

XX

PR 18-JAN-2000; 2000US-0176293P.

PR

PR 16-MAY-2000; 2000US-0204590P.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Achen MG, Hughes RA, Stacker S, Cendron A;

XX

DR WPI; 2001-442248/47.

XX

PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.

XX

PS Claim 49; Page 32; 102pp; English.

XX

CC The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGF (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.

CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy

XX

SQ Sequence 10 AA;

Query Match

Best Local Similarity 74.6%; Score 45.5; DB 4; Length 10;

Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CISVPLTSVPC 11
 DB 1 CISVPL-SVPC 10

RESULT 7
 AAU04533
 ID AAU04533 standard; peptide; 9 AA.
 XX
 AC AAU04533;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE VEGF based monocyclic peptide 11.
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..9 /note= "This bond cyclises the peptide"
 XX
 FN WO200152875-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 18-JAN-2001; 2001WO-US001533.
 XX
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Achen MG, Hughes RA, Stacker S, Cendron A;
 XX
 DR WPI; 2001-442248/47.
 XX
 PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX
 PS Claim 49; Page 32; 102pp; English.
 XX

The sequence represents a monomeric monocyclic peptide of the invention,
 whose 3-dimensional structure is modelled on the exposed loop of human
 VEGFD (vascular endothelial growth factor). The invention relates to a
 method of producing a monomeric monocyclic peptide by a measuring beta-
 beta carbon separation distances on opposite antiparallel strands of a
 peptide loop fragment from an exposed loop of a growth factor protein and
 cyclising the peptide by oxidising the cysteine residues. The monocyclic
 peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 peptides) and a cyclic peptide with at least one amino acid deleted prior
 to cyclisation are used to interfere with angiogenesis,
 neovascularisation or lymphangiogenesis in a mammal with a condition
 characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 The condition is diabetic retinopathy, psoriasis, arthropathy,
 hemangioma, vascularised malignant or benign tumour, post-recovery
 cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 trauma, substance-induced neovascularisation of the liver, excessive
 hormone-related angiogenic dysfunction, diabetes induced neovascular
 sequelae, hypertension induced neovascular sequelae, or chronic liver
 infection. The peptides are also used to modulate vascular permeability
 in a mammal (the mammal has a condition characterised by fluid
 accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 or brain). The peptides are used to image blood vessels and lymphatic
 vasculature. The monomeric and bicyclic peptides are used to interfere
 with at least one biological activity induced by VEGF, VEGF-C or -D and

CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 9 AA;

Query Match 67.2%; Score 41; DB 4; Length 9;
 Best Local Similarity 81.8%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 CISVPLTSVPC 11
 DB 1 CISVPL--VPC 9

RESULT 8
 ADK65202
 ID ADK65202 standard; peptide; 9 AA.
 XX
 AC ADK65202;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human VEGF-D-derived peptide #18 for anti-angiogenesis treatment.
 XX
 KW antiangiogenic; cytostatic; antiinflammatory; immunosuppressive;
 KW ophthalmological; gynecological; antiarteriosclerotic; virucide;
 KW hepatotropic; dermatological; anti-HIV; antidiabetic; antipsoriatic;
 KW antirheumatic; antiarthritic; antithyroid; immunization; angiogenesis;
 KW vascular endothelial growth factor; VEGF; neuropilin;
 KW placental growth factor; tumor; neoplasias; metastases; inflammation;
 KW autoimmunity; eye disease; arthritis; endometriosis; arteriosclerosis;
 KW edema; hepatitis; Kaposi sarcoma; diabetes; psoriasis;
 KW rheumatoid arthritis; thyroiditis; diabetic retinopathy;
 KW transplant rejection; macular degeneration; neovascular glaucoma;
 KW hemangioma; angiofibroma.
 XX
 OS Homo sapiens.
 XX
 FN WO2003086450-A1.
 XX
 PD 23-OCT-2003.
 XX
 PF 11-APR-2003; 2003WO-CU0000004.
 XX
 PR 15-APR-2002; 2002CU-00000076.
 XX
 PA (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
 XX
 PI Bequet Romero M, Acevedo Castro BE, Gavilondo Cowley JV;
 PI Fernandez Molina LE, Lopez Ochoa O, Silva Rodriguez RDIC;
 PI Musachio Lasa A, Galban Rodriguez E, Vazquez Blomquist DM;
 XX
 DR WPI; 2003-833615/77.
 XX
 PT Active immunization against angiogenic proteins, useful for treating e.g.
 PT tumors and inflammation, particularly contains vascular endothelial
 PT growth factor or its receptor.
 XX
 PS Disclosure; Page 18; 53pp; Spanish.
 XX

The invention relates to an active immunization against angiogenic
 proteins comprising administration of a vaccination composition (A),
 optionally containing an adjuvant, that comprises polypeptides (I),
 directly associated with an increase in angiogenesis, their variants, or
 their encoding polynucleotides (II). Angiogenesis-associated polypeptides
 are: members of the vascular endothelial growth factor (VEGF) family,
 especially the 121, 165 or 189 isoforms of VEGF-A, the 167 isoform of
 VEGF-B, or VEGF-C or -D; a (co-)receptor of VEGF, particularly VEGFR-1,
 2 or -3; NRP-1 or -2 (members of the neuropilin family); or placental
 growth factor. (A) is used for treatment or prevention of tumors in
 mammals, particularly humans but also farm animals and pets, also many
 other conditions associated with excessive angiogenesis, specifically

CC malignant or benign neoplasias (and their metastases), acute or chronic
 CC inflammation, autoimmunity and eye diseases (claimed). Among the diseases
 CC that may be treated are arthritis, endometriosis, arteriosclerosis,
 CC edema, infectious diseases (hepatitis and Kaposi sarcoma), diabetes,
 CC psoriasis, rheumatoid arthritis, thyroiditis, diabetic retinopathy,
 CC transplant rejection, macular degeneration, neovascular glaucoma,
 CC hemangioma and angiofibroma. The method destroys cells that are the
 CC source of angiogenic proteins, rather than just neutralizing the activity
 CC of such proteins (as in passive immunization). This sequence represents
 CC an immunisation peptides of the invention derived from the VEGF proteins.
 XX
 SQ Sequence 9 AA;

Query Match 59.0%; Score 36; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVPLTSV 9
 Db 2 ISVPLTSV 9

RESULT 9
 ADK65204
 ID ADK65204 standard; peptide; 9 AA.
 AC ADK65204;
 XX

DT 06-MAY-2004 (first entry)

DE Human VEGF-D-derived peptide #20 for anti-angiogenesis treatment.

XX antiangiogenic; cytostatic; antiinflammatory; immunosuppressive;
 KW ophthalmological; gynecological; antiarteriosclerotic; virucide;
 KW hepatotropic; dermatological; anti-HIV; antidiabetic; antipsoriatic;
 KW antirheumatic; antiarthritic; antithyroid; immunization; angiogenesis;
 KW vascular endothelial growth factor; VEGF; neuropilin;
 KW placental growth factor; tumor; neoplasias; metastases; inflammation;
 KW autoimmunity; eye disease; arthritis; endometriosis; arteriosclerosis;
 KW edema; hepatitis; Kaposi sarcoma; diabetes; psoriasis;
 KW rheumatoid arthritis; thyroiditis; diabetic retinopathy;
 KW transplant rejection; macular degeneration; neovascular glaucoma;
 KW hemangioma; angiofibroma.

XX Homo sapiens.

XX WO2003086450-A1.

XX 23-OCT-2003.

PF 11-APR-2003; 2003WO-CU0000004.

PR 15-APR-2002; 2002CU-000000076.

XX (INGG-) CENT ING GENETICA & BIOTECHNOLOGIA.

XX Bequet Romero M, Acevedo Castro BE, Gavilondo Cowley JV;
 PI Fernandez Molina LE, Lopez Ocejo O, Silva Rodriguez RDLG;
 PI Musachio Lasa A, Galban Rodriguez E, Vazquez Blomquist DM;
 XX WPI; 2003-833615/77.

XX Active immunization against angiogenic proteins, useful for treating e.g.
 PT tumors and inflammation, particularly contains vascular endothelial
 PT growth factor or its receptor.

PS Disclosure; Page 18; 53pp; Spanish.

XX The invention relates to an active immunization against angiogenic
 CC proteins comprising administration of a vaccination composition (A),
 CC optionally containing an adjuvant, that comprises polypeptides (I)
 CC directly associated with an increase in angiogenesis, their variants, or
 CC their encoding polynucleotides (II). Angiogenesis-associated polypeptides

CC are: members of the vascular endothelial growth factor (VEGF) family,
 CC especially the 121, 165 or 189 isoforms of VEGF-A, the 167 isoform of
 CC VEGF-B, or VEGF-C or -D; a (co-)receptor of VEGF, particularly VEGFR-1,
 CC 2 or -3; NRP-1 or -2 (members of the neuropilin family); or placental
 CC growth factor. (A) is used for treatment or prevention of tumors in
 CC mammals, particularly humans but also farm animals and pets, also many
 CC other conditions associated with excessive angiogenesis, specifically
 CC malignant or benign neoplasias (and their metastases), acute or chronic
 CC inflammation, autoimmunity and eye diseases (claimed). Among the diseases
 CC that may be treated are arthritis, endometriosis, arteriosclerosis,
 CC edema, infectious diseases (hepatitis and Kaposi sarcoma), diabetes,
 CC psoriasis, rheumatoid arthritis, thyroiditis, diabetic retinopathy,
 CC transplant rejection, macular degeneration, neovascular glaucoma,
 CC hemangioma and angiofibroma. The method destroys cells that are the
 CC source of angiogenic proteins, rather than just neutralizing the activity
 CC of such proteins (as in passive immunization). This sequence represents
 CC an immunisation peptides of the invention derived from the VEGF proteins.
 XX
 SQ Sequence 9 AA;

Query Match 57.4%; Score 35; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPLTSVP 10
 Db 1 VPLTSVP 7

RESULT 10
 AAU04529
 ID AAU04529 standard; peptide; 9 AA.
 AC AAU04529;
 XX

DT 26-SEP-2001 (first entry)

DE VEGF based monocyclic peptide 7.

XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.

XX Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 1..9 /note= "This bond cyclises the peptide"

XX WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

XX 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Hughes RA, Stacker S, Cendron A;

XX WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.

XX Claim 49; Page 32; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention,

CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy

XX SQ Sequence 9 AA;

Query Match 52.5%; Score 32; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;

QY 3 SVPLTSV 9
 |||||
 Db 2 SVPLTSV 8

RESULT 11

AARS58418
 ID AARS58418 standard; protein; 8 AA.

XX AARS58418;

XX 25-MAR-2003 (revised)

DT 13-APR-1995 (first entry)

XX Partial peptide 7 from TSAR C46.9-2 binding domain.

XX TSAR; totally synthetic affinity reagent; synthetic; binding domain;
 KW effector domain; concatenated heterofunctional protein; linker; direct;
 KW rapid; detection; screening; treatment; monoclonal antibody; MAB; C46;
 KW anti-carcinoma; antigen; anti-CEA.

XX Synthetic.

XX WO9418318-A1.

XX 18-AUG-1994.

XX 01-FEB-1994; 94WO-US000977.

XX 01-FEB-1993; 93US-00013416.

PR 30-DEC-1993; 93US-00176500.

PR 31-JAN-1994; 94US-00189331.

XX (UYN-C) UNIV NORTH CAROLINA.

XX Kay BK, Fowlkes DM;

XX WPI; 1994-279739/34.

PT Identifying proteins or peptide(s) which bind a ligand - by screening a

PT recombinant vector library expressing fusion proteins comprising a
 PT binding domain and an effector domain.
 XX Example 7.5; Page 108; 255pp; English.
 XX AARS8412-42 are overlapping 8-mer peptides of the binding domain of TSAR
 CC (Totally Synthetic Affinity Reagents) peptide TSAR C46.9-2 (AARS8411).
 CC These bind (partially) a monoclonal antibody, ie. anti-CEA C46 (anti
 CC carcinoembryonic antigen). TSAR peptides are generated using generic
 CC oligonucleotides (see AAQ70470-73 for examples). TSARs are concatenated
 CC heterofunctional proteins or peptides, comprising at least two functional
 CC regions - a binding domain with affinity for a ligand and a second
 CC effector peptide portion that is chemically or biologically active. They
 CC may further comprise a linker peptide between the 2 domains. The TSARs or
 CC compns. comprising a TSAR binding domain can be used in vivo to deliver
 CC a chemically or biologically active moiety, eg. metal ion, radioisotope,
 CC peptide, toxin or enzyme, to the specific target or on the cell. They can
 CC also replace the function of macromolecules eg. monoclonal or polyclonal
 CC antibodies and therefore circumvent the need for complex methods of
 CC hybridoma formation or in vivo antibody production. The TSARs are easily
 CC characterised and have designed activity allowing direct and rapid
 CC detection in a screening process. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX SQ Sequence 8 AA;

Query Match 49.2%; Score 30; DB 2; Length 8;
 Best Local Similarity 62.5%; Pred. No. 1.8e+06;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVPLTS 8
 |||||
 Db 1 CVSAFQTS 8

RESULT 12

AAR34703
 ID AAR34703 standard; peptide; 9 AA.

XX AAR34703;

XX 14-MAY-2003 (first entry)

XX CA125/MUC16 O-glycosylation site #1.

XX CA125; antigen; cancer; gene therapy; vaccine; MUC16.

XX Unidentified.

XX WO200292836-A2.

XX 21-NOV-2002.

XX 09-MAY-2002; 2002WO-US014768.

XX 11-MAY-2001; 2001US-0290480P.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

XX Lloyd KO, Yin BWT;

XX WPI; 2003-129305/12.

XX New isolated nucleic acid molecule comprising sequences encoding the
 PT CA125 protein, useful for diagnosing, preventing and/or treating cancer,
 PT e.g. ovarian, pancreatic, breast, endometrial or lung carcinomas.

XX Disclosure; Page 19; 70pp; English.

XX The invention relates to a nucleic acid molecule encoding an ovarian
 CC cancer antigen, CA125. Nucleic acid molecules, vaccine and methods are
 CC useful for diagnosing, preventing and treating cancer, e.g. pancreatic,
 CC lung, ovarian, breast or endometrial carcinoma. The invention is useful

CC in gene therapy and as vaccines. The present sequence is CA125/MUC16 O-
XX glycosylation site
SQ Sequence 9 AA;

Query Match 49.2%; Score 30; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 SVPLTSVP 10
||| |||
Db 2 SVPTTSTP 9

RESULT 13
AAW12561
ID AAW12561 standard; peptide; 10 AA.

XX AC AAW12561;

DT 08-APR-1997 (first entry)

DE SH2 binding peptide core sequence #11.

KW Core peptide; src homology region 2 binding peptide; SH2; cell growth;
KW differentiation; regulation; receptor tyrosine kinase pathway; cancer;
KW signal transduction pathway; non-insulin dependent diabetes;
KW insulin-resistant diabetes.

XX OS Synthetic.

PH Key Location/Qualifiers
FT Modified-site 3 /label= OTHER

FT /note= "given in the patent as pI, no further details
FT given. May be intended to be phosphotyrosine"

XX PN WO9623813-A1.

XX PD 08-AUG-1996.

XX PF 31-JAN-1996; 96WO-US001544.

XX PR 01-FEB-1995; 95US-00382100.

XX PA (AFFY-) AFFYMAX TECHNOLOGIES NV.

XX PI Patel DV, Gordeev MF, Gordon E, Grove JR, Hart CP, Kim MH;
PI Szardenings AK;

XX DR WPI; 1996-371373/37.

XX PT Peptide(s) which bind to SH2 domains - are used to treat diseases
PT associated with aberrant cell growth, differentiation or regulation
PT associated with defects in receptor tyrosine kinase pathways.

XX PS Claim 8; Page 116; 203pp; English.

XX CC The sequences given in AAW12551-70 represent core peptides of an src
CC homology region 2 (SH2) binding peptide which correspond to the formula:
CC Z7-X-Z8-X X = any D- or L- amino acid; Z7 = phosphotyrosine or its
CC isostere; Z8 = asparagine or its isostere; the amino terminus is
CC acylated, and the peptide is less than 14 residues in length, with the
CC proviso that if Z7 is phosphotyrosine and Z8 is asparagine, then the
CC peptide is not GDGZ7XZ8XPLLL. SH2 binding peptides containing these core
CC peptides are used to treat of diagnose diseases associated with aberrant
CC cell growth, differentiation or regulation which is associated with
CC defects in receptor tyrosine kinase pathways, by partially blocking or
CC inhibiting a cellular signal transduction pathway. The disease may be
CC cancer, a developmental or differentiation disease or insulin-resistant
CC (or non-insulin dependent) diabetes

XX SQ Sequence 10 AA;

Query Match 49.2%; Score 30; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CISVPLT 7
||: |||
Db 2 CINVPT 8

RESULT 14
AAW12615

ID AAW12615 standard; peptide; 11 AA.

XX AC AAW12615;

DT 08-APR-1997 (first entry)

DE SH2 binding peptide core sequence #21.

KW Core peptide; src homology region 2 binding peptide; SH2; cell growth;
KW differentiation; regulation; receptor tyrosine kinase pathway; cancer;
KW signal transduction pathway; non-insulin dependent diabetes;
KW insulin-resistant diabetes.

XX OS Synthetic.

XX PN WO9623813-A1.

XX PD 08-AUG-1996.

XX PF 31-JAN-1996; 96WO-US001544.

XX PR 01-FEB-1995; 95US-00382100.

XX PA (AFFY-) AFFYMAX TECHNOLOGIES NV.

XX PI Patel DV, Gordeev MF, Gordon E, Grove JR, Hart CP, Kim MH;
PI Szardenings AK;

XX DR WPI; 1996-371373/37.

XX PT Peptide(s) which bind to SH2 domains - are used to treat diseases
PT associated with aberrant cell growth, differentiation or regulation
PT associated with defects in receptor tyrosine kinase pathways.

XX PS Claim 13; Page 117; 203pp; English.

XX CC This sequence represents a core peptide of an src homology region 2 (SH2)
CC binding peptide corresponding to the formula: Z7-X-Z8-X X = any D- or L-
CC amino acid; Z7 = phosphotyrosine or its isostere; Z8 = asparagine or its
CC isostere; the amino terminus is acylated, and the peptide is less than 14
CC residues in length, with the proviso that if Z7 is phosphotyrosine and Z8
CC is asparagine, then the peptide is not GDGZ7XZ8XPLLL. SH2 binding
CC peptides containing this core peptide are used to treat of diagnose
CC diseases associated with aberrant cell growth, differentiation or
CC regulation which is associated with defects in receptor tyrosine kinase
CC pathways, by partially blocking or inhibiting a cellular signal
CC transduction pathway. The disease may be cancer, a developmental or
CC differentiation disease or insulin-resistant (or non-insulin dependent)
CC diabetes

XX SQ Sequence 11 AA;

Query Match 49.2%; Score 30; DB 2; Length 11;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CISVPLT 7
||: |||
Db 2 CINVPT 8

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RESULT 15
ADK06442
ID ADK06442 standard; peptide; 9 AA.
XX
AC ADK06442;
XX
DT 06-MAY-2004 (first entry)
XX
DE Hepatitis C virus CTL epitope peptide #4272.
XX
KW pathogenic virus; alternative reading frame; antigenic determinant;
KW virucide; vaccine; therapeutic agent; infection; epitope peptide;
KW HLA-allele; CTL.
XX
OS Hepatitis C virus.
XX
PN WO2004011650-A2.
XX
PD 05-FEB-2004.
XX
PF 24-JUL-2003; 2003WO-EP008112.
XX
PR 24-JUL-2002; 2002AT-00001124.
PR 11-JUL-2003; 2003EP-00450171.
XX
PA (INTE-) INTERCELL AG.
XX
PI Mattner F, Schmidt W, Habel A;
XX
DR WPI; 2004-169243/16.
XX
PT New polypeptide encoded by an alternative reading frame of a pathogenic
PT virus comprising an antigenic determinant, useful for treating or
PT preventing an infection with the pathogenic virus.
XX
PS Claim 14; Page 139; 220pp; English.
XX
CC This invention relates to a novel polypeptide encoded by an alternative
CC reading frame of a pathogenic virus, where the polypeptide starts with a
CC methionine amino acid residue, which comprises an antigenic determinant
CC and more than 7 amino acid residues. The invention may be useful for the
CC production of compounds with a virucide activity or the development of a
CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
CC agent. It is also useful for the manufacture of a medicament for treating
CC or preventing an infection with the pathogenic virus. The present
CC sequence is that of a hepatitis C virus CTL epitope peptide of the
CC invention.
XX
SQ Sequence 9 AA;
Query Match 47.5%; Score 29; DB 8; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 CISPVLTS 8
|:|:|:|
DB 1 CLSLPVSS 8

```

Search completed: April 1, 2005, 11:08:15
Job time : 119 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 11:04:25 ; Search time 45 Seconds
(without alignments)
81.056 Million cell updates/sec

Title: US-09-761-636A-7

Perfect score: 61

Sequence: 1 CISVPLTSVPC 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 193427

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	11	9 US-09-761-636A-7	Sequence 7, Appli
2	59	96.7	11	9 US-09-761-636A-23	Sequence 23, Appli
3	57	93.4	11	9 US-09-761-636A-26	Sequence 26, Appli
4	54	88.5	11	9 US-09-761-636A-24	Sequence 24, Appli
5	52	85.2	11	9 US-09-761-636A-25	Sequence 25, Appli
6	45.5	74.6	10	9 US-09-761-636A-13	Sequence 13, Appli
7	41	67.2	9	9 US-09-761-636A-14	Sequence 14, Appli
8	32	52.5	9	9 US-09-761-636A-10	Sequence 10, Appli
9	29	47.5	9	15 US-10-245-871-332	Sequence 332, App
10	29	47.5	9	15 US-10-253-286-332	Sequence 332, App
11	29	47.5	9	16 US-10-649-873-38	Sequence 38, Appli
12	29	47.5	11	14 US-10-126-845-89	Sequence 89, Appli
13	29	47.5	11	15 US-10-398-104-155	Sequence 155, App

14	29	47.5	11	15	US-10-398-104-156	Sequence 156, App
15	28	45.9	9	15	US-10-154-884B-11221	Sequence 11221, A
16	27	44.3	9	15	US-10-154-884B-11228	Sequence 11228, A
17	27	44.3	9	15	US-10-154-884B-11250	Sequence 11250, A
18	27	44.3	9	15	US-10-154-884B-11254	Sequence 11254, A
19	27	44.3	9	15	US-10-154-884B-11258	Sequence 11258, A
20	27	44.3	9	15	US-10-154-884B-11259	Sequence 11259, A
21	27	44.3	9	15	US-10-154-884B-11265	Sequence 11265, A
22	27	44.3	9	15	US-10-154-884B-11275	Sequence 11275, A
23	27	44.3	9	15	US-10-154-884B-11280	Sequence 11280, A
24	27	44.3	11	15	US-10-398-104-172	Sequence 172, App
25	27	44.3	11	17	US-10-615-343-8	Sequence 8, Appli
26	26	42.6	9	13	US-10-066-151-20	Sequence 20, Appli
27	26	42.6	9	15	US-10-358-052-20	Sequence 20, Appli
28	26	42.6	10	11	US-09-833-245-1011	Sequence 1011, Ap
29	25	41.0	9	13	US-10-066-151-19	Sequence 19, Appli
30	25	41.0	9	15	US-10-358-052-19	Sequence 19, Appli
31	25	41.0	9	15	US-10-428-335-52	Sequence 52, Appli
32	25	41.0	9	16	US-10-471-895-10	Sequence 10, Appli
33	25	41.0	10	10	US-09-572-404B-2047	Sequence 2047, Ap
34	25	41.0	10	17	US-10-615-343-6	Sequence 6, Appli
35	25	41.0	11	14	US-10-126-845-12	Sequence 12, Appli
36	25	41.0	11	14	US-10-126-845-70	Sequence 70, Appli
37	25	41.0	11	15	US-10-116-275-100	Sequence 100, App
38	25	41.0	11	16	US-10-764-235-12	Sequence 12, Appli
39	24	39.3	5	10	US-09-886-135-5	Sequence 5, Appli
40	24	39.3	5	17	US-10-891-122-5	Sequence 5, Appli
41	24	39.3	7	9	US-09-761-636A-11	Sequence 11, Appli
42	24	39.3	7	14	US-10-220-033-28	Sequence 28, Appli
43	24	39.3	7	15	US-10-620-378-19	Sequence 19, Appli
44	24	39.3	9	10	US-09-935-430-249	Sequence 249, App
45	24	39.3	9	10	US-09-935-430-322	Sequence 322, App

ALIGNMENTS

RESULT 1
US-09-761-636A-7
; Sequence 7, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-7

Query Match 100.0%; Score 61; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CISVPLTSVPC 11

Db 1 CISVPLTSVPC 11

RESULT 2

US-09-761-636A-23

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; Sequence 23, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Steven
; APPLICANT: STACKER, Richard
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-23
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Query Match 96.7%; Score 59; DB 9; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0046;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CTSVPLTSVPC 11
Db 1 CTSVPLTSVPC 11
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RESULT 3
US-09-761-636A-26
; Sequence 26, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-26
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Query Match 93.4%; Score 57; DB 9; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.0098;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CTSVPLTSVPC 11
Db 1 CTSVPLTSVPC 11
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RESULT 4
US-09-761-636A-24
; Sequence 24, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
```

```
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-24
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Best Local Similarity 72.7%; Pred. No. 0.003;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 CTSVPLTSVPC 11
Db 1 CITIPLTSLPC 11
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RESULT 5
US-09-761-636A-25
; Sequence 25, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-25
```

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Query Match 85.2%; Score 52; DB 9; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.003;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 CTSVPLTSVPC 11
Db 1 CTSVPLTSVPC 11
```

```
RESULT 6
US-09-761-636A-13
; Sequence 13, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
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; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-13

Query Match          74.6%; Score 45.5; DB 9; Length 10;
Best Local Similarity 90.9%; Pred. No. 0.65;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 C1SVPLTSPVC 11
Db 1 C1SVPL-SVPC 10

RESULT 7
US-09-761-636A-14
; Sequence 14, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-14

Query Match          67.2%; Score 41; DB 9; Length 9;
Best Local Similarity 81.8%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 C1SVPLTSPVC 11
Db 1 C1SVPL--VPC 9

RESULT 8
US-09-761-636A-10
; Sequence 10, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16

; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-10

Query Match          52.5%; Score 32; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLTSV 9
Db 2 SVPLTSV 8

RESULT 9
US-10-245-871-332
; Sequence 332, Application US/10245871
; Publication No. US20030235594A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2013
; CURRENT APPLICATION NUMBER: US/10/245,871
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 332
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-245-871-332

Query Match          47.5%; Score 29; DB 15; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VPLTSTVP 10
Db 2 VPITSTP 8

RESULT 10
US-10-253-286-332
; Sequence 332, Application US/10253286
; Publication No. US20040058881A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2015
; CURRENT APPLICATION NUMBER: US/10/253,286
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 332
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-253-286-332

Query Match          47.5%; Score 29; DB 15; Length 9;
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Best Local Similarity 71.4%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VPLTSVP 10
Db 2 VPISTP 8

RESULT 11
US-10-649-873-38
; Sequence 38, Application US/10649873
; Publication No. US2004017152A1
; GENERAL INFORMATION:
; APPLICANT: Biokine Therapeutics Ltd.
; APPLICANT: Peled, Amnon
; APPLICANT: Eizenberg, Orly
; APPLICANT: Vaizel-Ohayon, Dalit
; TITLE OF INVENTION: NOVEL CHEMOKINE BINDING PEPTIDES CAPABLE OF MODULATING THE
; TITLE OF INVENTION: BIOLOGICAL ACTIVITY OF CHEMOKINES
; FILE REFERENCE: 26732
; CURRENT APPLICATION NUMBER: US/10/649,873
; CURRENT FILING DATE: 2003-08-28
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-649-873-38

Query Match 47.5%; Score 29; DB 16; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVPC 11
Db 3 PFTKLPC 9

RESULT 12
US-10-126-845-89
; Sequence 89, Application US/10126845
; Publication No. US20030181367A1
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20058
; CURRENT APPLICATION NUMBER: US/10/126,845
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D form peptide
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(11)
; OTHER INFORMATION: D form retroinversion peptide
US-10-126-845-89

Query Match 47.5%; Score 29; DB 14; Length 11;
Best Local Similarity 45.5%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CISVPLTSVPC 11

us-09-761-636a-7.closed.rapb

Db 1 CLLVPELLVAC 11

RESULT 13
US-10-398-104-155
; Sequence 155, Application US/10398104
; Publication No. US20040047880A1
; GENERAL INFORMATION:
; APPLICANT: De Bolle, Xavier Thomas
; APPLICANT: Letesson, Jean-Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Mertens, Pascal Yvon
; APPLICANT: Poolman, Jan
; APPLICANT: Voet, Pierre
; TITLE OF INVENTION: COMPONENT FOR VACCINE
; FILE REFERENCE: B45242
; CURRENT APPLICATION NUMBER: US/10/398,104
; CURRENT FILING DATE: 2003-01-04
; PRIOR APPLICATION NUMBER: PCT/EP01/11409
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: GB 0024200.8
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 155
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LOS peptide mimotope sequence
US-10-398-104-155

Query Match 47.5%; Score 29; DB 15; Length 11;
Best Local Similarity 27.3%; Pred. No. 3.4e+02;
Matches 3; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 CISVPLTSVPC 11
Db 1 CVTIPIRGTC 11

RESULT 14
US-10-398-104-156
; Sequence 156, Application US/10398104
; Publication No. US20040047880A1
; GENERAL INFORMATION:
; APPLICANT: De Bolle, Xavier Thomas
; APPLICANT: Letesson, Jean-Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Mertens, Pascal Yvon
; APPLICANT: Poolman, Jan
; APPLICANT: Voet, Pierre
; TITLE OF INVENTION: COMPONENT FOR VACCINE
; FILE REFERENCE: B45242
; CURRENT APPLICATION NUMBER: US/10/398,104
; CURRENT FILING DATE: 2003-01-04
; PRIOR APPLICATION NUMBER: PCT/EP01/11409
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: GB 0024200.8
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LOS peptide mimotope sequence
US-10-398-104-156

Query Match 47.5%; Score 29; DB 15; Length 11;
Best Local Similarity 36.4%; Pred. No. 3.4e+02;
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Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CISVPLTSVPC 11
 | : | : ||
Db 1 CFAPPYDPLPC 11

RESULT 15

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US-10-154-884B-11221
; Sequence 11221, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Cotixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11221
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11221

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Query Match 45.9%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.3e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CISVPLT	7
		: : :	
Db	2	CLSVFVS	8

Search completed: April 1, 2005, 11:12:08
Job time : 45 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 10:06:39 ; Search time 43 Seconds
(without alignments)
22.568 Million cell updates/sec

Title: US-09-761-636A-5

Perfect score: 72

Sequence: 1 CASELGKSTNTFC 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 143084

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	38.9	9	3 US-09-258-754-63	Sequence 63, Appl
2	28	38.9	9	3 US-09-042-107-63	Sequence 63, Appl
3	28	38.9	9	4 US-09-722-250D-63	Sequence 63, Appl
4	28	38.9	9	4 US-09-676-475A-63	Sequence 63, Appl
5	27	37.5	13	1 US-07-732-114A-2	Sequence 2, Appli
6	27	37.5	13	1 US-08-170-114A-2	Sequence 2, Appli
7	26	36.1	9	3 US-08-660-092-70	Sequence 70, Appl
8	26	36.1	9	4 US-09-160-513-70	Sequence 70, Appl
9	26	36.1	13	3 US-09-258-754-219	Sequence 219, App
10	26	36.1	13	3 US-09-042-107-219	Sequence 219, App
11	26	36.1	13	4 US-09-722-250D-219	Sequence 219, App
12	26	36.1	13	4 US-09-428-082B-170	Sequence 170, App
13	26	36.1	13	4 US-09-676-475A-219	Sequence 219, App
14	24.5	34.0	12	4 US-08-182-967-12	Sequence 12, Appl
15	24	33.3	7	2 US-08-645-193B-3	Sequence 3, Appli
16	24	33.3	9	6 5217869-110	Patent No. 5217869
17	24	33.3	9	6 5217869-110	Patent No. 5217869
18	24	33.3	11	3 US-08-866-545-24	Sequence 24, Appl
19	24	33.3	11	4 US-09-428-082B-116	Sequence 116, App
20	24	33.3	11	4 US-09-627-775-24	Sequence 24, Appl
21	24	33.3	11	4 US-09-744-072-27	Sequence 27, Appl
22	24	33.3	13	3 US-09-258-754-183	Sequence 183, App
23	24	33.3	13	3 US-09-042-107-183	Sequence 183, App
24	24	33.3	13	4 US-08-182-967-11	Sequence 11, Appl
25	24	33.3	13	4 US-09-722-250D-183	Sequence 183, App
26	24	33.3	13	4 US-09-747-802-5	Sequence 5, Appli
27	24	33.3	13	4 US-09-676-475A-183	Sequence 183, App

28	23.5	32.6	11	1 US-07-732-114A-6	Sequence 6, Appli
29	23.5	32.6	11	1 US-08-170-114A-6	Sequence 6, Appli
30	23	31.9	7	2 US-08-645-193B-7	Sequence 7, Appli
31	23	31.9	7	2 US-08-645-193B-59	Sequence 59, Appl
32	23	31.9	9	3 US-08-660-092-150	Sequence 150, App
33	23	31.9	9	3 US-08-660-092-151	Sequence 151, App
34	23	31.9	9	3 US-08-660-092-152	Sequence 152, App
35	23	31.9	9	4 US-09-160-513-150	Sequence 150, App
36	23	31.9	9	4 US-09-160-513-151	Sequence 151, App
37	23	31.9	9	4 US-09-160-513-152	Sequence 152, App
38	23	31.9	10	1 US-08-250-789A-91	Sequence 91, Appl
39	23	31.9	10	4 US-09-489-847-344	Sequence 344, App
40	23	31.9	11	1 US-08-212-433A-30	Sequence 30, Appl
41	23	31.9	11	3 US-08-716-256-30	Sequence 30, Appl
42	23	31.9	11	4 US-09-069-827A-35	Sequence 35, Appl
43	23	31.9	11	4 US-09-744-072-30	Sequence 30, Appl
44	23	31.9	11	4 US-09-744-072-31	Sequence 31, Appl
45	23	31.9	11	5 PCT-US95-03239-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-09-258-754-63
; Sequence 63, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-63

Query Match 38.9%; Score 28; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 KSTNTFC 13
Db 3 RSTNTGC 9

RESULT 2
US-09-042-107-63
; Sequence 63, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 9

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-63

Query Match 38.9%; Score 28; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 KSTNTFC 13
:|||||
Db 3 RSTNTGC 9

RESULT 3
US-09-722-250D-63
; Sequence 63, Application US/09722250D
; Patent No. 6610651
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250D
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-63

Query Match 38.9%; Score 28; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 KSTNTFC 13
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Db 3 RSTNTGC 9

RESULT 4
US-09-676-475A-63
; Sequence 63, Application US/09676475A
; Patent No. 6784153
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; FILE REFERENCE: P-LA 4377
; CURRENT APPLICATION NUMBER: US/09/676,475A
; CURRENT FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-676-475A-63

Query Match 38.9%; Score 28; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 KSTNTFC 13
:|||||
Db 3 RSTNTGC 9

RESULT 5
US-07-732-114A-2
; Sequence 2, Application US/07732114A
; Patent No. 5298396
; GENERAL INFORMATION:
; APPLICANT: KOTZIN, BRIAN L.
; APPLICANT: MARRACK, PHILIPPA
; APPLICANT: KAPPLER, JOHN
; APPLICANT: FALTARD, XAVIER
; TITLE OF INVENTION: METHOD FOR IDENTIFYING T CELLS
; TITLE OF INVENTION: INVOLVED IN AUTOIMMUNE DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beaton & Swanson, P.C.
; STREET: 4582 South Ulster Street Parkway, #403
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80237
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/732,114A
; FILING DATE: 18-JULY-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/488,353
; FILING DATE: 2-MARCH-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/437,370
; FILING DATE: 15-NOVEMBER-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 850-9900
; TELEFAX: (303) 850-9401
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-07-732-114A-2

Query Match 37.5%; Score 27; DB 1; Length 13;
Best Local Similarity 54.5%; Pred. No. 2.9e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CASELGKSTNT 11
:|||||
Db 1 CASSLYGTRNT 11

RESULT 6
US-08-170-114A-2
; Sequence 2, Application US/08170114A
; Patent No. 5776708
; GENERAL INFORMATION:
; APPLICANT: KOTZIN, BRIAN L.
; APPLICANT: MARRACK, PHILIPPA

APPLICANT: KAPPLER, JOHN
APPLICANT: PALIARD, XAVIER
TITLE OF INVENTION: METHOD FOR IDENTIFYING T CELLS
TITLE OF INVENTION: INVOLVED IN AUTOIMMUNE DISEASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0 (a) For Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/170,114A
FILING DATE: 20-DECEMBER-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/732,114
FILING DATE: 18-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07,488,353
FILING DATE: 2-MARCH-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07,437,370
FILING DATE: 15-NOVEMBER-1989
ATTORNEY/AGENT INFORMATION:
NAME: Julie L. Bernard
REGISTRATION NUMBER: 36,450
REFERENCE/DOCKET NUMBER: NJH217.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-170-114A-2

Query Match 37.5%; Score 27; DB 1; Length 13;
Best Local Similarity 54.5%; Pred. No. 2.9e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CASELGKSTNT 11
DB 1 CASSLYGTRNT 11

RESULT 7
US-08-660-092-70
Sequence 70, Application US/08660092
Patent No. 6207160
GENERAL INFORMATION:
APPLICANT: Victoria, Edward J.
APPLICANT: Marquis, David M.
APPLICANT: Jones, David S.
APPLICANT: Yu, Lin
TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES
TITLE OF INVENTION: THEREOF AND METHODS OF TREATMENT FOR aPL ANTIBODY-MEDIATED
TITLE OF INVENTION: PATHOLOGIES
NUMBER OF SEQUENCES: 216
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,092
FILING DATE: 06-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Park, Freddie K.
REGISTRATION NUMBER: 35,636
REFERENCE/DOCKET NUMBER: 25231-20061.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-660-092-70

Query Match 36.1%; Score 26; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELGK 7
DB 1 CAGVLGK 7

RESULT 8
US-09-160-513-70
Sequence 70, Application US/09160513
Patent No. 6410775
GENERAL INFORMATION:
APPLICANT: Victoria, Edward J.
APPLICANT: Marquis, David M.
APPLICANT: Jones, David S.
APPLICANT: Yu, Lin
TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES THEREOF AND METHODS O
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,513
FILING DATE: 1998-DEC-24
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CATHERINE M. POLIZZI
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 25231-20061.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids

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/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-09-160-513-70

Query Match 36.1%; Score 26; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELGK 7
Db 1 CAGVLCK 7

RESULT 9
US-09-258-754-219
; Sequence 219, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 219
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-219

Query Match 36.1%; Score 26; DB 3; Length 13;
Best Local Similarity 30.8%; Pred. No. 4.2e+02;
Matches 4; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
Db 1 CGSHCGQLCKSLC 13

RESULT 10
US-09-042-107-219
; Sequence 219, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 219
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-219

Query Match 36.1%; Score 26; DB 3; Length 13;
Best Local Similarity 30.8%; Pred. No. 4.2e+02;
Matches 4; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
Db 1 CGSHCGQLCKSLC 13

RESULT 11
US-09-722-250D-219
; Sequence 219, Application US/09722250D
; Patent No. 6610651
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250D
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 219
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-219

Query Match 36.1%; Score 26; DB 4; Length 13;
Best Local Similarity 30.8%; Pred. No. 4.2e+02;
Matches 4; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
Db 1 CGSHCGQLCKSLC 13

RESULT 12
US-09-428-082B-170
; Sequence 170, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-PA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 170
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CALMODULIN ANTAGONIST PEPTIDE
US-09-428-082B-170

Query Match 36.1%; Score 26; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NTFC 13
Db 8 NTFC 11
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RESULT 13
US-09-676-475A-219
; Sequence 219, Application US/09676475A
; Patent No. 6784153
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LA 4377
; CURRENT FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: US/09/676,475A
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 219
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-676-475A-219
Query Match 36.1%; Score 26; DB 4; Length 13;
Best Local Similarity 30.8%; Pred. No. 4.2e+02;
Matches 4; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 CASELGKSTNTEC 13
Db 1 CGSHCGQLCKSLC 13

RESULT 14
US-08-182-967-12
; Sequence 12, Application US/08182967
; Patent No. 6413516
; GENERAL INFORMATION:
; APPLICANT: Chang, Jennie C.C.
; APPLICANT: Brostoff, Steven W.
; APPLICANT: Carlo, Dennis J.
; TITLE OF INVENTION: Peptides and Methods Against Psoriasis
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,967
; FILING DATE: 14-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/462,471
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,867
; FILING DATE: 14-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/644,611
; FILING DATE: 22-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/530,229
; FILING DATE: 30-MAY-1990
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/382,085
; FILING DATE: 18-JUL-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/382,086
; FILING DATE: 18-JUL-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/326,314
; FILING DATE: 21-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 9830
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-182-967-12
Query Match 34.0%; Score 24.5; DB 4; Length 12;
Best Local Similarity 63.6%; Pred. No. 7e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 CASELGKSTNT 11
Db 1 CASSL-NSLNT 10

RESULT 15
US-08-645-193B-3
; Sequence 3, Application US/08645193B
; Patent No. 5962253
; GENERAL INFORMATION:
; APPLICANT: Kupke, Thomas
; APPLICANT: Gotz, Friedrich
; APPLICANT: Kempter, Christoph
; APPLICANT: Jung, Gunther
; TITLE OF INVENTION: Oxidative Decarboxylation of Peptides
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,193B
; FILING DATE: 13-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmord, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0652.1540000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-645-193B-3

Query Match 33.3%; Score 24; DB 2; Length 7;
Best Local Similarity 66.7%; Pred No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 STNTFC 13
| | : | |
Db 1 SFNSFC 6

Search completed: April 1, 2005, 10:42:36
Job time : 44 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 10:48:43 ; Search time 39 Seconds
(without alignments)
19.737 Million cell updates/sec

Title: US-09-761-636A-6

Perfect score: 46

Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 606

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	37.0	6	2 S29637	jacalin beta-II ch
2	17	37.0	6	2 I37263	Y protein - human
3	15	32.6	6	2 JU0355	lipopeptide WS1279
4	15	32.6	7	2 B39040	calsequestrin, fas
5	15	32.6	8	2 S39622	metallothionein is
6	15	32.6	8	2 S19288	acylase - Kluyvera
7	15	32.6	8	2 S69165	ferredoxin a2 - Ja
8	14	30.4	6	2 B31263	dihydrofolate redu
9	14	30.4	6	2 S29881	Na+/K+-exchanging
10	14	30.4	7	1 XEVDGD	galactose oxidase
11	14	30.4	8	2 B47594	aspartate kinase
12	13	28.3	5	2 A32014	tram protein - Esc
13	13	28.3	8	2 A59495	Vesicle associated
14	13	28.3	8	2 A37521	R-phycoerythrin ga
15	12	26.1	6	2 H48394	glycoprotein compo
16	12	26.1	7	2 B34818	vicilin 57K chain
17	12	26.1	7	2 A12016	formylglycinamide
18	12	26.1	8	2 PC1002	leucine-RNA ligas
19	11	23.9	4	2 A41890	protein D - Escher
20	11	23.9	5	2 B22565	R-phycoerythrin al
21	11	23.9	5	2 A44692	fulicin - giant Af
22	11	23.9	5	2 A26830	mitosis inhibiting
23	11	23.9	6	2 A31263	dihydrofolate redu
24	11	23.9	7	2 I46868	alpha-myosin heavy
25	11	23.9	7	2 A58512	venom heptapeptide
26	11	23.9	8	2 P70554	T-cell receptor be
27	11	23.9	8	2 C61512	variant surface gl
28	10	21.7	4	2 S55238	pallidipin - assas
29	10	21.7	5	2 A60803	neuropeptide - sea

30	10	21.7	5	2 PT0610	T-cell receptor be
31	10	21.7	6	2 S11556	hydrogensulfite re
32	10	21.7	6	2 S60293	tubulin beta-3 cha
33	10	21.7	7	2 S71870	glutathione transf
34	10	21.7	7	2 B33882	cadmium-binding he
35	10	21.7	7	2 S45648	Na+-transporting A
36	10	21.7	7	2 S09066	globulin IV alpha
37	10	21.7	7	2 PT0529	T-cell receptor be
38	10	21.7	7	2 S08606	hypothetical prote
39	10	21.7	8	2 A61597	cytochrome P450 AL
40	10	21.7	8	2 S29272	tocopherol-binding
41	10	21.7	8	2 I57532	gene Taislow prote
42	10	21.7	8	2 D61512	variant surface gl
43	10	21.7	8	2 I57018	gene Ctrr protein
44	10	21.7	8	2 A25836	L-serine ammonia-1
45	9	19.6	3	3 A22565	R-phycoerythrin al

ALIGNMENTS

RESULT 1

S29637 jacalin beta-II chain - Artocarpus champeden (fragment)

C:Species: Artocarpus champeden

C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998

C:Accession: S29637

R:Ngoc, L.D.; Brillard, M.; Hoebeke, J.

Biochim. Biophys. Acta 1156, 219-222, 1993

A:Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kD

A:Reference number: S29635; MUID:93152601; PMID:8427879

A:Accession: S29637

A:Molecule type: protein

A:Residues: 1-6 <NGO>

A:Experimental source: seed

A:Complex: heterotetramer; two alpha and two beta chains

C:Function:

A:Description: seed storage protein

A:Note: lectin for D-galactosyl-beta-1->3-N-acetylgalactosamine

C:Keywords: heterotetramer; lectin; seed; storage protein

Query Match 37.0%; Score 17; DB 2; Length 6;

Best Local Similarity 75.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 NEES 5

Db 1 NEQS 4

RESULT 2

I37263

Y protein - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Nov-1999

C:Accession: I37263

R:Waechter, G.; Habener, J.F.

Endocrinology 131, 2010-2015, 1992

A:Title: Novel testis germ cell-specific transcript of the CREB gene contains an alternat

A:Reference number: I37263; MUID:93010691; PMID:1396344

A:Accession: I37263

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-6 <RES>

A:Cross-references: EMBL:X68994; NID:G396171; PIDN:CAA48780.1; PID:G579816

C:Genetics:

A:Gene: CREB

Query Match 37.0%; Score 17; DB 2; Length 6;

Best Local Similarity 75.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 1; Gaps 0;

Matches 3; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Oy 5 SLIC 8

Db |||
1 SLFC 4

RESULT 3

JU0355
lipopeptide WS1279 [validated] - Streptomyces willmorei
C;Species: Streptomyces willmorei
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: JU0355
R;Tsuda, Y.; Okada, Y.; Tanaka, M.; Shigematsu, N.; Hori, Y.; Goto, T.; Hashimoto, M.
Chem. Pharm. Bull. 39, 607-611, 1991
A;Title: Structure and synthesis of an immunosensitive lipopeptide, WS1279, of microbial origin
A;Reference number: JU0355; MUID:91300586; PMID:2070441
A;Accession: JU0355
A;Molecule type: protein
A;Residues: 1-6 <TSU>
A;Note: the structure was confirmed by synthesis
A;Keywords: blocked amino end; lipoprotein
F;1/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status experimental
F;1/Modified site: fatty acylated amino end (Cys) #status experimental

Query Match 32.6%; Score 15; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 CN 2
|||
Db 1 CN 2

RESULT 4

B39040
calsequestrin, fast skeletal muscle - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 23-Feb-1997
C;Accession: B39040
R;Cala, S.E.; Jones, L.R.
J. Biol. Chem. 266, 391-398, 1991
A;Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casein
A;Reference number: A39040; MUID:91093153; PMID:1985907
A;Accession: B39040
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <CAL>
C;Keywords: phosphoprotein; skeletal muscle

Query Match 32.6%; Score 15; DB 2; Length 7;

Best Local Similarity 60.0%; Pred. No. 2.8e+05; Mismatches 1; Indels 0; Gaps 0;

QY 2 NEESL 6
: |||
Db 2 DEEDL 6

RESULT 5

S59622
metallothionein isoform a, cadmium-binding - Ariantha arbustorum (terrestrial snail) (fragment)
C;Species: Ariantha arbustorum
C;Date: 19-Mar-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: S59622
R;Berger, B.; Hunziker, P.E.; Hauer, C.R.; Birchler, N.; Dallinger, R.
Biochem. J. 311, 951-957, 1995
A;Title: Mass spectrometry and amino acid sequencing of two cadmium-binding metallothionein
A;Reference number: S59621; MUID:96067616; PMID:7487956
A;Accession: S59622
A;Molecule type: protein
A;Residues: 1-8 <BER>
A;Cross-references: UNIPROT:P55946
C;Superfamily: metallothionein
C;Keywords: chelation; metal binding; metal-thiolate cluster

Query Match 32.6%; Score 15; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 CN 2
|||
Db 1 CN 2

RESULT 6

S19288
acylase - Kluyvera cryocrescens
C;Species: Kluyvera cryocrescens
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S19288
R;Martin, J.; Slade, A.; Aicken, A.; Arche, R.; Virden, R.
Biochem. J. 280, 659-662, 1991
A;Title: Chemical modification of serine at the active site of penicillin acylase from Kluyvera
A;Reference number: S19288; MUID:92109664; PMID:1764029
A;Accession: S19288
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <MAR>
A;Cross-references: UNIPROT:Q7M124

Query Match 32.6%; Score 15; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 CN 2
|||
Db 1 CN 2

RESULT 7

S69165
ferredoxin a2 - Japanese radish (fragment)
C;Species: Kaiware daikon (Japanese radish)
C;Date: 10-Mar-1998 #sequence_revision 10-Mar-1998 #text_change 09-Jul-2004
C;Accession: S69165
R;Obata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shin, M.
Arch. Biochem. Biophys. 316, 797-802, 1995
A;Title: Four ferredoxins from Japanese radish leaves.
A;Reference number: S69164; MUID:95168867; PMID:7864635
A;Accession: S69165
A;Molecule type: protein
A;Residues: 1-8 <OBA>
A;Cross-references: UNIPROT:Q7M1F1
C;Keywords: 2Fe-2S; electron transfer; iron-sulfur protein

Query Match 32.6%; Score 15; DB 2; Length 8;

Best Local Similarity 40.0%; Pred. No. 2.8e+05; Mismatches 2; Indels 0; Gaps 0;

QY 3 EESLI 7
||| : :
Db 4 EEDIV 8

RESULT 8

B31263
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C;Accession: B31263
R;Peterson, D.S.; Walliker, D.; Wellem, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
A;Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase (EC 1.5.1.3) of Plasmodium falciparum confers resistance to pyrimethamine
A;Reference number: A94217; MUID:89057886; PMID:2904149
A;Accession: B31263
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-6 <PET>

C;Keywords: methyltransferase; NADP; oxidoreductase

Query Match 30.4%; Score 14; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NEESL 6
| | | |
Db 2 NWESI 6

RESULT 9
S29881
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 19-Apr-2002
C;Accession: S29881
R;Walderhaug, M.O.; Post, R.L.; Saccomani, G.; Leonard, R.T.; Briskin, D.P.
J. Biol. Chem. 260, 3852-3859, 1985
A;Title: Structural relatedness of three ion-transport adenosine triphosphatases around
A;Reference number: S29881; PMID:85131201; PMID:3156136
A;Accession: S29881
A;Molecule type: protein
A;Residues: 1-6 <WAL>
A;Experimental source: kidney
C;Keywords: ATP; heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein;
F;4/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 30.4%; Score 14; DB 2; Length 6;
Best Local Similarity 20.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEES 5
| | | |
Db 2 CSDKT 6

RESULT 10
XEYDGD
galactose oxidase inhibitor - fungus (Cladobotryum dendroides)
C;Species: Cladobotryum dendroides
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Accession: A01341
R;Avigad, G.; Markus, Z.
Fed. Proc. 31, 447, 1972
A;Reference number: A01341
A;Accession: A01341
A;Molecule type: protein
A;Residues: 1-7 <AVI>
A;Cross-references: UNIPROT:P06294
C;Comment: The mycelia of this imperfect fungus produce the metalloenzyme galactose oxidase, an apoenzyme, may inactivate the enzyme by binding to its prosthetic copper group.
C;Superfamily: galactose oxidase inhibitor
C;Keywords: copper

Query Match 30.4%; Score 14; DB 1; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 NEES 5
| | | |
Db 4 NTES 7

RESULT 11
B47594
aspartate kinase (EC 2.7.2.4) beta chain - Corynebacterium flavum (strain N13) (fragment)
C;Species: Corynebacterium flavum
C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 19-Dec-1997
C;Accession: B47594
R;Pollettie, M.T.; Peoples, O.P.; Agoropoulou, C.; Sinskey, A.J.
J. Bacteriol. 175, 4096-4103, 1993
A;Title: Gene structure and expression of the Corynebacterium flavum N13 ask-asd operon.

A;Reference number: A47594; MUID:93308089; PMID:8100567

A;Accession: B47594
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-8 <FOL>
C;Keywords: phosphotransferase

Query Match 30.4%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 EESLI 7
| | | |
Db 2 BEAVL 6

RESULT 12
A32014
tram protein - Escherichia coli plasmid R100 (fragment)
C;Species: Escherichia coli
C;Date: 22-Jun-1989 #sequence_revision 22-Jun-1989 #text_change 09-Jul-2004
C;Accession: A32014
R;Inamoto, S.; Yoshioka, Y.; Ohtsubo, E.
J. Bacteriol. 170, 2749-2757, 1988
A;Title: Identification and characterization of the products from the traJ and traY genes
A;Reference number: A32014; MUID:88227859; PMID:2836369
A;Accession: A32014
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5 <INA>
A;Cross-references: UNIPROT:P13973
C;Genetics:
A;Genome: plasmid
C;Keywords: DNA binding

Query Match 28.3%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NEE 4
| | | |
Db 2 NDE 4

RESULT 13
A59495
Vesicle associated membrane protein - Mus musculus
C;Species: Mus musculus
C;Date: 04-Apr-2004 #sequence_revision 04-Apr-2004 #text_change 04-Apr-2004
C;Accession: A59495
R;Brahmaraju, M.; Shoen, M.; Laloraya, M.; Kumar, P.
Submitted to the Protein Sequence Database, March 2004
A;Description: Spatio-temporal organization of Vam6P and SNAP on mouse spermatozoa and t

A;Reference number: A59495
A;Accession: A59495
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <KUM>
A;Experimental source: strain Swiss
A;Note: Soluble N-ethylmaleimide-sensitive factor-attachment protein receptor (SNARE) protein trafficking through the formation of complexes between proteins present on vesicle and t

Query Match 28.3%; Score 13; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EESLI 7
| | | |
Db 3 BEWLL 7

RESULT 14
A37521

R-phycoerythrin gamma-E chain - red alga (Gastroclonium coulteri) (fragment)
C;Species: Gastroclonium coulteri
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 09-Jul-2004
C;Accession: A37521; J22565
R;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A;Reference number: A22565; MUID:85182601; PMID:3886644
A;Accession: A37521
A;Molecule type: protein
A;Residues: 1-8 <KLO>
A;Cross-references: UNIPROT:Q7M267

Query Match 28.3%; Score 13; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. NO. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SLIC 8
DB 4 ALAC 7

RESULT 15
H48394
glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C;Accession: H48394
R;Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
II-like sequences.
A;Reference number: A48394; MUID:93250576; PMID:8485470
A;Accession: H48394
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-6 <MAT>
A;Experimental source: milk
A;Note: sequence extracted from NCBI backbone (NCBIP:131518)
C;Keywords: glycoprotein

Query Match 26.1%; Score 12; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. NO. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ESLIC 8
DB 2 ELLGC 6

Search completed: April 1, 2005, 10:56:27
Job time : 40 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 10:42:43 ; Search time 116 Seconds
(without alignments)
35.316 Million cell updates/sec

Title: US-09-761-636A-6

Perfect score: 46

Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 790

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	DB	ID	Description
1	18	39.1	8	2	Q9SAY7	Q9say7 dioscorea t
2	16	34.8	7	2	Q67113	Q67113 influenza a
3	16	34.8	7	2	O42564	O42564 fugu rubrip
4	15	32.6	8	2	Q7M1F1	Q7m1f1 raphanus sa
5	15	32.6	8	2	Q7M124	Q7m124 kluyvera ci
6	14	30.4	7	1	IGAO_DACDE	P06294 dactylium d
7	14	30.4	8	2	Q8IV87	Q8iv87 homo sapien
8	14	30.4	8	2	Q7OY84	Q7oy84 plectranthu
9	13	28.3	5	1	TRM3_ECOLI	P13973 escherichia
10	13	28.3	7	2	O55184	O55184 rattus norv
11	13	28.3	8	1	PLP_BRANA	P81707 brassica na
12	13	28.3	8	1	VAM6_MOUSE	P83853 mus musculu
13	13	28.3	8	2	Q7M267	Q7m267 gastrocioni
14	13	28.3	8	2	O32560	O32560 escherichia
15	12	26.1	7	1	UF03_MOUSE	P38641 mus musculu
16	12	26.1	8	1	UPA1_HUMAN	P30087 homo sapien
17	12	26.1	8	1	VTIN_ALOVR	P83233 aloe vera (
18	12	26.1	8	2	Q15890	Q15890 homo sapien
19	12	26.1	8	2	Q15895	Q15895 homo sapien
20	12	26.1	8	2	Q71UR9	Q71ur9 homo sapien
21	12	26.1	8	2	Q9BYI5	Q9byi5 homo sapien
22	12	26.1	8	2	Q9BF82	Q9bf82 ursus arcto
23	12	26.1	8	2	Q9BF83	Q9bf83 canis famil
24	12	26.1	8	2	Q9BF84	Q9bf84 panthera on
25	12	26.1	8	2	Q9BF85	Q9bf85 leopardus p
26	12	26.1	8	2	Q9BF86	Q9bf86 felis silve
27	12	26.1	8	2	Q9BF87	Q9bf87 tapirus ind
28	12	26.1	8	2	Q9BF88	Q9bf88 equus cabal
29	12	26.1	8	2	Q9BF89	Q9bf89 okapia john
30	12	26.1	8	2	Q9BF90	Q9bf90 tragelaphus
31	12	26.1	8	2	Q9BF91	Q9bf91 hippopotamu

32	12	26.1	8	2	Q9BF92	Q9bf92 tursiops tr
33	12	26.1	8	2	Q9BF93	Q9bf93 megaptera n
34	12	26.1	8	2	Q9BF94	Q9bf94 nycteris th
35	12	26.1	8	2	Q9BF95	Q9bf95 roussettus l
36	12	26.1	8	2	Q9BF96	Q9bf96 pteropus gi
37	12	26.1	8	2	Q9BF97	Q9bf97 artibeus ja
38	12	26.1	8	2	Q9BF98	Q9bf98 callimico g
39	12	26.1	8	2	Q9BF99	Q9bf99 hylobates c
40	12	26.1	8	2	Q9BFA0	Q9bfa0 macaca mula
41	12	26.1	8	2	Q9BFA1	Q9bfa1 ateles fusc
42	12	26.1	8	2	Q9BFA2	Q9bfa2 tarsius ban
43	12	26.1	8	2	Q9BFA3	Q9bfa3 lemur catta
44	12	26.1	8	2	Q9BFA4	Q9bfa4 tupaia mino
45	12	26.1	8	2	Q9BFAS	Q9bfas cynocephalu

ALIGNMENTS

RESULT 1
Q9SAY7 PRELIMINARY; PRT; 8 AA.
AC Q9SAY7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Phosphoglucose isomerase (Fragment).
OS Dioscorea tokoro.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Dioscoreales; Dioscoreaceae;
OC Dioscorea.
OX NCBI_taxid=64475;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20279211; PubMed=10821191; DOI=10.1007/s004380051201;
RA Terauchi R., Kahl G.;
RT "Rapid isolation of promoter sequences by TAIL-PCR: the 5'-flanking
RT regions of Pal and Pgi genes from yams (Dioscorea).";
RL Mol. Gen. Genet. 263:554-560(2000).
DR EMBL; AB016716; BAA32235.1; -.
DR GO; GO:0016853; F:isomerase activity; IEA.
KW Isomerase.
FT NON_TER
SQ SEQUENCE 8 AA; 839 MW; F7B05731B5A1ADD6 CRC64;
Query Match 39.1%; Score 18; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLIC 8
Db 5 TLIC 8
RESULT 2
Q67113 PRELIMINARY; PRT; 7 AA.
AC Q67113;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Influenza virus type A (Udorn/72) hemagglutinin (seg 4) cDNA, 3' end.
(Fragment).
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_taxid=11320;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81001892; PubMed=7407922; DOI=10.1016/0092-8674(80)90486-9;
RA Dhar R., Chanock R.M., Lai C.-J.;
RT "Nonviral oligonucleotides at the 5' terminus of cytoplasmic influenza
RT viral mRNA deduced from cloned complete genomic sequences.";

```
RL Cell 21:495-500(1980).
DR EMBL; M25045; AAA43202.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 834 MW; 605EB0544EA40030 CRC64;

Query Match 34.8%; Score 16; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 CNEESLIC 8
DB 3 CN----IC 6

RESULT 3
ID O42564 PRELIMINARY; PRT; 7 AA.
AC O42564;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Truncated voltage-gated sodium channel alpha subunit (Fragment).
GN Name=Scn8a;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97442476; PubMed=9295353; DOI=10.1074/jbc.272.38.24008;
RA Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
RT two-domain protein in fetal brain and non-neuronal cells.";
RL J. Biol. Chem. 272:24008-24015(1997).
DR EMBL; U97673; AAB80916.1; -.
DR GO; GO:0005216; F:ion channel activity; IEA.
KW Ionic channel.
FT NON_TER 1
SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

Query Match 34.8%; Score 16; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 LIC 8
DB 3 LVC 5

RESULT 4
QY7M1F1 PRELIMINARY; PRT; 8 AA.
AC Q7M1F1;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Ferredoxin a2 (Fragment).
OS Raphanus sativus var. niger (Chinese radish).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Raphanus.
OX NCBI_TaxID=41679;
RN [1]
RP SEQUENCE.
RX MEDLINE=95168867; PubMed=7864635; DOI=10.1006/abbi.1995.1106;
RA Obata S., Nishimura M., Negai K., Sakihama N., Shin M.;
RT "Four ferredoxins from Japanese radish leaves.";
RL Arch. Biochem. Biophys. 316:797-802(1995).
DR PIR; S69165; S69165.
FT NON_TER 1
FT NON_TER 8

RL Cell 21:495-500(1980).
DR EMBL; M25045; AAA43202.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 834 MW; 605EB0544EA40030 CRC64;

Query Match 34.8%; Score 16; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 CNEESLIC 8
DB 3 CN----IC 6

RESULT 3
ID O42564 PRELIMINARY; PRT; 7 AA.
AC O42564;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Truncated voltage-gated sodium channel alpha subunit (Fragment).
GN Name=Scn8a;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97442476; PubMed=9295353; DOI=10.1074/jbc.272.38.24008;
RA Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
RT two-domain protein in fetal brain and non-neuronal cells.";
RL J. Biol. Chem. 272:24008-24015(1997).
DR EMBL; U97673; AAB80916.1; -.
DR GO; GO:0005216; F:ion channel activity; IEA.
KW Ionic channel.
FT NON_TER 1
SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

Query Match 34.8%; Score 16; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 LIC 8
DB 3 LVC 5

RESULT 4
QY7M1F1 PRELIMINARY; PRT; 8 AA.
AC Q7M1F1;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Ferredoxin a2 (Fragment).
OS Raphanus sativus var. niger (Chinese radish).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Raphanus.
OX NCBI_TaxID=41679;
RN [1]
RP SEQUENCE.
RX MEDLINE=95168867; PubMed=7864635; DOI=10.1006/abbi.1995.1106;
RA Obata S., Nishimura M., Negai K., Sakihama N., Shin M.;
RT "Four ferredoxins from Japanese radish leaves.";
RL Arch. Biochem. Biophys. 316:797-802(1995).
DR PIR; S69165; S69165.
FT NON_TER 1
FT NON_TER 8

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RESULT 7
Q81V87 ID Q81V87 PRELIMINARY; PRT; 8 AA.
AC Q81V87;
DT 01-WAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE D10712.2 (Serine palmitoyltransferase, long chain base subunit 2-
DE like (Aminotransferase 2), variant 1) (Fragment).
GN Name=SPTLC2L;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith M.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050320; CAD54807.1; -.
DR GO; GO:0008483; F:transaminase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Aminotransferase; Transferase.
FT NON_TER 1
SQ SEQUENCE 8 AA; 908 MW; 8E533682CEBEB042 CRC64;

Query Match 30.4%; Score 14; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 LIC 8
DB :||
1 VIC 3

RESULT 8
Q70Y84 ID Q70Y84 PRELIMINARY; PRT; 8 AA.
AC Q70Y84;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ribosomal protein (Fragment).
GN Name=rpsl6;
OS Plectranthus buchananii.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Plectranthus.
OX NCBI_TaxID=204181;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;
RA Paton A., Springate D.A., Sudde S., Otiemo D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basilis and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ053379; CAD45500.1; -.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 945 MW; 6EA415A5BEAB5863 CRC64;

Query Match 30.4%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CNEES 5
DB :||
4 CSSRS 8

RESULT 9
TRM3_ECOLI ID TRM3_ECOLI STANDARD; PRT; 5 AA.
AC P13973;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE TraM protein (Fragment).
GN Name=traM;
OS Escherichia coli.
OG Plasmid IncFII R100.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88227859; PubMed=2836369;
RA Inamoto S., Yoshioka Y., Ohtsubo E.;
RT "Identification and characterization of the products from the traJ and
RT tray genes of plasmid R100.";
RL J. Bacteriol. 170:2749-2757(1988).
CC -!- FUNCTION: Transfer gene protein. Is involved in the conjugation
CC process of bacterial cells for the exchange of plasmid DNA.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the traM family.

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DR EMBL; M20941; -. NOT_ANNOTATED_CDS.
DR PIR; A32014; A32014.
KW Conjugation; DNA-binding; Plasmid.
FT NON_TER 1
SQ SEQUENCE 5 AA; 634 MW; 6B1B1AA443500000 CRC64;

Query Match 28.3%; Score 13; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NEE 4
DB :||
2 NDE 4

RESULT 10
O55184 ID O55184 PRELIMINARY; PRT; 7 AA.
AC O55184;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Orphan receptor TR4-NS (Fragment).
GN Name=TR4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley;
RX MEDLINE=96198747; PubMed=8612486; DOI=10.1210/en.137.5.1562;
RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
RA Detera-Wadleigh S.D.;
RT "Splice variants of rat TR4 orphan receptor: differential expression
RT of novel sequences in the 5'-untranslated region and C-terminal
RT domain.";
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RL Endocrinology 137:1562-1571 (1996).
RP [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=96299786; PubMed=8661150; DOI=10.1006/geno.1996.0368;
RA Yoshikawa T., DuPont B.R., Leach R.J., Deters-Wadleigh S.D.;
RT "New variants of the human and rat nuclear hormone receptor, TR4:
RT expression and chromosomal localization of the human gene.";
RL Genomics 35:361-366 (1996).
DR EMBL; U59454; AAB91433.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 7 AA; 663 MW; 6DDAA8787EB05350 CRC64;

Query Match 28.3%; Score 13; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 IC 8
Db 2 IC 3

RESULT 11
PLP_BRANA STANDARD; PRT; 8 AA.
ID FLP_BRANA
AC F81707;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Plastidial lipid-associated protein (Fragment).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Topaz; TISSUE=Tapetum;
RX MEDLINE=99349136; PubMed=10420651;
RA Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,
RA Murphy D.J.;
RT "Composition and role of tapetal lipid bodies in the biogenesis of the
RT pollen coat of Brassica napus.";
RL Planta 208:588-598 (1999).
CC -!- FUNCTION: May play a structural role in the elaioplast, a tapetum-
CC specific plastidial lipid organelle.
CC -!- TISSUE SPECIFICITY: Tapetum of anthers.
KW Direct protein sequencing.
FT NON_TER 8
SQ SEQUENCE 8 AA; 989 MW; 9D7B1AA452CAA042 CRC64;

Query Match 28.3%; Score 13; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NEE 4
Db 5 NDE 7

RESULT 12
VAM6_MOUSE STANDARD; PRT; 8 AA.
ID VAM6_MOUSE
AC P83853;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Vam6-like protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Sperm;
RA Bramaraju M., Shueb M., Laloraya M., Kumar G.P.;
RT "Spatio-temporal organization of Vam6P and SNAP on mouse spermatozoa
RT and their involvement in sperm-zona pellucida interactions.";
RL Submitted (MAR-2004) to Swiss-Prot.
CC -!- FUNCTION: May play a role in clustering and fusion of late
CC endosomes and lysosomes (By similarity).
CC -!- SUBUNIT: Homooligomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and associated with the
CC membranes of lysosomes and late endosomes (By similarity).
KW Direct protein sequencing; Protein transport; Transport.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1075 MW; 2CD727337B1B037B CRC64;

Query Match 28.3%; Score 13; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RESLI 7
Db 3 BEWLL 7

RESULT 13
Q7M267 PRELIMINARY; PRT; 8 AA.
ID Q7M267
AC Q7M267;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE R-phycoerythrin gamma-E chain (Fragment).
OS Gastroclonium coulteri (Red alga).
OC Eukaryota; Rhodophyta; Florideophyceae; Rhodomeniales; Champiaceae;
OC Gastroclonium.
OX NCBI_TaxID=2773;
RN [1]
RP SEQUENCE.
RX MEDLINE=85182601; PubMed=3886644;
RA Klotz A.V., Glazer A.N.;
RT "Characterization of the bilin attachment sites in R-phycoerythrin.";
RL J. Biol. Chem. 260:4856-4863 (1985).
DR PIR; A37521; A37521.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 880 MW; 180EBDD72DD9D5B7 CRC64;

Query Match 28.3%; Score 13; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SLIC 8
Db 4 ALAC 7

RESULT 14
O32560 PRELIMINARY; PRT; 8 AA.
ID O32560
AC O32560;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Propionate kinase (Fragment).
GN Name:tdcD;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=W3110;
RX MEDLINE=99449059; PubMed=10520749;
RA Hessler C., Sawers G.;
RT "The tdcE gene in Escherichia coli W3110 is separated from the rest of
RL DNA Seq. 9:183-188(1998).
DR EMBL; AJ001620; CAA04875.1; -.
KW Kinase.
FT GO: GO:0016301; F:kinase activity; IEA.
SQ SEQUENCE 8 AA; 1000 MW; 3A505EB044140DC4 CRC64;

Query Match      28.3%; Score 13; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 IC 8
Db 5 IC 6

RESULT 15
UF03 MOUSE
ID UF03 MOUSE STANDARD; PRT; 7 AA.
AC P38641.
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of fibroblasts (P36) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins using
RL preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.1, its MW is: 36 kDa.
KW Direct protein sequencing.
FT NON_TER 7
SQ SEQUENCE 7 AA; 842 MW; 6AA72B1DB1B1180 CRC64;

Query Match      26.1%; Score 12; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NEES 5
Db 1 HEAA 4

Search completed: April 1, 2005, 10:55:37
Job time : 116 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 10:41:48 ; Search time 117 Seconds
(without alignments)
26.445 Million cell updates/sec

Title: US-09-761-636A-6

Perfect score: 46

Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 160390

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A: Geneseq 16DEC04: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	8	AAU04525	Aau04525 VEGF base
2	43	93.5	8	AAU04539	Aau04539 VEGF base
3	42	91.3	8	AAU04541	Aau04541 VEGF base
4	41	89.1	8	AAU04538	Aau04538 VEGF base
5	39	84.8	8	AAU04540	Aau04540 VEGF base
6	30	65.2	8	AAR24954	Aar24954 Conformal
7	30	65.2	8	AAY54526	Aay54526 Human CD4
8	26	56.5	8	AAR73351	Aar73351 Human TSH
9	26	56.5	8	AAR73350	Aar73350 Human TSH
10	26	56.5	8	AAY57040	Aay57040 Feline im
11	26	56.5	8	AAU08451	Aau08451 Peptide A
12	25	54.3	8	AAR80365	Aar80365 Protein p
13	25	54.3	8	AAW49750	Aaw49750 Glutamine
14	25	54.3	8	AAW48644	Aaw48644 Membrane
15	25	54.3	8	ABG35021	Abg35021 Endostati
16	24	52.2	8	AAU08460	Aau08460 Peptide C
17	24	52.2	8	ADO49161	Ado49161 Human car
18	23	50.0	7	AAW25915	Aaw25915 Beta-2-ni
19	23	50.0	8	AAR73349	Aar73349 Human TSH
20	23	50.0	8	AAR73348	Aar73348 Human TSH
21	23	50.0	8	AAW12848	Aaw12848 RGD-bind
22	23	50.0	8	AAW48852	Aaw48852 Membrane
23	23	50.0	8	AAW48662	Aaw48662 Membrane
24	23	50.0	8	AAW48640	Aaw48640 Membrane
25	23	50.0	8	AAW06526	Aaw06526 Claudin-2

26	23	50.0	8	AAU04525	AAU04525 standard; peptide; 8 AA.
27	23	50.0	8	AAU04525	AAU04525
28	23	50.0	8	AAU04525	AAU04525
29	23	50.0	8	AAU04525	AAU04525
30	23	50.0	8	AAU04525	AAU04525
31	23	50.0	8	AAU04525	AAU04525
32	23	50.0	8	AAU04525	AAU04525
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34	23	50.0	8	AAU04525	AAU04525
35	23	50.0	8	AAU04525	AAU04525
36	23	50.0	8	AAU04525	AAU04525
37	23	50.0	8	AAU04525	AAU04525
38	22	47.8	6	AAU04525	AAU04525
39	22	47.8	6	AAU04525	AAU04525
40	22	47.8	7	AAU04525	AAU04525
41	22	47.8	7	AAU04525	AAU04525
42	22	47.8	8	AAU04525	AAU04525
43	22	47.8	8	AAU04525	AAU04525
44	22	47.8	8	AAU04525	AAU04525
45	22	47.8	8	AAU04525	AAU04525

ALIGNMENTS

RESULT 1
AAU04525
ID AAU04525 standard; peptide; 8 AA.
XX
AC AAU04525;
XX
DT 26-SEP-2001 (first entry)
XX
DE VEGF based monocyclic peptide 2.
XX
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..8 /note= "This bond cyclises the peptide"
XX
PN WO200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX
(LUDW-) LUDWIG INST CANCER RES.
XX
PI Achen MG, Hughes RA, Stacker S, Cendron A;
XX
WPI; 2001-442248/47.
XX
PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.
XX
PS Claim 49; Page 32; 102pp; English.
XX
CC The sequence represents a monomeric monocyclic peptide of the invention,
CC whose 3-dimensional structure is modelled on the expose loop of human
CC VEGF (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a

26	23	50.0	8	AAU04525	AAU04525
27	23	50.0	8	AAU04525	AAU04525
28	23	50.0	8	AAU04525	AAU04525
29	23	50.0	8	AAU04525	AAU04525
30	23	50.0	8	AAU04525	AAU04525
31	23	50.0	8	AAU04525	AAU04525
32	23	50.0	8	AAU04525	AAU04525
33	23	50.0	8	AAU04525	AAU04525
34	23	50.0	8	AAU04525	AAU04525
35	23	50.0	8	AAU04525	AAU04525
36	23	50.0	8	AAU04525	AAU04525
37	23	50.0	8	AAU04525	AAU04525
38	22	47.8	6	AAU04525	AAU04525
39	22	47.8	6	AAU04525	AAU04525
40	22	47.8	7	AAU04525	AAU04525
41	22	47.8	7	AAU04525	AAU04525
42	22	47.8	8	AAU04525	AAU04525
43	22	47.8	8	AAU04525	AAU04525
44	22	47.8	8	AAU04525	AAU04525
45	22	47.8	8	AAU04525	AAU04525

26	23	50.0	8	AAU04525	AAU04525
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28	23	50.0	8	AAU04525	AAU04525
29	23	50.0	8	AAU04525	AAU04525
30	23	50.0	8	AAU04525	AAU04525
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35	23	50.0	8	AAU04525	AAU04525
36	23	50.0	8	AAU04525	AAU04525
37	23	50.0	8	AAU04525	AAU04525
38	22	47.8	6	AAU04525	AAU04525
39	22	47.8	6	AAU04525	AAU04525
40	22	47.8	7	AAU04525	AAU04525
41	22	47.8	7	AAU04525	AAU04525
42	22	47.8	8	AAU04525	AAU04525
43	22	47.8	8	AAU04525	AAU04525
44	22	47.8	8	AAU04525	AAU04525
45	22	47.8	8	AAU04525	AAU04525

26	23	50.0	8	AAU04525	AAU04525
27	23	50.0	8	AAU04525	AAU04525
28	23	50.0	8	AAU04525	AAU04525
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30	23	50.0	8	AAU04525	AAU04525
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32	23	50.0	8	AAU04525	AAU04525
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35	23	50.0	8	AAU04525	AAU04525
36	23	50.0	8	AAU04525	AAU04525
37	23	50.0	8	AAU04525	AAU04525
38	22	47.8	6	AAU04525	AAU04525
39	22	47.8	6	AAU04525	AAU04525
40	22	47.8	7	AAU04525	AAU04525
41	22	47.8	7	AAU04525	AAU04525
42	22	47.8	8	AAU04525	AAU04525
43	22	47.8	8	AAU04525	AAU04525
44	22	47.8	8	AAU04525	AAU04525
45	22	47.8	8	AAU04525	AAU04525

26	23	50.0	8	AAU04525	AAU04525
27	23	50.0	8	AAU04525	AAU04525
28	23	50.0	8	AAU04525	AAU04525
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36	23	50.0	8	AAU04525	AAU04525
37	23	50.0	8	AAU04525	AAU04525
38	22	47.8	6	AAU04525	AAU04525
39	22	47.8	6	AAU04525	AAU04525
40	22	47.8	7	AAU04525	AAU04525
41	22	47.8	7	AAU04525	AAU04525
42	22	47.8	8	AAU04525	AAU04525
43	22	47.8	8	AAU04525	AAU04525
44	22	47.8	8	AAU04525	AAU04525
45	22	47.8	8	AAU04525	AAU04525

26	23	50.0	8	AAU04525	AAU04525
27	23	50.0	8	AAU04525	AAU04525
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30	23	50.0	8	AAU04525	AAU04525
31	23	50.0	8	AAU04525	AAU04525
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33	23	50.0	8	AAU04525	AAU04525
34	23	50.0	8	AAU04525	AAU04525
35	23	50.0	8	AAU04525	AAU04525
36	23	50.0	8	AAU04525	AAU04525
37	23	50.0	8	AAU04525	AAU04525
38	22	47.8	6	AAU04525	AAU04525
39	22	47.8	6	AAU04525	AAU04525
40	22	47.8	7	AAU04525	AAU04525
41	22	47.8	7	AAU04525	AAU04525
42	22	47.8	8	AAU04525	AAU04525
43	22	47.8	8	AAU04525	AAU04525
44	22	47.8	8	AAU04525	AAU04525
45	22	47.8	8	AAU04525	AAU04525

26	23	50.0	8	AAU04525	AAU04525
27	23	50.0	8	AAU04525	AAU04525
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33	23	50.0	8	AAU04525	AAU04525
34	23	50.0	8	AAU04525	AAU04525
35	23	50.0	8	AAU04525	AAU04525
36	23	50.0	8	AAU04525	AAU04525
37	23	50.0	8	AAU04525	AAU04525
38	22	47.8	6	AAU04525	AAU04525
39	22	47.8	6	AAU04525	AAU04525
40	22	47.8	7	AAU04525	AAU04525
41	22	47.8	7	AAU04525	AAU04525
42	22	47.8	8	AAU04525	AAU04525
43	22	47.8	8	AAU04525	AAU04525
44	22	47.8	8	AAU04525	AAU04525
45	22	47.8	8	AAU04525	AAU04525

Aab17353	Integrin- Aae08176	Peptide #
Aae08176	Peptide #	
Aag03955	Human pro-	
Abg34987	Human pro-	
Abg34987	Human pro-	
Aau81097	Integrin- Aab72952	Integrin
Aab72952	Integrin	
Adj73106	Integrin	
Adj52741	CH1 delet	
Adj51702	CH1 delet	
Adl95915	Antibody-	
Adl95907	Antibody-	
Adl95907	Antibody-	
Aay64349	Partial p	
Aay64349	Cadherin-	
Aay64350	Cadherin-	
Adl71410	Phase-disl	
Aay70546	Peptide 1	
Aay70546	Membrane	
Aay44874	Membrane	
Aay44874	Membrane	
Aay48637	Membrane	
Aay48637	Membrane	
Aay48637	Membrane	

CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 46; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
 Db |||||
 1 CNEESLIC 8

RESULT 2
 AAU04539
 ID AAU04539 standard; peptide; 8 AA.
 XX
 AC AAU04539;
 XX
 DT 26-SEP-2001 (first entry)
 DE
 DE VEGF based monocyclic peptide 17.
 XX

Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 OS
 XX Synthetic.

Key Location/Qualifiers
 FH Disulfide-bond 1..8
 FT /note= "This bond cyclises the peptide"
 XX

PN WO200152875-A1.
 XX
 PD 26-JUL-2001.

PF 18-JAN-2001; 2001WO-US001533.
 XX
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.

PI Achen MG, Hughes RA, Stacker S, Cendron A;
 XX
 DR WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclising a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine

PT residues.

PS Example 25; Page 47; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the exposed loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 8 AA;

Query Match 93.5%; Score 43; DB 4; Length 8;
 Best Local Similarity 87.5%; Pred. No. 1.8e+06;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
 Db |||||
 1 CNEETLIC 8

RESULT 3
 AAU04541
 ID AAU04541 standard; peptide; 8 AA.
 XX
 AC AAU04541;

XX
 DT 26-SEP-2001 (first entry)
 XX
 DE VEGF based monocyclic peptide 19.
 XX

Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.

Key Location/Qualifiers
 FH Disulfide-bond 1..8
 FT /note= "This bond cyclises the peptide"
 XX

PN WO200152875-A1.
 XX
 PD 26-JUL-2001.

PF 18-JAN-2001; 2001WO-US001533.
 XX
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.

XX

(LUDW-) LUDWIG INST CANCER RES.
 Achen MG, Hughes RA, Stacker S, Cendron A;
 WPI; 2001-442248/47.
 Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.
 Example 25; Page 47; 102pp; English.
 The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the exposed loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain). The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy
 Sequence 8 AA;
 Query Match 91.3%; Score 42; DB 4; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CNEESLIC 8
 |||||:
 Db 1 CNEESVVC 8
 RESULT 4
 AAU04538
 ID AAU04538 standard; peptide; 8 AA.
 XX
 AC AAU04538;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE VEGF based monocyclic peptide 16.
 XX
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key
 FT Disulfide-bond 1..8
 FT Disulfide-bond 1..8 /note= "This bond cyclises the peptide"
 XX

PN W0200152875-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 18-JAN-2001; 2001WO-US001533.
 XX
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Achen MG, Hughes RA, Stacker S, Cendron A;
 XX
 WPI; 2001-442248/47.
 XX
 Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.
 Example 25; Page 47; 102pp; English.
 The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the exposed loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain). The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy
 Sequence 8 AA;
 Query Match 89.1%; Score 41; DB 4; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CNEESLIC 8
 |||||:
 Db 1 CNEESLIC 8
 RESULT 5
 AAU04540
 ID AAU04540 standard; peptide; 8 AA.
 XX
 AC AAU04540;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE VEGF based monocyclic peptide 18.
 XX
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour;

KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.

OS Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 1..8 /note= "This bond cyclises the peptide"

FT WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2003; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

PR 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Hughes RA, Stacker S, Cendron A;

PI WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.

XX Example 25; Page 47; 102pp; English.

CC The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the exposed loop of human
 CC VEGF (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis.

CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy

XX Sequence 8 AA;

Query Match 84.8%; Score 39; DB 4; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEESLIC 8

DB 1 CNEESLIC 8

RESULT 6

AAR24954

ID AAR24954 standard; protein; 8 AA.

XX AAR24954;
 XX 25-MAR-2003 (revised)
 DT 04-DEC-1992 (first entry)
 XX Conformationally constrained HIV inhibitory peptide.
 DE Human immunodeficiency virus; AIDS; envelope glycoproteins; CD4;
 KW cell surface protein; infection.
 XX Synthetic.
 OS Key Location/Qualifiers
 PH Disulfide-bond 1..8
 FT Region 1..2
 FT /note= "conformationally constraining gp."
 FT Peptide 3..6
 FT /note= "beta-turn or beta-turn mimic tetrapeptide"
 FT Region 7..8
 FT /note= "conformationally constraining gp."
 XX WO9209625-A1.
 XX 11-JUN-1992.
 XX 27-NOV-1991; 91WO-US008873.
 XX 29-NOV-1990; 90US-00619782.
 XX (SMIK) SMITHLINE BEECHAM CORP.
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX Bhatnagar PK, Jarlais RLD, Dixon JS, Hendrickson WA, Kopple KD;
 PI Kwong P, Peishoff CE, Ryu SE, Truneh A, Sweet RW;
 XX WPI; 1992-217018/26.
 XX Conformationally constrained peptides used for inhibiting HIV - by
 PT mimicking the stereochemical regions of the CD4 receptor protein.
 XX Example; Page 24; 37pp; English.
 CC The peptide is conformationally constrained by groups attached to each
 CC side. The peptide mimics a beta turn and can bind to at least one HIV
 CC envelope protein, thus inhibiting infection. It inhibits the interaction
 CC between HIV envelope glycoproteins and human cell-surface protein CD4 by
 CC mimicking structures of CD4. See also AAR24950-R24959 and AAR25122.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 8 AA;
 SQ Query Match 65.2%; Score 30; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CNEESLIC 8
 DB 1 CNOGSFLC 8
 RESULT 7
 AAY54526
 ID AAY54526 standard; peptide; 8 AA.
 XX AAY54526;
 AC AAY54526;
 XX 25-APR-2000 (first entry)
 DT Human CD4 protein target antigenic peptide p1615.
 DE Human; CD4 protein; antigenic peptide; CDR2-like domain; apoptosis;
 KW syncytia formation; human immune deficiency virus; HIV binding;

CD4-Class II interaction; immunisation; CD4 surface complex; immune response; transplant rejection; autoimmune disease; cyclic; rheumatoid arthritis; systemic lupus erythematosus; psoriasis.

Synthetic.
Homo sapiens.

Key Location/Qualifiers
Disulfide-bond 1...8 /note= "this peptide is conformationally restricted by cyclisation"

W09967294-A1.
29-DEC-1999.
21-JUN-1999; 99WO-US014030.
20-JUN-1998; 98US-00100409.
(UNBI-) UNITED BIOMEDICAL INC.
Wang CY;
WPI; 2000-160579/14.
New antigenic peptide from the CDR2 domain of CD4, for immunization against e.g. human immune deficiency virus.
Disclosure; Page 63; 106pp; English.

The present sequence represents a target antigenic peptide derived from the CDR2-like domain of the human CD4 protein. The peptide is cyclised by the addition of cysteine residues at either end. The specification describes antigenic peptides derived from the CDR2-like domain of CD4 (amino acids 27-66 of AAV54500). These antigenic peptides present neutralising receptor/co-receptor effector sites of the CDR2-like domain. The peptides evoke effective antibody responses by having optimised site-specificity. The induced antibodies block human immune deficiency virus (HIV) binding and syncytia formation. They may also block CD4-Class II interactions with other cells, deliver signals to T cells (inhibiting normal CD4+-mediated immunoregulatory functions) or induce apoptosis of CD4 cells by simultaneous engagement of T cell receptors. Conjugates and peptides containing the antigenic peptides are used for active immunisation to generate antibodies against CD4 surface complexes, especially to prevent binding of HIV to CD4 and thus HIV infection, but also to treat undesirable immune responses such as transplant rejection, or autoimmune diseases (rheumatoid arthritis, systemic lupus erythematosus or psoriasis). These conjugates produce high-titre antibodies which are broadly neutralising against primary isolates from all classes of HIV-1 and of HIV-2. The peptides may include a promiscuous T helper epitope that is active in genetically diverse subjects

Query Match 65.2%; Score 30; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
||:|:|
DB 1 CNOGSFLC 8

RESULT 8
AAR73351
ID AAR73351 standard; peptide; 8 AA.
XX
AC AAR73351;
XX
DT 12-DEC-1995 (first entry)
XX
DE Human TSH receptor (residues 301-308).

XX thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody;
KW affinity; detection.
XX
OS Synthetic.
XX
PN JP07089991-A.
XX
PD 04-APR-1995.
XX
PF 28-SEP-1993; 93JP-00240853.
XX
PR 28-SEP-1993; 93JP-00240853.
XX
PA (MTP) MITSUBISHI PETROCHEMICAL CO LTD.
XX
DR WPI; 1995-167251/22.
XX
PT Novel polypeptide(s) having affinity for the human TSH receptor antibody
PT - used in detection of the TSH antibody.
XX
PS Example 1; Page 25; 54pp; Japanese.
XX
CC Peptides with affinity to human TSH (thyroid stimulating hormone)
CC receptor antibody are used for detection of the antibody. (See also
CC AAR73201-592)
XX
SQ Sequence 8 AA;

Query Match 56.5%; Score 26; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEESL 6
||:|:
DB 1 CNESSM 6

RESULT 9
AAR73350
ID AAR73350 standard; peptide; 8 AA.
XX
AC AAR73350;
XX
DT 12-DEC-1995 (first entry)
XX
DE Human TSH receptor (residues 291-298).
XX
KW thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody;
KW affinity; detection.
XX
OS Synthetic.
XX
PN JP07089991-A.
XX
PD 04-APR-1995.
XX
PF 28-SEP-1993; 93JP-00240853.
XX
PR 28-SEP-1993; 93JP-00240853.
XX
PA (MTP) MITSUBISHI PETROCHEMICAL CO LTD.
XX
DR WPI; 1995-167251/22.
XX
PT Novel polypeptide(s) having affinity for the human TSH receptor antibody
PT - used in detection of the TSH antibody.
XX
PS Example 1; Page 25; 54pp; Japanese.
XX
CC Peptides with affinity to human TSH (thyroid stimulating hormone)
CC receptor antibody are used for detection of the antibody. (See also
CC AAR73201-592)
XX

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XX SQ Sequence 8 AA;
Query Match      56.5%; Score 26; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CNEESL 6
Db 3 CNESSM 8

RESULT 10
AAU08451
ID AAY57040 standard; peptide; 8 AA.
XX AC AAY57040;
XX DT 21-FEB-2000 (first entry)
XX DE Feline immunodeficiency virus immunogenic fragment.
XX KW Feline immunodeficiency virus; FIV; infection; diagnosis; gp130; p55;
XX KW immunogenic fragment; antibody; env precursor; gag precursor; cat;
XX KW antibody binding composition.
XX OS Feline immunodeficiency virus.
XX PI Alitalo K, Jeltsch MM;
XX PN EP962774-A1.
XX PD 08-DEC-1999.
XX PF 14-MAY-1999; 99EP-00303760.
XX PR 15-MAY-1998; 98US-0085615P.
XX PR 03-JUN-1998; 98US-00089878.
XX PA (IDEX-) IDEX LAB INC.
XX PI Groat RG, Mermer B, O'Connor TP;
XX WPI; 2000-025671/03.
XX PT Diagnosing Feline Immunodeficiency Virus infection.
XX PS Disclosure; Page 4; 15pp; English.
XX CC This sequence is an immunogenic fragment of feline immunodeficiency virus
CC (FIV) glycoprotein 130. Peptides AAY57038-Y57039 (also fragments of
CC gp130) are used in the invention as capture polypeptides when diagnosing
CC FIV infection. The invention relates to an antibody binding composition
CC which consists of an enhanced capture polypeptide, which contains an
CC immunogenic fragment of FIV gag precursor p55, and a second fragment
CC which is part of the env precursor gp130, and an antibody-binding
CC detection composition. The invention also includes a device for
CC performing an assay which determines whether a feline is infected with
CC FIV. The novel method is used for the diagnosis of Feline
CC Immunodeficiency Virus infection

XX SQ Sequence 8 AA;
Query Match      56.5%; Score 26; DB 3; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 1 CNEESLIC 8
Db 1 CNQNOFFC 8

RESULT 11
AAU08451
ID AAU08451 standard; peptide; 8 AA.

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XX AAU08451;
XX AC 21-NOV-2001 (first entry)
XX DT Peptide A6 encoded by human VEGF-A forward primer A6-F.
XX DE Human; vascular endothelial growth factor; VEGF-A; vasculogenesis;
XX KW angiogenesis; blood vessel; cancer; proliferative retinopathy; psoriasis;
XX KW age-related macular degeneration; rheumatoid arthritis; cardiovascular;
XX KW primer; mutant; mutein.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200162942-A2.
XX PD 30-AUG-2001.
XX PF 26-FEB-2001; 2001WO-US006113.
XX PR 25-FEB-2000; 2000US-0185205P.
XX PR 18-MAY-2000; 2000US-0205331P.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PA (LICN) LICENTIA OY.
XX PI Alitalo K, Jeltsch MM;
XX WPI; 2001-536640/59.
XX DR N-PSDB; AAS12807.
XX PT Polypeptides that bind cellular receptors for vascular endothelial growth
XX PS factors, polynucleotides encoding them.
XX CC Claim 9; Fig 7C; 261pp; English.
XX CC The present invention relates to polypeptides that bind cellular
XX CC receptors for vascular endothelial growth factors (VEGFs), the
XX CC polynucleotides encoding them, and their use for identifying agents that
XX CC modulate interactions between VEGFs and their receptors, VEGFs and their
XX CC receptors play an important role in vasculogenesis, the development of
XX CC the embryonic vasculature from early differentiating endothelial cells
XX CC and angiogenesis, the process of forming new blood vessels from pre-
XX CC existing ones. Modulators of interactions between VEGF and its receptors
XX CC may be used to treat dysfunction of the endothelial cell regulatory
XX CC system. Such disorders include cancers, abnormal angiogenesis, rheumatoid
XX CC proliferative retinopathies, age-related macular degeneration, rheumatoid
XX CC arthritis and psoriasis. The polypeptides of the invention exhibit unique
XX CC receptor binding profiles compared to known naturally occurring VEGFs.
XX CC AAU08446-AAU08454 represent the peptides A1-A9 which are encoded by human
XX CC VEGF-A forward primers used in the methods of the present invention
XX SQ Sequence 8 AA;
Query Match      56.5%; Score 26; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CNEESL 6
Db 3 CNDEGL 8

RESULT 12
AAR80365
ID AAR80365 standard; peptide; 8 AA.
XX AC AAR80365;
XX DT 19-APR-1996 (first entry)
XX DE Protein polymeric adhesion substrate glutamine donor peptide #15.

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XX KW Pendant group; repeating unit; enzyme recognition site; sealant; fibrin;
XX KW enzymatic cross-linking; biocompatible material; structural integrity;
XX KW medical adhesive; wound closure; tissue repair; transglutaminase;
XX KW protein polymer adhesive substrate.
XX OS Synthetic.
XX FN WO9523611-A1.
XX PD 08-SEP-1995.
XX PF 03-MAR-1995; 95WO-US002728.
XX PR 03-MAR-1994; 94US-00205518.
XX PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
XX PI Cappello J;
XX DR WPI; 1995-320413/41.
XX PT Protein polymers comprising repeating units and sequences - capable of
XX PT enzyme-catalysed covalent bond formation useful as a biocompatible
XX PT material for wound closure and tissue repair.
XX PS Example 9; Page 75; 138pp; English.
XX CC The peptides AAR0351-70 are examples of glutamine donor peptides which
XX CC can be used to generate protein polymeric adhesion substrate (PPAS)
XX CC contg. repeats of non-fibrin cross-linking donor peptide sequences (see
XX CC AAR0345-50 for examples of PPAS proteins). The PPAS proteins can be used
XX CC as substrates in enzymatic cross-linking reactions catalysed by a
XX CC transglutaminase enzyme e.g. Factor VIII or XIII. The polymers can be
XX CC used in biological systems where in situ formation of a biocompatible
XX CC material with structural integrity is required e.g. as medical adhesives
XX CC and sealants or for wound closure or tissue repair.
XX SQ Sequence 8 AA;

Query Match 54.3%; Score 25; DB 2; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.8e+06;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db | : : ||
1 CGQSKVIC 8

RESULT 13
AAW49750
ID AAW49750 standard; peptide; 8 AA.
XX AC AAW49750;
XX DT 25-MAR-2003 (revised)
XX DT 12-OCT-1998 (first entry)
XX DE Glutamine donor peptide.
XX KW Protein polymer; adhesive sealant; wound healing; cross-linking.
XX OS Synthetic.
XX PN US5773577-A.
XX PD 30-JUN-1998.
XX PF 02-MAR-1995; 95US-00397633.
XX PR 03-MAR-1994; 94US-00205518.
XX PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

Query Match 54.3%; Score 25; DB 2; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.8e+06;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db | : : ||
1 CGQSKVIC 8

RESULT 14
AAW48644
ID AAW48644 standard; peptide; 8 AA.
XX AC AAW48644;
XX DT 20-MAR-2003 (revised)
XX DT 10-DEC-1999 (first entry)
XX DE Membrane dipeptidase-binding lung homing peptide #15.
XX KW Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
XX KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
XX KW membrane dipeptidase.
XX OS Synthetic.
XX OS Homo sapiens.
XX FN WO9946284-A2.
XX PD 16-SEP-1999.
XX PF 10-MAR-1999; 99WO-US005284.
XX PR 13-MAR-1998; 98US-00042107.
XX PR 26-FEB-1999; 99US-00258754.
XX PA (BURN-) BURNHAM INST.
XX PI Rajotte D, Pasqualini R, Ruoslahti EI;
XX DR WPI; 1999-571717/48.
XX PT New peptides which selectively home to organs or tissues, used for, e.g.
XX PT identifying target ligands and for therapy of pathological conditions.
XX PS Example 6; Page 144; 193pp; English.
XX PA

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XX PI Cappello J;
XX DR WPI; 1998-387091/33.
XX PT New recombinant protein polymers - containing naturally occurring
XX PT repetitive units for crosslinking by enzymes, useful as medical adhesives
XX PT and sealants, depots and matrices.
XX PS Example 9; Col 49; 70pp; English.
XX CC This is an example of a glutamine donor peptide that can be utilised in
XX CC novel recombinant protein polymers of the invention. Such polymers (see
XX CC AAW49710-28) typically comprise a repetitive amino acid backbone of
XX CC repetitive units having a collagen, fibroin, elastin or keratin motif and
XX CC at least 2 enzyme recognition sequences comprising a glutamine and/or
XX CC lysine capable of enzyme catalysed isopeptide formation. The polymers are
XX CC capable of covalent crosslinking by enzymatic reaction to form products
XX CC which set quickly and have good adhesive properties and high strength.
XX CC They can be used as medical adhesives and sealants, in the closure of
XX CC wounds and repair of damaged tissues, prosthesis coatings, drug depots,
XX CC and matrices for the transplantation of cells. (Updated on 25-MAR-2003 to
XX CC correct PF field.)
XX SQ Sequence 8 AA;

Query Match 54.3%; Score 25; DB 2; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.8e+06;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db | : : ||
1 CGQSKVIC 8

RESULT 14
AAW48644
ID AAW48644 standard; peptide; 8 AA.
XX AC AAW48644;
XX DT 20-MAR-2003 (revised)
XX DT 10-DEC-1999 (first entry)
XX DE Membrane dipeptidase-binding lung homing peptide #15.
XX KW Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
XX KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
XX KW membrane dipeptidase.
XX OS Synthetic.
XX OS Homo sapiens.
XX FN WO9946284-A2.
XX PD 16-SEP-1999.
XX PF 10-MAR-1999; 99WO-US005284.
XX PR 13-MAR-1998; 98US-00042107.
XX PR 26-FEB-1999; 99US-00258754.
XX PA (BURN-) BURNHAM INST.
XX PI Rajotte D, Pasqualini R, Ruoslahti EI;
XX DR WPI; 1999-571717/48.
XX PT New peptides which selectively home to organs or tissues, used for, e.g.
XX PT identifying target ligands and for therapy of pathological conditions.
XX PS Example 6; Page 144; 193pp; English.
XX PA

```

CC The present invention describes peptides that selectively home to a
 CC tissue or organ. The peptides can be used for identifying an organ or
 CC tissue, for identifying a target molecule expressed by an organ or tissue
 CC or for treating an organ or tissue pathology, where the organ or tissue
 CC is selected from prostate, lung, skin, retina, pancreas, gut, ovary,
 CC adrenal gland, liver, and lymph node. The peptide bind to the membrane
 CC dipeptidase (MDP). AAY48618 to AAY49066 represent sequences which are
 CC used in the exemplification of the present invention. (Updated on 20-MAR-
 CC 2003 to correct PR field.)

XX Sequence 8 AA;
 SQ Query Match 54.3%; Score 25; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CNEESLIC 8
 | : | : |
 Db 1 CGNETLRC 8

RESULT 15

ABG35021

ID ABG35021 standard; peptide; 8 AA.

XX AC ABG35021;

XX DT 15-JUL-2002 (first entry)

XX DE Endostatin targeting peptide #20.

XX KW Targeting peptide; cancer; Hodgkin's disease; cytostatic;
 KW immunosuppressive; anti-inflammatory; antiarthritic; antiviral;
 KW antiatherosclerotic; antidiabetic; antibacterial; diabetes mellitus;
 KW inflammatory disease; arthritis; atherosclerosis; cancer;
 KW autoimmune disease; bacterial infection; viral infection.

XX OS Unidentified.

XX FN WO200220722-A2.

XX PD 14-MAR-2002.

XX PF 07-SEP-2001; 2001WO-US027702.

XX PR 08-SEP-2000; 2000US-0231266P.

XX PR 17-JAN-2001; 2001US-00765101.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Arap W, Pasqualini R;

XX DR WPI; 2002-383050/41.

XX PT Identifying targeting peptides useful for treating e.g. diabetes
 PT mellitus, inflammatory diseases, cancer, or autoimmune diseases,
 PT comprises exposing a sample to a phage display library and recovering
 PT phage bound to the sample.

XX PS Claim 56; Page 242; 298pp; English.

XX CC This invention relates to a novel method for identifying disease
 CC targeting peptides. The method comprises exposing a sample from an organ,
 CC tissue or cell type of interest, to a phage display library and
 CC recovering phage bound to the sample (the phage expresses targeting
 CC peptides). The peptides identified by the method of the invention may
 CC have cytostatic, immunosuppressive, anti-inflammatory, antiarthritic,
 CC antiatherosclerotic, antidiabetic, antibacterial and antiviral
 CC activities. The methods and composition are useful for identifying
 CC targeting peptides and one or more receptors for a targeting peptide. The
 CC targeting peptides are used for selective delivery of therapeutic agents,
 CC including gene therapy vectors and fusion proteins, to specific organs,
 CC tissues, or cell types in subject. The targeting peptide may also be used

CC for treating diseases such as diabetes mellitus, inflammatory diseases,
 CC arthritis, atherosclerosis, cancer, autoimmune diseases, bacterial and
 CC viral infections and Hodgkin's disease. The present sequence represents a
 CC targeting peptide of the invention
 XX Sequence 8 AA;

Query Match 54.3%; Score 25; DB 5; Length 8;
 Best Local Similarity 37.5%; Pred. No. 1.8e+06;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CNEESLIC 8
 | : | : |
 Db 1 CRRSFLC 8

Search completed: April 1, 2005, 10:53:30
 Job time : 117 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 10:55:44 ; Search time 93 Seconds
(without alignments)
28.524 Million cell updates/sec

Title: US-09-761-636A-6

Perfect score: 46

Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 311592847 residues

Total number of hits satisfying chosen parameters: 78585

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/2/pubpaa/FCT_NEW_PUB.pep.*
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6: /cgn2_6/ptodata/2/pubpaa/FCTUS_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	43	93.5	8	9	US-09-761-636A-20
3	42	91.3	8	9	US-09-761-636A-22
4	41	89.1	8	9	US-09-761-636A-19
5	39	84.8	8	9	US-09-761-636A-21
6	27	58.7	8	17	US-10-808-187-2445
7	26	56.5	8	9	US-09-795-006A-133
8	25	54.3	8	15	US-10-363-208-108
9	25	54.3	8	17	US-10-838-289-155
10	24	52.2	8	9	US-09-795-006A-142
11	23	50.0	7	10	US-09-827-345-14
12	23	50.0	8	9	US-09-840-277-25
13	23	50.0	8	9	US-09-185-908-115

14	23	50.0	8	15	US-10-609-217-457
15	23	50.0	8	15	US-10-363-208-74
16	23	50.0	8	15	US-10-363-208-82
17	23	50.0	8	15	US-10-632-388-457
18	23	50.0	8	15	US-10-651-723-457
19	23	50.0	8	15	US-10-645-761-457
20	23	50.0	8	15	US-10-666-696-457
21	23	50.0	8	15	US-10-653-048-457
22	23	50.0	8	17	US-10-838-289-136
23	23	50.0	8	17	US-10-838-289-147
24	23	50.0	8	17	US-10-838-289-270
25	22	47.8	6	14	US-10-006-869-3664
26	22	47.8	6	15	US-10-395-032-3664
27	22	47.8	7	14	US-10-006-869-3665
28	22	47.8	7	14	US-10-190-082-92
29	22	47.8	7	15	US-10-395-032-3665
30	22	47.8	8	14	US-10-006-869-1071
31	22	47.8	8	14	US-10-006-869-3624
32	22	47.8	8	15	US-10-395-032-1071
33	22	47.8	8	15	US-10-395-032-3624
34	22	47.8	8	17	US-10-838-289-141
35	22	47.8	8	17	US-10-838-289-154
36	22	47.8	5	14	US-10-838-289-313
37	21	45.7	5	14	US-10-006-869-3663
38	21	45.7	5	15	US-10-395-032-3663
39	21	45.7	6	14	US-10-006-869-985
40	21	45.7	6	14	US-10-006-869-2242
41	21	45.7	6	15	US-10-395-032-985
42	21	45.7	6	15	US-10-395-032-2242
43	21	45.7	7	14	US-10-006-869-989
44	21	45.7	7	14	US-10-006-869-2246
45	21	45.7	7	15	US-10-395-032-989

ALIGNMENTS

RESULT 1
US-09-761-636A-6
; Sequence 6, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-6

Query Match 100.0%; Score 46; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db 1 CNEESLIC 8

RESULT 2
US-09-761-636A-20

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; Sequence 20, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-20
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Query Match          93.5%; Score 43; DB 9; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 CNEESLIC 8
Db 1 CNEETLIC 8
```

```
RESULT 3
US-09-761-636A-22
; Sequence 22, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-22
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Query Match          91.3%; Score 42; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.3e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CNEESLIC 8
Db 1 CNEESVVC 8
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RESULT 4
US-09-761-636A-19
; Sequence 19, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
```

```
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-19
```

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Query Match          89.1%; Score 41; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.3e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 CNEESLIC 8
Db 1 CNEESLIC 8
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RESULT 5
US-09-761-636A-21
; Sequence 21, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-21
```

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Query Match          84.8%; Score 39; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.3e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
Qy 1 CNEESLIC 8
Db 1 CNEESFIC 8
```

```
RESULT 6
US-10-808-187-2445
; Sequence 2445, Application US/10808187
; Publication No. US2005000909A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
```

; TITLE OF INVENTION: RESPIRATORY SYNDROME (SARS)
; FILE REFERENCE: V9661.0078
; CURRENT APPLICATION NUMBER: US/10/808,187
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/468,139
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/471,200
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 2445
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-808-187-2445

Query Match 58.7%; Score 27; DB 17; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESL 6
|:|:|
Db 3 CNDLSL 8

RESULT 7
US-09-795-006A-133
; Sequence 133, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 133
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-795-006A-133

Query Match 56.5%; Score 26; DB 9; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEESL 6
|:|:|
Db 3 CNDLSL 8

RESULT 8
US-10-363-208-108
; Sequence 108, Application US/10363208
; Publication No. US20040048243A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774.P005PCT
; CURRENT APPLICATION NUMBER: US/10/363,208
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)-(8)
; OTHER INFORMATION: synthetic construct
US-10-363-208-108

Query Match 54.3%; Score 25; DB 15; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.3e+06;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
|:|:|
Db 1 CSRSFLC 8

RESULT 9
US-10-838-289-155
; Sequence 155, Application US/10838289
; Publication No. US20050058603A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Jiming
; APPLICANT: Ai, Hua
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
; FILE REFERENCE: NANOSHIELDS
; CURRENT APPLICATION NUMBER: US/10/838,289
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 60/502,429
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/467,389
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 155
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Lung homing peptide
US-10-838-289-155

Query Match 54.3%; Score 25; DB 17; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
|:|:|
Db 1 CGNETLRC 8

RESULT 10
US-09-795-006A-142
; Sequence 142, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al

; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAS AND PROTEINS
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 142
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-795-006A-142

Query Match 52.2%; Score 24; DB 9; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CNEESL 6
| | | |
Db 3 CNSEGL 8

RESULT 11
US-09-827-345-14
; Sequence 14, Application US/09827345
; Publication No. US20030021800A1
; GENERAL INFORMATION:
; APPLICANT: CHERMANN, JEAN-CLAUDE
; APPLICANT: LE CONTEL, CAROLE
; APPLICANT: GALEA, PASCALE
; TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING AN
; TITLE OF INVENTION: INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND
; TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF
; TITLE OF INVENTION: DIAGNOSIS
; FILE REFERENCE: 065691-0216
; CURRENT APPLICATION NUMBER: US/09/827,345
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/599,549
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: PCT/FR96/01006
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 08/973,551
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: FR 95/07914
; PRIOR FILING DATE: 1995-06-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-827-345-14

Query Match 50.0%; Score 23; DB 10; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CNEES 5
| | | |
Db 2 CNPES 6

RESULT 12

US-09-840-277-25
; Sequence 25, Application US/09840277
; Patent No. US20020168363A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: KOHNO, TADAHIKO
; APPLICANT: LACEY, DAVID LEE
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
; FILE REFERENCE: A-688A
; CURRENT APPLICATION NUMBER: US/09/840,277
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/198,919
; PRIOR FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 60/201,394
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Integrin antagonist peptide
US-09-840-277-25

Query Match 50.0%; Score 23; DB 9; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.3e+06;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CNEESLIC 8
| : | : |
Db 1 CWDGGLMC 8

RESULT 13
US-09-185-908-115
; Sequence 115, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; TITLE OF INVENTION: FUNCTIONS
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 115
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on mouse claudin-2 sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-185-908-115

Query Match 50.0%; Score 23; DB 9; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.3e+06;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CNEESLIC 8
| : | : |
Db 1 CRTSSYVC 8

RESULT 14
US-10-609-217-457
; Sequence 457, Application US/10609217
; Publication No. US200400044188A1

; GENERAL INFORMATION:
; APPLICANT: REIGE, ULRICH
; APPLICANT: LIU, CHUAN-PA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 457
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-609-217-457

Query Match 50.0%; Score 23; DB 15; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.3e+06;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 CNEESLIC 8
Db 1 CWDGGLMC 8

RESULT 15
US-10-363-208-74
; Sequence 74, Application US/10363208
; Publication No. US20040048243A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774.P005PCT
; CURRENT APPLICATION NUMBER: US/10/363,208
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(8)
; OTHER INFORMATION: synthetic construct
US-10-363-208-74

Query Match 50.0%; Score 23; DB 15; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.3e+06;
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 CNEESLIC 8
Db 1 CRASAMVC 8

Search completed: April 1, 2005, 11:06:05
Job time : 93 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 10:05:16 ; Search time 38 Seconds
(without alignments)
32.916 Million cell updates/sec

Title: US-09-761-636A-5
Perfect score: 72
Sequence: 1 CASELGKSTNTFC 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1828

Minimum DB seq length: 0
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33.5	46.5	12	2 PT0216	T-cell receptor be
2	30	41.7	12	2 S47394	T-cell antigen rec
3	29.5	41.0	13	2 S47357	T-cell antigen rec
4	29	40.3	12	2 S26549	T-cell receptor be
5	28	38.9	12	2 PH1463	T-cell receptor be
6	28	38.9	12	2 PH1466	T-cell receptor be
7	28	38.9	13	2 S47400	T-cell antigen rec
8	27	37.5	11	2 PT0217	T-cell receptor be
9	27	37.5	12	2 S47391	T-cell antigen rec
10	27	37.5	13	2 S47383	T-cell antigen rec
11	26	36.1	11	2 S57575	T-cell receptor V-
12	26	36.1	12	2 S47395	T-cell antigen rec
13	26	36.1	13	2 S47381	T-cell antigen rec
14	25.5	35.4	13	2 S47382	T-cell antigen rec
15	25	34.7	10	2 S23371	T-cell receptor al
16	25	34.7	11	2 PH0947	T-cell receptor be
17	25	34.7	12	2 PH0931	T-cell receptor be
18	25	34.7	12	2 PH1469	T-cell receptor be
19	24.5	34.0	12	2 PH1457	T-cell receptor be
20	24	33.3	11	2 PH1583	IG H chain V-D-J r
21	24	33.3	12	2 S26552	T-cell receptor be
22	24	33.3	12	2 S26554	T-cell receptor be
23	24	33.3	12	2 S26559	T-cell receptor be
24	24	33.3	12	2 S47363	T-cell antigen rec
25	24	33.3	12	2 PH1467	T-cell receptor be
26	24	33.3	12	2 PH1468	T-cell receptor be
27	24	33.3	13	2 S47390	T-cell antigen rec
28	23.5	32.6	12	2 PH1459	T-cell receptor be
29	23.5	32.6	13	2 S47377	T-cell antigen rec

30	23	31.9	12	2 S26553	T-cell receptor be
31	23	31.9	12	2 S26557	T-cell receptor be
32	23	31.9	12	2 S26556	T-cell receptor be
33	23	31.9	12	2 PH1462	T-cell receptor be
34	23	31.9	12	2 PH1470	T-cell receptor be
35	23	31.9	12	2 PH1464	T-cell receptor be
36	23	31.9	13	2 A23695	myosin heavy chain
37	22.5	31.2	12	2 S26541	T-cell receptor be
38	22.5	31.2	12	2 PH1458	T-cell receptor be
39	22.5	31.2	13	2 S47356	T-cell antigen rec
40	22.5	31.2	13	2 S47378	T-cell antigen rec
41	22.5	31.2	13	2 S47385	T-cell antigen rec
42	22	30.6	10	2 PH0927	T-cell receptor be
43	22	30.6	12	2 S26548	T-cell receptor be
44	22	30.6	12	2 S26547	T-cell receptor be
45	22	30.6	12	2 S26555	T-cell receptor be

ALIGNMENTS

RESULT 1

PT0216
T-cell receptor beta chain V-J region (4-I-G.4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C:Accession: PT0216
J.Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restrict
A:Reference number: PT0209; MUID:91217621; PMID:1902501
A:Accession: PT0216
A:Molecule type: mRNA
A:Residues: 1-12 <NAK>
C:Keywords: T-cell receptor

Query Match 46.5%; Score 33.5; DB 2; Length 12;
Best Local Similarity 72.7%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CASELGKSTNT 11
||| | :|||
Db 1 CASSLG-TTNT 10

RESULT 2

S47394
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47394; S47369
R.Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T ce
A:Reference number: S47355
A:Accession: S47394
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-12 <LEH>
A:Cross-references: EMBL:Z35714; NID:G527523; PIDN:CAA84783.1; PID:G527524; EMBL:Z35694;
C:Keywords: T-cell receptor

Query Match 41.7%; Score 30; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASELGKSTNTF 12
||| :|||
Db 1 CASSIGNGYTFF 12

RESULT 3

S47357

T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T cell
A:Reference number: S47355
A:Accession: S47357
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35681; NID:G527451; PIDN:CAA84750.1; PID:G527452
C:Keywords: T-cell receptor

Query Match 41.0%; Score 29.5; DB 2; Length 13;
Best Local Similarity 63.6%; Pred. No. 75;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 CASELGKSTNT 11
||| |::|
DB 1 CASS-GRSTD 10

RESULT 4
S26549
T-cell receptor beta chain (clone Cw3/A8, Cw3/Cas1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C:Accession: S26549; S26550
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A:Reference number: S26512; MUID:92364546; PMID:1380061
A:Accession: S26549
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Cross-references: EMBL:X67999
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/A8
A:Accession: S26550
A:Molecule type: mRNA
A:Residues: 1-12 <CA2>
A:Cross-references: EMBL:X68000
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 40.3%; Score 29; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 86;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELGKS 8
||| |::|
DB 1 CASSLGST 8

RESULT 5
PH1463
T-cell receptor beta chain (clone A24/10.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004
R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatib
A:Reference number: PH1430; MUID:93171821; PMID:8436911
A:Accession: PH1463
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Keywords: receptor; T-cell

Query Match 38.9%; Score 28; DB 2; Length 12;

Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELGKS 8
||| |::|
DB 1 CASSLGNT 8

RESULT 6
PH1466
T-cell receptor beta chain (clone A3/74.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004
C:Accession: PH1466
R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatib
A:Reference number: PH1430; MUID:93171821; PMID:8436911
A:Accession: PH1466
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Keywords: receptor; T-cell

Query Match 38.9%; Score 28; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELGK 7
||| |::|
DB 1 CASSLGQ 7

RESULT 7
S47400
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47400
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T ce
A:Reference number: S47355
A:Accession: S47400
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35678; NID:G527535; PIDN:CAA84747.1; PID:G527536
C:Keywords: T-cell receptor

Query Match 38.9%; Score 28; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASELGKSTNTF 12
||| |::|
DB 1 CASSVALATEAF 12

RESULT 8
PT0217
T-cell receptor beta chain V-J region (4-1-E.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C:Accession: PT0217
R:Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restrict
A:Reference number: PT0209; MUID:91217621; PMID:1902501
A:Accession: PT0217
A:Molecule type: mRNA
A:Residues: 1-11 <NAK>
C:Keywords: T-cell receptor

Query Match 37.5%; Score 27; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELG 6
|||: ||
Db 1 CASRLG 6

RESULT 9
S47391
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47391; S47386
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T cell epitopes
A:Reference number: S47355
A:Accession: S47391
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-12 <LEH>
A:Cross-references: EMBL:Z35712; NID:G527519; PIDN:CAA84781.1; PID:G527520; EMBL:Z35701;
C:Keywords: T-cell receptor

Query Match 37.5%; Score 27; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CASELGKSTNTF 12
|||: ||
Db 1 CASSTGSGYGYTF 12

RESULT 10
S47383
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47383
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T cell epitopes
A:Reference number: S47355
A:Accession: S47383
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35709; NID:G527513; PIDN:CAA84778.1; PID:G527514
C:Keywords: T-cell receptor

Query Match 37.5%; Score 27; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELGKS 8
|||: ||
Db 1 CASSNGGS 8

RESULT 11
S57575
T cell receptor V-J junctional alpha chain region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C:Accession: S57575
R:Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Arguet, V.P.
submitted to the EMBL Data Library, June 1995
A:Description: T cell receptor repertoire for a viral epitope in humans is diversified by T cell epitopes
A:Reference number: S57494
A:Accession: S57575

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-11 <BUR>
A:Cross-references: EMBL:Z49953; NID:G887510; PIDN:CAA90224.1; PID:G887511
C:Keywords: T-cell receptor

Query Match 36.1%; Score 26; DB 2; Length 11;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELGK 7
|||: ||
Db 1 CASQGGK 7

RESULT 12
S47395
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47395
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T cell epitopes
A:Reference number: S47355
A:Accession: S47395
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-12 <LEH>
A:Cross-references: EMBL:Z35715; NID:G527525; PIDN:CAA84784.1; PID:G527526
C:Keywords: T-cell receptor

Query Match 36.1%; Score 26; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CASELGKSTNTF 12
|||: ||
Db 1 CASQSGSYGYTF 12

RESULT 13
S47381
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47381
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T cell epitopes
A:Reference number: S47355
A:Accession: S47381
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35698; NID:G527487; PIDN:CAA84767.1; PID:G527488
C:Keywords: T-cell receptor

Query Match 36.1%; Score 26; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CASELGKSTNTF 12
|||: ||
Db 1 CASSTRSNTTEAF 12

RESULT 14
S47382
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47382; S47370

R:Lehner, P.J.
 Submitted to the EMBL Data Library, August 1994
 A:Description: Human H1A-A0201 restricted recognition of influenza A is dominated by T
 A:Reference number: S47355
 A:Accession: S47382
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-13 <LEH>
 A:Cross-references: EMBL:Z35687; NID:G527463; PIDN:CAA84756.1; PID:G527464; EMBL:Z35695;
 C:Keywords: T-cell receptor

Query Match 35.4%; Score 25.5; DB 2; Length 13;
 Best Local Similarity 54.5%; Pred. No. 3.9e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 CASELGKSTNT 11
 ||| : |||:
 Db 1 CASSM-RSTD 10

RESULT 15
 S23371
 T-cell receptor alpha chain J region - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
 C:Accession: S23371
 R:Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichman
 Eur. J. Immunol. 21, 2749-2754, 1991
 A>Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rheu
 A:Reference number: S23364; WUID:92037820; PMID:1657615
 A:Accession: S23371
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-10 <PLU>
 A:Cross-references: EMBL:X58166
 C:Keywords: T-cell receptor

Query Match 34.7%; Score 25; DB 2; Length 10;
 Best Local Similarity 62.5%; Pred. No. 3.8e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASELGKST 9
 : |||||
 Db 2 SCEAGKST 9

Search completed: April 1, 2005, 10:41:41
 Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 09:36:29 ; Search time 116 Seconds
(without alignments)
57.388 Million cell updates/sec

Title: US-09-761-636A-5

Perfect score: 72

Sequence: 1 CASELGKSTWTF 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 4955

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	27	37.5	13	2	Q8GZ5	Q8GZ5 fugu rubrip
2	26	36.1	9	2	Q6XSN9	Q6XSN9 botryosphae
3	26	36.1	10	2	Q69FL6	Q69FL6 photopsis s
4	26	36.1	10	2	Q69FL7	Q69FL7 photopsis s
5	26	36.1	13	2	Q69FL3	Q69FL3 pillidiella
6	26	36.1	13	2	Q69FP4	Q69FP4 botryosphae
7	26	36.1	13	2	Q6XDZ3	Q6XDZ3 guignardia
8	26	36.1	13	2	Q6XDZ4	Q6XDZ4 botryosphae
9	26	36.1	13	2	Q6XDZ6	Q6XDZ6 botryosphae
10	26	36.1	13	2	Q6XDZ7	Q6XDZ7 botryosphae
11	26	36.1	13	2	Q6XDZ8	Q6XDZ8 botryosphae
12	26	36.1	13	2	Q6XE03	Q6XE03 botryosphae
13	26	36.1	13	2	Q6XE05	Q6XE05 botryosphae
14	26	36.1	13	2	Q6XE07	Q6XE07 botryosphae
15	26	36.1	13	2	Q6XE18	Q6XE18 botryosphae
16	26	36.1	13	2	Q6XE20	Q6XE20 botryosphae
17	26	36.1	13	2	Q918T4	Q918T4 human papil
18	26	36.1	13	2	Q918T6	Q918T6 human papil
19	25	34.7	9	2	Q6Y5E3	Q6Y5E3 cercospora
20	25	34.7	9	2	Q6Y5E4	Q6Y5E4 phialophora
21	25	34.7	9	2	Q6Y5E5	Q6Y5E5 togninia fr
22	25	34.7	9	2	Q6Y5E8	Q6Y5E8 togninia no
23	25	34.7	9	2	Q6Y5G9	Q6Y5G9 togninia mi
24	25	34.7	13	2	Q6XE04	Q6XE04 botryosphae
25	23	31.9	12	1	PSB3_PHYPA	P80662 physcomitre
26	23	31.9	12	2	Q9P5E7	Q9P5E7 gallus gall
27	22	30.6	13	2	Q6R272	Q6R272 lactococcus
28	21	29.2	11	2	Q7M1D1	Q7M1D1 unidentified
29	21	29.2	12	2	Q85666	Q85666 reovirus ty
30	21	29.2	13	1	RAN6_RANCA	P82821 rana catesb
31	21	29.2	13	1	RAN7_RANCA	P82822 rana catesb

32	21	29.2	13	2	Q9GJU2	Q9GJU2 oviss aries
33	20	27.8	10	2	Q6MZE6	Q6MZE6 homo sapien
34	20	27.8	11	2	Q9TOL9	Q9TOL9 brassica ol
35	20	27.8	12	1	RAN5_RANCA	P82820 rana catesb
36	20	27.8	12	1	V23K_WSSV	P82005 white spot
37	20	27.8	12	2	Q9UR22	Q9UR22 cryptococcu
38	20	27.8	13	1	LIGA_TRAVE	P20011 trameetes ve
39	20	27.8	13	1	PSP_PINPS	P81668 pinus pinas
40	20	27.8	13	1	RAN8_RANCA	P82821 rana catesb
41	20	27.8	13	2	Q6TUI7	Q6TUI7 ascaris suu
42	20	27.8	13	2	Q8OWZ0	Q8OWZ0 rattus norv
43	19	26.4	11	2	Q6DW13	Q6DW13 bos taurus
44	19	26.4	12	2	Q61331	Q61331 mus musculu
45	19	26.4	13	2	O54809	O54809 mus musculu

ALIGNMENTS

RESULT 1
Q8QGZ5 PRELIMINARY; PRT; 13 AA.
ID Q8QGZ5
AC Q8QGZ5; (Created)
DT 01-JUN-2002 (TREMREL. 21, Last sequence update)
DT 01-JUN-2002 (TREMREL. 21, Last sequence update)
DT 01-JUN-2003 (TREMREL. 24, Last annotation update)
DE Guanine nucleotide binding protein (Fragment).
GN Name=Gnao;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97129408; PubMed=8973916;
RA Sarwal M.M., Sontag J.M., Hoang L., Brenner S., Wilkie T.M.;
RT "G protein alpha subunit multigene family in the Japanese puffer fish
Fugu rubripes: PCR from a compact vertebrate genome.";
RL Genome Res. 6:1207-1215(1996).
DR EMBL; L79891; AAL77640.1; -;
DR GO; GO:0004871; P:signal transducer activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR001019; Gprotein_alpha.
DR Pfam; PF00503; G-alpha; 1.
FT NON_TER 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1336 MW; 465859640B44B5B3 CRC64;

Query Match 37.5%; Score 27; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. NO. 7.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASELGKST 9
DB 1 AGESGKST 8

RESULT 2
Q6XSN9 PRELIMINARY; PRT; 9 AA.
ID Q6XSN9
AC Q6XSN9; (Created)
DT 05-JUL-2004 (TREMREL. 27, Last sequence update)
DT 05-JUL-2004 (TREMREL. 27, Last sequence update)
DT 05-JUL-2004 (TREMREL. 27, Last annotation update)
DE Elongation factor 1 alpha (Fragment).
OS Botryosphaeria parva.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
OC Dothideomycetes et Chaetothyriomycetes incertae sedis;
OC Botryosphaeriaceae; Botryosphaeria.
OX NCBI_TaxID=120390;
RN [1]

```

RP SEQUENCE FROM N.A.
RC STRAIN=CMW11062, CMW11064, CMW10089, CMW10094, CMW10095, and CMW11060;
RA Gezaghe A., Roux J., Slippers B., Wingfield M.J., Wingfield B.D.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY210481; AAP85509.1; -
DR EMBL; AY210482; AAP85510.1; -
DR EMBL; AY210483; AAP85511.1; -
DR EMBL; AY210484; AAP85512.1; -
DR EMBL; AY210485; AAP85513.1; -
DR EMBL; AY210486; AAP85514.1; -
DR EMBL; AY210487; AAP85515.1; -
DR GO; GO:0003746; F:translation elongation factor activity; IEA.
KW Elongation factor.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 861 MW; D5A97338772B1DDDD CRC64;

Query Match 36.1%; Score 26; DB 2; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.6e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGKST 9
Db 2 AAELGKGS 9

RESULT 3
Q69FL6 PRELIMINARY; PRT; 10 AA.
AC Q69FL6;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE Translation elongation factor 1 alpha (Fragment).
OS Phomopsis sp. R433R.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Diaporthales; Valsaceae; mitosporic Valsaceae;
OC Phomopsis.
OX NCBI_TaxID=251294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R433R;
RX MEDLINE=23358489; PubMed=15185979;
RA van Niekirk J.M., Groenewald J.Z., Verkley G.J.M., Fourie P.H.,
RA Wingfield M.J., Crous P.W.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY339353; AAR04082.1; -
DR GO; GO:0003746; F:translation elongation factor activity; IEA.
KW Elongation factor.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1007 MW; 726CD0B87338772B CRC64;

Query Match 36.1%; Score 26; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 8.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGKST 9
Db 1 AAELGKGS 8

RESULT 5
Q69FL3 PRELIMINARY; PRT; 13 AA.
AC Q69FL3;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE Translation elongation factor 1 alpha (Fragment).
OS Pilidiella diploidiella.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Diaporthales; Melanconidaceae; Schizoparme complex;
OC mitosporic Schizoparme; Pilidiella.
OX NCBI_TaxID=251300;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=STE-U 3931;
RX MEDLINE=23358489; PubMed=15185979;
RA van Niekirk J.M., Groenewald J.Z., Verkley G.J.M., Fourie P.H.,
RA Wingfield M.J., Crous P.W.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY339357; AAR04086.1; -
DR GO; GO:0003746; F:translation elongation factor activity; IEA.
KW Elongation factor.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1007 MW; 726CD0B87338772B CRC64;

Query Match 36.1%; Score 26; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 8.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGKST 9
Db 1 AAELGKGS 8

RESULT 4
Q69FL7 PRELIMINARY; PRT; 10 AA.
AC Q69FL7;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE Translation elongation factor 1 alpha (Fragment).
OS Phomopsis sp. R338E.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Diaporthales; Valsaceae; mitosporic Valsaceae;
OC Phomopsis.
OX NCBI_TaxID=251293;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R338E;
RX MEDLINE=23358489; PubMed=15185979;
RA van Niekirk J.M., Groenewald J.Z., Verkley G.J.M., Fourie P.H.,
RA Wingfield M.J., Crous P.W.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY339353; AAR04082.1; -
DR GO; GO:0003746; F:translation elongation factor activity; IEA.
KW Elongation factor.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1007 MW; 726CD0B87338772B CRC64;

Query Match 36.1%; Score 26; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 8.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGKST 9
Db 1 AAELGKGS 8

RESULT 5
Q69FL3 PRELIMINARY; PRT; 13 AA.
AC Q69FL3;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE Translation elongation factor 1 alpha (Fragment).
OS Pilidiella diploidiella.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Diaporthales; Melanconidaceae; Schizoparme complex;
OC mitosporic Schizoparme; Pilidiella.
OX NCBI_TaxID=251300;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=STE-U 3931;
RX MEDLINE=23358489; PubMed=15185979;
RA van Niekirk J.M., Groenewald J.Z., Verkley G.J.M., Fourie P.H.,
RA Wingfield M.J., Crous P.W.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY339357; AAR04086.1; -
DR GO; GO:0003746; F:translation elongation factor activity; IEA.
KW Elongation factor.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1007 MW; 726CD0B87338772B CRC64;

Query Match 36.1%; Score 26; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 8.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGKST 9
Db 1 AAELGKGS 8

```



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KW Elongation factor.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1394 MW; 726C85FF1812972B CRC64;

Query Match 36.1%; Score 26; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGKST 9
Db 4 AAELGKGS 11

RESULT 6
Q69FF4 ID Q69FF4 PRELIMINARY; PRT; 13 AA.
AC Q69FF4;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE Elongation factor-1 alpha (Fragment).
OS Botryosphaeria australis.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
OC Dothideomycetes et Chaetothryiomycetes incertae sedis;
OC Botryosphaeriaceae; Botryosphaeria.
OX NCBI_TaxID=240362;
RN [1]
RP SEQUENCE FROM N.A.
RA Slippers B., Vermeulen G., Crous P.W., Coutinho T.A., Wingfield B.D.,
RA Wingfield M.J.;
RT "Multiple gene sequences delimit Botryosphaeria australis sp. nov. as
a sister species to B. lutea.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY339268; AAQ75709.1; -
DR EMBL; AY339269; AAQ75709.1; -
DR EMBL; AY339270; AAQ75710.1; -
DR EMBL; AY339271; AAQ75711.1; -
DR GO; GO:0003746; F:translation elongation factor activity; IEA.
KW Elongation factor.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1394 MW; D5F1817FF18C1DDD CRC64;

Query Match 36.1%; Score 26; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGKST 9
Db 6 AAELGKGS 13

RESULT 7
Q6XDZ3 ID Q6XDZ3 PRELIMINARY; PRT; 13 AA.
AC Q6XDZ3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Translation elongation factor 1 alpha (Fragment).
OS Guignardia philoprina.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
OC Dothideomycetes et Chaetothryiomycetes incertae sedis;
OC Botryosphaeriaceae; Guignardia.
OX NCBI_TaxID=121617;
RN [1]
RP SEQUENCE FROM N.A.
RA Slippers B., Crous P.W., Denman S., Coutinho T.A., Wingfield B.D.,
RA Wingfield M.J.;
RT "Combined multiple gene genealogies and phenotypic characters
differentiate several species previously identified as Botryosphaeria
dothidea.";

KW Elongation factor.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1394 MW; 726C85FF1812972B CRC64;

Query Match 36.1%; Score 26; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGKST 9
Db 4 AAELGKGS 11

RESULT 8
Q6XDZ4 ID Q6XDZ4 PRELIMINARY; PRT; 13 AA.
AC Q6XDZ4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Translation elongation factor 1 alpha (Fragment).
OS Botryosphaeria stevensii.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
OC Dothideomycetes et Chaetothryiomycetes incertae sedis;
OC Botryosphaeriaceae; Botryosphaeria.
OX NCBI_TaxID=85927;
RN [1]
RP SEQUENCE FROM N.A.
RA Slippers B., Crous P.W., Denman S., Coutinho T.A., Wingfield B.D.,
RA Wingfield M.J.;
RT "Combined multiple gene genealogies and phenotypic characters
differentiate several species previously identified as Botryosphaeria
dothidea.";
RL Mycologia 96:83-101(2004).
DR EMBL; AY236904; AAP87169.1; -
DR GO; GO:0003746; F:translation elongation factor activity; IEA.
KW Elongation factor.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1394 MW; D5F1817FF18C1DDD CRC64;

Query Match 36.1%; Score 26; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGKST 9
Db 6 AAELGKGS 13

RESULT 9
Q6XDZ6 ID Q6XDZ6 PRELIMINARY; PRT; 13 AA.
AC Q6XDZ6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Translation elongation factor 1 alpha (Fragment).
OS Botryosphaeria obtusa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
OC Dothideomycetes et Chaetothryiomycetes incertae sedis;
OC Botryosphaeriaceae; Botryosphaeria.
OX NCBI_TaxID=66732;
RN [1]
RP SEQUENCE FROM N.A.
RA Slippers B., Crous P.W., Denman S., Coutinho T.A., Wingfield B.D.,
RA Wingfield M.J.;
RT "Combined multiple gene genealogies and phenotypic characters
differentiate several species previously identified as Botryosphaeria
dothidea.";
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RT dothidea."; RT
 RL Mycologia 96:83-101(2004).
 DR EMBL; AY236902; AAP87165.1; -.
 DR EMBL; AY236903; AAP87167.1; -.
 DR GO; GO:0003746; F:translation elongation factor activity; IEA.
 KW Elongation factor.
 FT NON_TER 1
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1394 MW; D5F1817FF18C1DDD CRC64;

Query Match 36.1%; Score 26; DB 2; Length 13;
 Best Local Similarity 62.5%; Pred. No. 1.1e+03;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGKST 9
 |:|||||:
 Db 6 AAELGKGS 13

RESULT 10

Q6XDZ7 PRELIMINARY; PRT; 13 AA.
 ID Q6XDZ7;
 AC Q6XDZ7;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Translation elongation factor 1 alpha (Fragment).
 OS Botryosphaeria rhodina.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
 OC Dothideomycetes et Chaetothryiomycetes incertae sedis;
 OC Botryosphaeriaceae; Botryosphaeria.
 OX NCBI_TaxID=45133;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Slippers B., Crous P.W., Denman S., Countinho T.A., Wingfield B.D.,
 RA Wingfield M.J.;
 RT "Combined multiple gene genealogies and phenotypic characters
 RT differentiate several species previously identified as Botryosphaeria
 RT dothidea.";
 RL Mycologia 96:83-101(2004).
 DR EMBL; AY236901; AAP87165.1; -.
 DR GO; GO:0003746; F:translation elongation factor activity; IEA.
 KW Elongation factor.
 FT NON_TER 1
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1394 MW; D5F1817FFC3A1DDD CRC64;

Query Match 36.1%; Score 26; DB 2; Length 13;
 Best Local Similarity 62.5%; Pred. No. 1.1e+03;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGKST 9
 |:|||||:
 Db 6 AAELGKGS 13

RESULT 11

Q6XDZ8 PRELIMINARY; PRT; 13 AA.
 ID Q6XDZ8;
 AC Q6XDZ8;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Translation elongation factor 1 alpha (Fragment).
 OS Botryosphaeria rhodina.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
 OC Dothideomycetes et Chaetothryiomycetes incertae sedis;
 OC Botryosphaeriaceae; Botryosphaeria.
 OX NCBI_TaxID=45133;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Slippers B., Crous P.W., Denman S., Countinho T.A., Wingfield B.D.,
 RA Wingfield M.J.;

RT "Combined multiple gene genealogies and phenotypic characters
 RT differentiate several species previously identified as Botryosphaeria
 RT dothidea.";
 RL Mycologia 96:83-101(2004).
 DR EMBL; AY236900; AAP87164.1; -.
 DR GO; GO:0003746; F:translation elongation factor activity; IEA.
 KW Elongation factor.
 FT NON_TER 1
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1394 MW; D5F1817FF18C1DDD CRC64;

Query Match 36.1%; Score 26; DB 2; Length 13;
 Best Local Similarity 62.5%; Pred. No. 1.1e+03;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGKST 9
 |:|||||:
 Db 6 AAELGKGS 13

RESULT 12

Q6XE03 PRELIMINARY; PRT; 13 AA.
 ID Q6XE03;
 AC Q6XE03;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
 DE Translation elongation factor 1 alpha (Fragment).
 OS Botryosphaeria dothidea.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
 OC Dothideomycetes et Chaetothryiomycetes incertae sedis;
 OC Botryosphaeriaceae; Botryosphaeria.
 OX NCBI_TaxID=55169;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Slippers B., Crous P.W., Denman S., Countinho T.A., Wingfield B.D.,
 RA Wingfield M.J.;
 RT "Combined multiple gene genealogies and phenotypic characters
 RT differentiate several species previously identified as Botryosphaeria
 RT dothidea.";
 RL Mycologia 96:83-101(2004).
 DR EMBL; AY236895; AAP87159.1; -.
 DR EMBL; AY236896; AAP87160.1; -.
 DR EMBL; AY236897; AAP87161.1; -.
 DR EMBL; AY236898; AAP87162.1; -.
 DR EMBL; AY236899; AAP87163.1; -.
 DR GO; GO:0003746; F:translation elongation factor activity; IEA.
 KW Elongation factor.
 FT NON_TER 1
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1394 MW; D5F1817FF18C1DDD CRC64;

Query Match 36.1%; Score 26; DB 2; Length 13;
 Best Local Similarity 62.5%; Pred. No. 1.1e+03;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGKST 9
 |:|||||:
 Db 6 AAELGKGS 13

RESULT 13

Q6XE05 PRELIMINARY; PRT; 13 AA.
 ID Q6XE05;
 AC Q6XE05;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
 DE Translation elongation factor 1 alpha (Fragment).
 OS Botryosphaeria lutea.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
 OC Dothideomycetes et Chaetothryiomycetes incertae sedis;
 OC Botryosphaeriaceae; Botryosphaeria.

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OX NCBI_TaxID=120395;
RP SEQUENCE FROM N.A.
RA Slippers B., Crous P.W., Denman S., Coutinho T.A., Wingfield B.D.,
RA Wingfield M.J.;
RT "Combined multiple gene genealogies and phenotypic characters
RT differentiate several species previously identified as Botryosphaeria
RT dothidea.";
RL Mycologia 96:83-101(2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Slippers B., Vermeulen G., Crous P.W., Coutinho T.A., Wingfield B.D.,
RA Wingfield M.J.;
RT "Multiple gene sequences delimit Botryosphaeria australis sp. nov. as
RT a sister species to B. lutea.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY236893; AAP87157.1; -
DR EMBL; AY339265; AAQ75705.1; -
DR EMBL; AY339266; AAQ75706.1; -
DR EMBL; AY339267; AAQ75707.1; -
DR GO; GO:0003746; F:translation elongation factor activity; IEA.
KW Elongation factor.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1394 MW; D5F1817FF18C1DDD CRC64;

Query Match 36.1%; Score 26; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGKST 9
DB 6 AAELGKGS 13

RESULT 14
QXEQ07 PRELIMINARY; PRT; 13 AA.
AC Q6XE07;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Translation elongation factor 1 alpha (Fragment).
OS Botryosphaeria eucalyptorum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
OC Dothideomycetes et Chaetothyriomycetes incertae sedis;
OC Botryosphaeriaceae; Botryosphaeria.
OX NCBI_TaxID=233969;
RN [1]
RP SEQUENCE FROM N.A.
RA Slippers B., Crous P.W., Denman S., Coutinho T.A., Wingfield B.D.,
RA Wingfield M.J.;
RT "Combined multiple gene genealogies and phenotypic characters
RT differentiate several species previously identified as Botryosphaeria
RT dothidea.";
RL Mycologia 96:83-101(2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Slippers B., Vermeulen G., Crous P.W., Coutinho T.A., Wingfield B.D.,
RA Wingfield M.J.;
RT "Multiple gene sequences delimit Botryosphaeria australis sp. nov. as
RT a sister species to B. lutea.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY236891; AAP87155.1; -
DR EMBL; AY336892; AAP87156.1; -
DR EMBL; AY339266; AAQ75704.1; -
DR GO; GO:0003746; F:translation elongation factor activity; IEA.
KW Elongation factor.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1394 MW; D5F1817FF18C1DDD CRC64;

Query Match 36.1%; Score 26; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGKST 9
DB 6 AAELGKGS 13

RESULT 15
QXEX18 PRELIMINARY; PRT; 13 AA.
AC Q6XE18;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Translation elongation factor 1 alpha (Fragment).
OS Botryosphaeria parva.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
OC Dothideomycetes et Chaetothyriomycetes incertae sedis;
OC Botryosphaeriaceae; Botryosphaeria.
OX NCBI_TaxID=120390;
RN [1]
RP SEQUENCE FROM N.A.
RA Slippers B., Crous P.W., Denman S., Coutinho T.A., Wingfield B.D.,
RA Wingfield M.J.;
RT "Combined multiple gene genealogies and phenotypic characters
RT differentiate several species previously identified as Botryosphaeria
RT dothidea.";
RL Mycologia 96:83-101(2004).
DR EMBL; AY236880; AAP87144.1; -
DR EMBL; AY236881; AAP87145.1; -
DR EMBL; AY236882; AAP87146.1; -
DR EMBL; AY236883; AAP87147.1; -
DR EMBL; AY236884; AAP87148.1; -
DR EMBL; AY236885; AAP87149.1; -
DR EMBL; AY236886; AAP87150.1; -
DR EMBL; AY236887; AAP87151.1; -
DR EMBL; AY236888; AAP87152.1; -
DR EMBL; AY236889; AAP87153.1; -
DR EMBL; AY236890; AAP87154.1; -
DR GO; GO:0003746; F:translation elongation factor activity; IEA.
KW Elongation factor.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1394 MW; D5F1817FF18C1DDD CRC64;

Query Match 36.1%; Score 26; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGKST 9
DB 6 AAELGKGS 13

Search completed: April 1, 2005, 10:40:51
Job time : 117 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 09:33:38 ; Search time 117 Seconds
(without alignments)
42.973 Million cell updates/sec

Title: US-09-761-636A-5

Perfect score: 72

Sequence: 1 CASELGKSTNTFC 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 544453

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	13	4	Aau04524 VEGF base
2	69	95.8	13	4	Aau04534 VEGF base
3	65	90.3	13	4	Aau04535 VEGF base
4	65	90.3	13	4	Aau04537 VEGF base
5	61	84.7	13	4	Aau04536 VEGF base
6	32	44.4	12	3	Aay57039 Feline im
7	32	44.4	13	5	Abj04094 Immunoglo
8	31	43.1	9	7	Adi15745 HLA-A2 re
9	30	41.7	13	3	Aay66781 T cell an
10	29	40.3	10	4	Aab75626 HLA class
11	29	40.3	13	3	Aay66787 T cell an
12	29	40.3	13	5	Abj04095 Immunoglo
13	28	38.9	9	2	Aay48678 Membrane
14	28	38.9	9	3	Aab10896 Human 9p7
15	28	38.9	9	5	Aae26783 Fibrin bi
16	28	38.9	9	8	Adi36130 Fibrin bi
17	28	38.9	10	3	Aab10895 Human 9p7
18	28	38.9	13	5	Abj04091 Immunoglo
19	28	38.9	13	5	Abj04088 Immunoglo
20	27	37.5	9	5	Abj04570 Bone marr
21	27	37.5	10	2	Aam42705 Antigenic
22	27	37.5	10	4	Aam43317 Mycoplasma
23	27	37.5	12	2	Aaw34877 Human tau
24	27	37.5	12	2	Aaw34865 Human tau
25	27	37.5	12	4	Aau28829 DPI trypt

26	27	37.5	12	4	Aau26477 Depressio
27	27	37.5	12	5	Abg67372 Human ADP
28	27	37.5	12	6	Ada23476 Alzheimer
29	27	37.5	13	3	Aab26567 Human Ige
30	27	37.5	13	4	Aau16900 Peptide #
31	27	37.5	13	5	Abj00485 Human Ige
32	27	37.5	13	5	Abj04090 Immunoglo
33	27	37.5	13	5	Abj04092 Immunoglo
34	27	37.5	13	5	Abj04093 Immunoglo
35	26	36.1	8	4	Aau08458 Peptide C
36	26	36.1	9	2	Aaw83264 NPF motif
37	26	36.1	9	2	Aaw67159 aPL immun
38	26	36.1	9	2	Aaw97980 Human syn
39	26	36.1	9	3	Aay76718 SCP-1 HLA
40	26	36.1	9	6	Abp74688 Human SCP
41	26	36.1	9	7	Adc09547 Epitope w
42	26	36.1	10	4	Aag84316 Arabidops
43	26	36.1	10	4	Aag96997 Human com
44	26	36.1	10	4	Aag96549 Human com
45	26	36.1	10	5	Abp47552 N. mening

ALIGNMENTS

RESULT 1
AAU04524
ID AAU04524 standard; peptide; 13 AA.
XX
AC AAU04524;
XX
DT 26-SEP-2001 (first entry)
XX
DE VEGF based monocyclic peptide 1.
XX
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..13 /note= "This bond cyclises the peptide"
XX
PN WO200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Achen MG, Hughes RA, Stackner S, Cendron A;
XX
DR WPI; 2001-442248/47.
XX
PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.
XX
PS Claim 49; Page 32; 102pp; English.
XX
CC The sequence represents a monomeric monocyclic peptide of the invention,
CC whose 3-dimensional structure is modelled on the expose loop of human
CC VEGF (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis.
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 13 AA;

Query Match 100.0%; Score 72; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
 DB 1 CASELGKSTNTFC 13

RESULT 2

AAU04534
 ID AAU04534 standard; peptide; 13 AA.

AC AAU04534;

DT 26-SEP-2001 (first entry)

DE VEGF based monocyclic peptide 12.

XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.

OS Synthetic.

XX Key Location/Qualifiers
 FH Disulfide-bond 1..13

FT /note= "This bond cyclises the peptide"

PN WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

PR 18-JAN-2000; 2000US-0176293P.

PR 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

PI Achen MG, Hughes RA, Stackler S, Cendron A;

XX WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine

PT residues.

PS Example 25; Page 47; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the exposed loop of human
 CC VEGF (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 13 AA;

Query Match 95.8%; Score 69; DB 4; Length 13;

Best Local Similarity 92.3%; Pred. No. 9e-05;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13

DB 1 CASELGKSTNTFC 13

RESULT 3

AAU04535

ID AAU04535 standard; peptide; 13 AA.

XX AAU04535;

DT 26-SEP-2001 (first entry)

XX VEGF based monocyclic peptide 13.

XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.

OS Synthetic.

XX Key Location/Qualifiers
 FH Disulfide-bond 1..13

FT /note= "This bond cyclises the peptide"

XX WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

PR 16-MAY-2000; 2000US-0204590P.

XX

PA (LUDW-) LUDWIG INST CANCER RES.
 XX Achen MG, Hughes RA, Stacker S, Cendron A;
 PI
 XX WPI; 2001-442248/47.
 DR
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX
 XX Example 25; Page 47; 102pp; English.
 PS
 XX The sequence represents a monomeric monocyclic peptide of the invention,
 XX whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidizing the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides), and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 13 AA;
 Query Match 90.3%; Score 65; DB 4; Length 13;
 Best Local Similarity 84.6%; Pred. No. 0.00043;
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CASELGKSTNTFC 13
 DB 1 CASELGKSTNTFC 13
 |||||:|||||
 RESULT 4
 ID AAU04537 standard; peptide; 13 AA.
 XX
 AC AAU04537;
 XX
 XX 26-SEP-2001 (first entry)
 DT
 XX VEGF based monocyclic peptide 15.
 DE
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 1..13
 FT /note= "This bond cyclises the peptide"
 XX

PN WO200152875-A1.
 XX
 PD 26-JUL-2001.
 XX
 XX 18-JAN-2001; 2001WO-US001533.
 XX
 XX 18-JAN-2000; 2000US-0176293P.
 PR
 PR 16-MAY-2000; 2000US-0204590P.
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA
 XX Achen MG, Hughes RA, Stacker S, Cendron A;
 PI
 XX WPI; 2001-442248/47.
 DR
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX
 XX Example 25; Page 47; 102pp; English.
 PS
 XX The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidizing the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides), and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 13 AA;
 Query Match 90.3%; Score 65; DB 4; Length 13;
 Best Local Similarity 84.6%; Pred. No. 0.00043;
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CASELGKSTNTFC 13
 DB 1 CASELGKSTNTFC 13
 |||||:|||||
 RESULT 5
 ID AAU04536 standard; peptide; 13 AA.
 XX
 AC AAU04536;
 XX
 XX 26-SEP-2001 (first entry)
 DT
 XX VEGF based monocyclic peptide 14.
 DE
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;

XX 08-NOV-2003; 2001WO-EP012933.
 XX
 XX 08-NOV-2000; 2000EP-00124418.
 PR
 XX (AFFI-) AFFINA IMMUNTECHNIK GMBH.
 PA
 PI Egner R, Winkler D, Roenspeck W, Kunze R;
 DR WPI; 2002-557447/59.
 XX
 XX New immunoglobulin-binding peptides, useful for removing autoantibodies
 PT from serum, e.g. for treating rheumatism, also related solid phases.
 PT
 XX Claim 3; Page 40; 54pp; German.
 PS
 XX The present invention relates to immunoglobulin binding peptides. These
 CC can be used to remove autoantibodies from solutions, particularly
 CC autoantibodies associated with autoimmune diseases such as rheumatism,
 CC multiple sclerosis and myasthenia gravis, from body fluids. The present
 CC sequence is a peptide of the invention
 XX
 XX Sequence 13 AA;
 SQ
 Query Match 44.4%; Score 32; DB 5; Length 13;
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CASELGGK 7
 DB |||||
 2 CASHLOK 8
 RESULT 8
 ADI15745
 ID ADI15745 standard; peptide; 9 AA.
 XX
 AC ADI15745;
 XX
 XX 22-APR-2004 (first entry)
 DT
 XX HLA-A2 restricted cytotoxic T lymphocyte recognised peptide #88.
 DE
 XX tumour; antigen; human leukocyte antigen; HLA-A2; HLA-A26;
 KW cytotoxic T-cell; CTL; vaccine; cancer; colorectal cancer;
 KW stomach cancer; buccal cancer; renal cancer; lung cancer;
 KW gynecological cancer; prostate cancer.
 XX
 OS Synthetic.
 XX
 PN WO2003008450-A1.
 XX
 PD 30-JAN-2003.
 XX
 PF 11-JUN-2002; 2002WO-JP005799.
 XX
 XX 12-JUN-2001; 2001JP-00177058.
 PR
 PR 21-AUG-2001; 2001JP-00250728.
 XX
 XX (ITOH/) ITOH K.
 PA
 XX Itoh K, Shichijo S;
 PI WPI; 2003-267996/26.
 DR
 XX Tumor antigen peptides recognized by human leukocyte antigen (HLA)-A2 or
 PT HLA-A26 restricted cytotoxic T-cells for treatment and prevention of
 PT cancer including preparation of cancer vaccines.
 XX
 PS Claim 1; SEQ ID NO 89; 323pp; Japanese.
 XX
 XX The invention relates to a tumour antigen peptide recognised by human
 CC leukocyte antigen (HLA)-A2 or HLA-A26 restricted cytotoxic T-cells (CTL)

CC and/or capable of inducing CTL. The tumour antigen peptide is useful for
 CC the treatment, prevention, diagnosis and vaccine production for cancers
 CC including colorectal, stomach, buccal, lung, gynecological and
 CC prostate cancer. The present sequence represents a peptide recognised by
 CC HLA-A2 restricted cytotoxic T lymphocytes.
 XX
 SQ Sequence 9 AA;
 Query Match 43.1%; Score 31; DB 7; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 7 KSTNTFC 13
 DB |||||
 1 KLTNTYC 7
 RESULT 9
 AAY66781
 ID AAY66781 standard; peptide; 13 AA.
 XX
 AC AAY66781;
 XX
 XX 11-APR-2000 (first entry)
 DT
 XX T cell antigen receptor Vbeta 5 chain peptide.
 DE
 XX Rheumatoid arthritis; arthrosis deformans; T-cell antigen receptor;
 KW Vbeta chain; autoantigen; immunological tolerance.
 KW
 XX Homo sapiens.
 OS
 XX WO9963084-A1.
 PN
 XX 09-DEC-1999.
 PD
 XX 28-MAY-1999; 99WO-JP002814.
 PF
 XX 29-MAY-1998; 98JP-00149855.
 PR
 PR 14-OCT-1998; 98JP-00328761.
 XX
 XX (TORI) TORII PHARM CO LTD.
 PA
 XX Nishioka K, Yoshino S;
 PI WPI; 2000-086978/07.
 DR
 DR N-PSDB; AA296511.
 XX
 XX T-cell antigen receptor V-beta chain CDR3 region sequences accumulated in
 PT synovial membranes of rheumatoid arthritis patients.
 PS
 XX Example 3; Page 25; 136pp; Japanese.
 CC
 CC The invention relates to peptide sequences present in the synovial fluid
 CC and membranes of rheumatoid arthritis patients, arising from the CDR
 CC region of oligoclonal pathogenic T-cell antigen receptor Vbeta chains.
 CC Compositions which contain autoantigenic peptide binding specifically to
 CC T-cells expressing receptors containing the peptide sequences, which
 CC include antigen-specific immunological tolerance to rheumatoid arthritis
 CC can be used for the treatment and prevention of rheumatoid arthritis. The
 CC invention can be used for the diagnosis, treatment and prevention of
 CC rheumatoid arthritis. Sequences AAY66771-958 represent peptides from the
 CC various Vbeta chains of T cell antigen receptor
 XX
 SQ Sequence 13 AA;
 Query Match 41.7%; Score 30; DB 3; Length 13;
 Best Local Similarity 41.7%; Pred. No. 4e+02;
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CASELGGKSTNTF 12
 DB |||||
 2 CASSIGTNEQF 13

```

RESULT 10
AAB75626
ID AAB75626 standard; peptide; 10 AA.
XX
AC AAB75626;
XX
DT 10-APR-2001 (first entry)
XX
DE HLA class I binding motif in HOM-TES-84 SEQ ID NO:29.
XX
KW Human; cancer associated antigen precursor; cancer associated antigen;
KW seminoma; HLA; human leukocyte antigen; cytostatic; gene therapy;
KW vaccine; cancer.
XX
OS Homo sapiens.
XX
PN WO200100874-A2.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-US017207.
XX
PR 30-JUN-1999; 99US-00346498.
XX
PS (LUDW-) LUDWIG INST CANCER RES.
XX
PI Sahin U, Tureci O, Pfreundschuh M;
XX
DR WPI; 2001-112465/12.
XX
PT Diagnosing a disorder characterized by expression of a human cancer
PT associated antigen precursor, comprises detecting interaction of an agent
PT with a nucleic acid molecule encoding the antigen precursor.
XX
PS Example 10; Page 62; 126pp; English.
XX
CC The present invention describes a method for diagnosing a disorder
CC characterised by expression of a human cancer associated antigen (CAA)
CC precursor (I) coded by a NA Group 1 nucleic acid molecule (NI) comprising
CC contacting the biological sample with an agent (A) that specifically
CC binds to NI, (I) or its fragment, complexed with an human leukocyte
CC antigen (HLA) molecule and determining the interaction between the agent
CC and NI or (I). (I) has cytostatic activity and can be used in gene
CC therapy and vaccine production. The method can be used for treating a
CC subject with a condition characterised by expression of (I) in cells of a
CC subject. AAB75607 and AAB75608 represent proteins from human cancer
CC associated antigen precursors, and AAB75609 to AAB75802 represent HLA
CC class I binding motifs in human cancer associated antigen precursors
CC given in the exemplification of the present invention
XX
SQ Sequence 10 AA;
Query Match 40.3%; Score 29; DB 4; Length 10;
Best Local Similarity 60.0%; Pred.No. 4.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 4 ELGKSTNTFC 13
DB 1 KLGPSFNTNC 10
RESULT 11
AAY66787
ID AAY66787 standard; peptide; 13 AA.
XX
AC AAY66787;
XX
DT 11-APR-2000 (first entry)
XX
DE T cell antigen receptor Vbeta 10 chain peptide.
XX
KW Rheumatoid arthritis; arthrosis deformans; T-cell antigen receptor;
KW Vbeta chain; autoantigen; immunological tolerance.
XX
OS Homo sapiens.
XX
PN WO9963084-A1.
XX
PD 09-DEC-1999.
XX
PF 28-MAY-1999; 99WO-JP002814.
XX
PR 29-MAY-1998; 98JP-00149855.
PR 14-OCT-1998; 98JP-00328761.
XX
PA (TORI) TORII PHARM CO LTD.
XX
PI Nishioka K, Yoshino S;
XX
DR WPI; 2000-086978/07.
DR N-PSDB; AA296517.
XX
PT T-cell antigen receptor V-beta chain CDR3 region sequences accumulated in
PT synovial membranes of rheumatoid arthritis patients.
XX
PS Example 3; Page 29; 136pp; Japanese.
XX
CC The invention relates to peptide sequences present in the synovial fluid
CC and membranes of rheumatoid arthritis patients, arising from the CDR
CC region of oligoclonal pathogenic T-cell antigen receptor Vbeta chains.
CC Compositions which contain autoantigenic peptides binding specifically to
CC T-cells expressing receptors containing the peptide sequences, which
CC include antigen-specific immunological tolerance to rheumatoid arthritis
CC can be used for the treatment and prevention of rheumatoid arthritis. The
CC invention can be used for the diagnosis, treatment and prevention of
CC rheumatoid arthritis. Sequences AA16771-958 represent peptides from the
CC various Vbeta chains of T cell antigen receptor
XX
SQ Sequence 13 AA;
Query Match 40.3%; Score 29; DB 3; Length 13;
Best Local Similarity 66.7%; Pred.No. 5.9e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CASELKGKST 9
DB 2 CASSKGKST 10
RESULT 12
ABJ04095
ID ABJ04095 standard; peptide; 13 AA.
XX
AC ABJ04095;
XX
DT 01-OCT-2002 (first entry)
XX
DE Immunoglobulin binding peptide #15.
XX
KW Immunoglobulin binding peptide; autoimmune disease; rheumatoid arthritis;
KW multiple sclerosis; myasthenia gravis; immunosuppressive; antirheumatic;
KW neuroprotective.
XX
OS Synthetic.
XX
PN WO200238592-A2.
XX
PD 16-MAY-2002.
XX
PF 08-NOV-2001; 2001WO-EP012933.
XX
PR 08-NOV-2000; 2000EP-00124418.
XX
PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.

```

XX PI Egner R, Winkler D, Roenspeck W, Kunze R;
XX WPI; 2002-557447/59.
XX New immunoglobulin-binding peptides, useful for removing autoantibodies
XX from serum, e.g. for treating rheumatism, also related solid phases.
XX Claim 3; Page 40; 54pp; German.
XX The present invention relates to immunoglobulin binding peptides. These
XX can be used to remove autoantibodies from solutions, particularly
XX autoantibodies associated with autoimmune diseases such as rheumatism,
XX multiple sclerosis and myasthenia gravis, from body fluids. The present
XX sequence is a peptide of the invention
XX Sequence 13 AA;
SQ
Query Match 40.3%; Score 29; DB 5; Length 13;
Best Local Similarity 71.4%; Pred. No. 5.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CASELKG 7
Db 2 CATHLKG 8
||: |||
||: |||
RESULT 13
AAAY48678
ID AAY48678 standard; peptide; 9 AA.
XX AC AAY48678;
XX 20-MAR-2003 (revised)
XX 10-DEC-1999 (first entry)
XX Membrane dipeptidase-binding lung homing peptide #49.
DE Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
XX prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
XX membrane dipeptidase.
XX Synthetic.
OS Homo sapiens.
XX WO9946284-A2.
XX 16-SEP-1999.
XX 10-MAR-1999; 99WO-US005284.
XX 13-MAR-1998; 98US-00042107.
XX 26-FEB-1999; 99US-00258754.
XX (BURN-) BURNHAM INST.
XX Rajotte D, Pasqualini R, Ruoslahti EI;
XX WPI; 1999-571717/48.
XX New peptides which selectively home to organs or tissues, used for, e.g.
XX identifying target ligands and for therapy of pathological conditions.
XX Example 6; Page 144; 193pp; English.
XX The present invention describes peptides that selectively home to a
XX tissue or organ. The peptides can be used for identifying an organ or
XX tissue, for identifying a target molecule expressed by an organ or tissue
XX or for treating an organ or tissue pathology, where the organ or tissue
XX is selected from prostate, lung, skin, retina, pancreas, gut, ovary,
XX adrenal gland, liver, and lymph node. The peptide bind to the membrane
XX dipeptidase (MDP). AAY48618 to AAY49066 represent sequences which are
XX used in the exemplification of the present invention. (Updated on 20-MAR-

XX 2003 to correct PR field.)
XX Sequence 9 AA;
SQ
Query Match 38.9%; Score 28; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 7 KSTNTFC 13
Db 3 RSTNTGC 9
: || || |
: || || |
RESULT 14
AAB10896
ID AAB10896 standard; protein; 9 AA.
XX AC AAB10896;
XX 26-JAN-2001 (first entry)
XX Human 9D7 protein immunogenic fragment SEQ ID NO: 55.
XX Tumor-associated antigen; 9D7; human; cytostatic; immunogenic;
XX immunotherapy; cancer; cellular anticancer vaccine; diagnostic; kidney;
XX lung; colon; breast; carcinoma; Hodgkin's lymphoma.
XX Homo sapiens.
XX DE19909503-A1.
XX 07-SEP-2000.
XX 04-MAR-1999; 99DE-01009503.
XX 04-MAR-1999; 99DE-01009503.
XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
XX Klade C, Adolf G, Sommergruber W, Heider K;
XX WPI; 2000-588357/56.
XX New tumor-associated antigen 9D7, useful e.g. for immunotherapy of cancer
XX and for producing diagnostic or therapeutic antibodies.
XX Claim 6; Page 45; 50pp; German.
XX This invention describes a novel tumor-associated antigen, designated 9D7
XX which has cytostatic activity. The invention also describes a method for
XX isolating (a) a polypeptide (I) that includes (S1) as part of its
XX sequence; (b) an immunogenic protein fragment or peptide (II) derived
XX from 9D7; (c) a pharmaceutical composition containing at least 1 of 9D7,
XX (I) or (II) as active ingredients; (d) an isolated DNA (III) encoding a
XX protein (IV) with the immunogenic properties of 9D7 or its fragments; (e)
XX a recombinant DNA (IIIA) that includes (III); and (f) antibodies (Ab)
XX directed against 9D7, (I) or (II). 9D7, or its derived immunogenic
XX peptides, are used to induce a humoral and/or cellular response for use
XX in vivo or ex vivo immunotherapy of cancer. DNA (III) that encodes 9D7
XX can be used similarly and cells that express 9D7 are useful for
XX anticancer vaccines. Antibodies (Ab) specific for 9D7 are useful for
XX imaging, diagnosing and monitoring cancers, also, when conjugated to
XX cytotoxins or radionuclide, as therapeutic agents. Peptides derived from
XX 9D7 may also be used diagnostically to test for an immune response. 9D7-
XX associated cancers are particularly kidney, lung, colon and breast
XX carcinoma and Hodgkin's lymphoma. AAB10874-B10899 represent immunogenic
XX fragments of the human tumor-associated antigen 9D7 which is described in
XX the method of the invention
XX Sequence 9 AA;
SQ
Query Match 38.9%; Score 28; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.8e+06;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELGK 7
| | | |
Db 3 CGSRLGK 9

RESULT 15
AAE26783
ID AAE26783 standard; peptide; 9 AA.
XX
AC AAE26783;
XX
DT 13-DEC-2002 (first entry)
XX
DE Fibrin binding peptide #36.
XX
KW Fibrin binding peptide; thrombosis; pulmonary embolism; atherosclerosis;
KW myocardial infarct; ischaemia; imaging; rheumatoid arthritis; vasotropic;
KW anaemia; hypoxia; tumour; diabetic retinopathy; autoimmune disorder;
KW inflammatory disorder; angiogenesis; stroke; cerebroprotective.
XX
OS Unidentified.
XX
PN WO200255544-A2.
XX
PD 18-JUL-2002.
XX
PF 21-DEC-2001; 2001WO-US049534.
XX
PR 23-DEC-2000; 2000US-00747403.
XX
PA (DYAX-) DYAX CORP.
XX
PI Wescott CR, Beltzer JP, Sato AK;
XX
DR WPI; 2002-666875/71.
XX
PT Novel synthetic fibrin-binding moiety, useful for detecting, imaging or
PT localizing fibrin-containing clots by magnetic resonance imaging,
PT radioimaging and for treating diseases involving thrombus formation e.g.
PT stroke.
XX
PS Claim 4; Page 55; 89pp; English.
XX

CC binding peptide
XX
SQ Sequence 9 AA;
Query Match 38.9%; Score 28; DB 5; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 6 GKSTNTFC 13
| : | | |
Db 2 QGSRFTFC 9

Search completed: April 1, 2005, 10:38:43
Job time : 118 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2005, 10:40:58 ; Search time 93 Seconds
(without alignments)

46.352 Million cell updates/sec

Title: US-09-761-636A-5

Perfect score: 72

Sequence: 1 CASELGKSTNTFC 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 220024

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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- 3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09D_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	69	95.8	13	9	US-09-761-636A-15
3	65	90.3	13	9	US-09-761-636A-16
4	65	90.3	13	9	US-09-761-636A-18
5	61	84.7	13	9	US-09-761-636A-17
6	32	44.4	13	15	US-10-415-665-14
7	31	43.1	9	17	US-10-734-049A-89
8	30	41.7	10	14	US-10-208-304-14
9	29	40.3	13	15	US-10-415-665-15
10	28	38.9	9	14	US-10-034-974-55
11	28	38.9	9	17	US-10-838-289-170
12	28	38.9	13	15	US-10-415-665-8
13	28	38.9	13	15	US-10-415-665-11

14	27	37.5	10	10	US-09-573-822C-626	Sequence 626, Appl
15	27	37.5	10	14	US-10-271-343-19	Sequence 19, Appl
16	27	37.5	12	9	US-09-142-613-23	Sequence 22, Appl
17	27	37.5	12	10	US-09-791-393-262	Sequence 262, Appl
18	27	37.5	12	10	US-09-791-389-262	Sequence 262, Appl
19	27	37.5	12	14	US-10-014-340-84	Sequence 84, Appl
20	27	37.5	13	14	US-10-322-210-67	Sequence 67, Appl
21	27	37.5	13	14	US-10-304-443-67	Sequence 67, Appl
22	27	37.5	13	15	US-10-362-527-269	Sequence 269, Appl
23	27	37.5	13	15	US-10-415-665-10	Sequence 10, Appl
24	27	37.5	13	15	US-10-415-665-13	Sequence 13, Appl
25	27	37.5	13	15	US-10-415-665-13	Sequence 13, Appl
26	26	36.1	8	9	US-09-795-006A-140	Sequence 140, Appl
27	26	36.1	9	15	US-10-117-937-572	Sequence 572, Appl
28	26	36.1	9	15	US-10-044-844-70	Sequence 70, Appl
29	26	36.1	10	10	US-09-572-404B-2743	Sequence 2743, Appl
30	26	36.1	10	10	US-09-572-404B-3191	Sequence 3191, Appl
31	26	36.1	10	10	US-09-572-270A-956	Sequence 956, Appl
32	26	36.1	10	14	US-10-208-304-12	Sequence 12, Appl
33	26	36.1	10	14	US-10-208-304-13	Sequence 13, Appl
34	26	36.1	10	14	US-10-208-304-15	Sequence 15, Appl
35	26	36.1	10	14	US-10-208-304-16	Sequence 16, Appl
36	26	36.1	10	15	US-10-117-937-573	Sequence 573, Appl
37	26	36.1	10	15	US-10-398-104-128	Sequence 128, Appl
38	26	36.1	11	15	US-10-398-104-153	Sequence 153, Appl
39	26	36.1	11	15	US-10-398-104-268	Sequence 268, Appl
40	26	36.1	11	15	US-10-415-665-82	Sequence 82, Appl
41	26	36.1	12	9	US-09-142-613-10	Sequence 10, Appl
42	26	36.1	12	15	US-10-415-665-66	Sequence 66, Appl
43	26	36.1	12	15	US-10-415-665-74	Sequence 74, Appl
44	26	36.1	12	16	US-10-363-204-231	Sequence 231, Appl
45	26	36.1	12	17	US-10-938-056-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1

US-09-761-636A-5
; Sequence 5, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-5

Query Match 100.0%; Score 72; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.8e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13

DB 1 CASELGKSTNTFC 13

RESULT 2

US-09-761-636A-15

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; Sequence 15, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-15

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Query Match          95.8%; Score 69; DB 9; Length 13;
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Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CASELGKSTNTFC 13
Db 1 CASELGKSTNTFC 13

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RESULT 3
US-09-761-636A-16
; Sequence 16, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-16

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Query Match          90.3%; Score 65; DB 9; Length 13;
Best Local Similarity 84.6%; Pred. No. 0.00016;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CASELGKSTNTFC 13
Db 1 CASELGKSTNTFC 13

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RESULT 4
US-09-761-636A-18
; Sequence 18, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven

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; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-18

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Query Match          90.3%; Score 65; DB 9; Length 13;
Best Local Similarity 84.6%; Pred. No. 0.00016;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CASELGKSTNTFC 13
Db 1 CASELGKSTNTFC 13

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RESULT 5
US-09-761-636A-17
; Sequence 17, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-17

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Best Local Similarity 76.9%; Pred. No. 0.00083;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CASELGKSTNTFC 13
Db 1 CASELGKSTNTFC 13

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RESULT 6
US-10-415-665-14
; Sequence 14, Application US/10415665
; Publication No. US20040087765A1
; GENERAL INFORMATION:
; APPLICANT: Egner, Ralf
; APPLICANT: Kunze, Rudolf
; APPLICANT: Winkler, Dirk
; APPLICANT: Roenspeck, Wolfgang
; TITLE OF INVENTION: Peptides, Preparation Thereof and Use Thereof for
; TITLE OF INVENTION: Binding Immunoglobulins
; FILE REFERENCE: P68842USO

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; CURRENT APPLICATION NUMBER: US/10/415,665
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: PCT/EP01/12933
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: EP00124418.5
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence:
; OTHER INFORMATION: synthetic peptide having affinity for
; OTHER INFORMATION: immunoglobulins
US-10-415-665-14

Query Match 44.4%; Score 32; DB 15; Length 13;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELGK 7
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Db 2 CASHLGK 8
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RESULT 7

US-10-734-049A-89
; Sequence 89, Application US/10734049A
; Publication No. US20050042624A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyogo
; APPLICANT: SHICHIO, Shigeki
; TITLE OF INVENTION: TUMOR ANTIGEN
; FILE REFERENCE: Q-78382
; CURRENT APPLICATION NUMBER: US/10/734, 049A
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/JP02/05799
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: JP 2001/177058
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001/250728
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 408
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 89
; LENGTH: 9
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; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Designed peptide recognized by HLA-A2 restricted cytokine T
; OTHER INFORMATION: lymphocytes
US-10-734-049A-89

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Best Local Similarity 71.4%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 KSTNTFC 13
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Db 1 KLNTNYC 7
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RESULT 8

US-10-208-304-14
; Sequence 14, Application US/10208304
; Publication No. US20030124571A1
; GENERAL INFORMATION:
; APPLICANT: Larisch, Savit
; APPLICANT: Kim, Seong-Jin
; APPLICANT: Lechleider, Robert J.
; APPLICANT: Roberts, Anita B.

; APPLICANT: Yi, Youngaek
; TITLE OF INVENTION: NOVEL HUMAN SEPTIN AND USES THEREFOR
; FILE REFERENCE: 11613.42USWI
; CURRENT APPLICATION NUMBER: US/10/208, 304
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: PCT/US01/02466
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/178,866
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/258,725
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Drosophila
; ORGANISM: Drosophila
US-10-208-304-14

Query Match 41.7%; Score 30; DB 14; Length 10;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGKST 9
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Db 2 ASGLGKST 9
|||

RESULT 9

US-10-415-665-15
; Sequence 15, Application US/10415665
; Publication No. US20040087765A1
; GENERAL INFORMATION:
; APPLICANT: Egner, Ralf
; APPLICANT: Kunze, Rudolf
; APPLICANT: Winkler, Dirk
; APPLICANT: Roenspeck, Wolfgang
; TITLE OF INVENTION: Peptides, Preparation Thereof and Use Thereof for
; TITLE OF INVENTION: Binding Immunoglobulins
; FILE REFERENCE: P68842USO
; CURRENT APPLICATION NUMBER: US/10/415,665
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: PCT/EP01/12933
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: EP00124418.5
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence:
; OTHER INFORMATION: synthetic peptide having affinity for
; OTHER INFORMATION: immunoglobulins
US-10-415-665-15

Query Match 40.3%; Score 29; DB 15; Length 13;
Best Local Similarity 71.4%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELGK 7
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Db 2 CATHLGK 8
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RESULT 10

US-10-034-974-55
; Sequence 55, Application US/10034974
; Publication No. US20030143158A1
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP.

; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 626
; LENGTH: 10
; TYPE: PRT
; ORGANISM: mycoplasma genitalium
; FEATURE:
; OTHER INFORMATION: Sequence located in MG309 at 847-856 and may interact with Sequen
; OTHER INFORMATION: in this patent.
US-09-573-822C-626

Query Match 37.5%; Score 27; DB 10; Length 10;
Best Local Similarity 40.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 SELGKSTNIF 12
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DB 1 AKLSRTNSF 10

RESULT 15
US-10-271-343-19
; Sequence 19, Application US/10271343
; Publication No. US20030166003A1
; GENERAL INFORMATION:
; APPLICANT: Cochran, Andrea G.
; APPLICANT: Skelton, Nicholas J.
; APPLICANT: Starovasinik, Melissa A.
; TITLE OF INVENTION: A STRUCTURED PEPTIDE SCAFFOLD FOR DISPLAYING TURN LIBRARIES
; TITLE OF INVENTION: ON PHASE
; FILE REFERENCE: 11669.116US11
; CURRENT APPLICATION NUMBER: US/10/271,343
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/592,695
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 60/139,017
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Turn Peptide
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa is independently Trp, Tyr, Leu, Val, or Thr
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (5)..(5)
; OTHER INFORMATION: Xaa is D-pro
US-10-271-343-19

Query Match 37.5%; Score 27; DB 14; Length 10;
Best Local Similarity 55.6%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CASELGKST 9
| | | | |
DB 1 CTXEXGKLT 9

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2005, 07:04:23 ; Search time 19.9726 Seconds
(without alignments)
33.638 Million cell updates/sec

Title: US-09-761-636A-14

Perfect score: 52

Sequence: 1 CISVPLVPC 9

Scoring table: BLOSUM62

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	78.8	342	1	US-08-499-215-5
2	40	76.9	86	4	US-09-270-767-59896
3	38	73.1	44	4	US-09-341-461-10
4	38	73.1	198	4	US-09-673-763-10
5	38	73.1	589	4	US-09-328-352-6901
6	38	73.1	3623	4	US-09-341-461-2
7	37	71.2	64	4	US-09-513-999C-4539
8	37	71.2	168	4	US-09-252-991A-27872
9	36	69.2	455	4	US-09-489-039A-13375
10	35	67.3	48	4	US-09-270-767-34100
11	35	67.3	48	4	US-09-270-767-49317
12	35	67.3	90	4	US-09-252-991A-20960
13	35	67.3	309	4	US-09-640-211A-2187
14	35	67.3	370	4	US-09-640-211A-823
15	35	67.3	556	4	US-09-949-016-7027
16	35	67.3	565	4	US-09-949-016-10036
17	35	67.3	1440	3	US-09-357-251-37
18	35	67.3	1512	3	US-09-443-184-48
19	34	65.4	96	4	US-09-540-236-2315
20	34	65.4	147	4	US-09-252-991A-23997
21	34	65.4	215	1	US-08-107-684B-11
22	34	65.4	424	4	US-09-949-016-7642
23	34	65.4	571	4	US-09-902-540-16194
24	34	65.4	833	4	US-09-949-016-9530
25	34	65.4	966	4	US-09-949-016-6669
26	34	65.4	1164	4	US-09-902-540-12627
27	34	65.4	1876	2	US-08-609-049A-12

28	34	65.4	1876	2	US-08-609-049A-28	Sequence 28, Appl
29	34	65.4	1876	3	US-09-170-996-12	Sequence 12, Appl
30	34	65.4	1876	3	US-09-170-996-28	Sequence 28, Appl
31	33	63.5	20	3	US-09-461-697-169	Sequence 169, App
32	33	63.5	32	3	US-09-461-697-167	Sequence 167, App
33	33	63.5	168	4	US-09-270-767-40328	Sequence 40328, A
34	33	63.5	168	4	US-09-270-767-55544	Sequence 55544, A
35	33	63.5	322	4	US-09-543-681A-4992	Sequence 4992, Ap
36	33	63.5	344	4	US-09-270-767-58767	Sequence 58767, A
37	33	63.5	621	4	US-09-270-767-43417	Sequence 43417, A
38	33	63.5	762	4	US-09-270-767-40204	Sequence 40204, A
39	33	63.5	762	4	US-09-270-767-55420	Sequence 55420, A
40	33	63.5	994	4	US-09-543-681A-7288	Sequence 7288, Ap
41	33	63.5	1253	1	US-07-920-281C-3	Sequence 3, Appli
42	33	63.5	1253	3	US-08-466-277-3	Sequence 3, Appli
43	33	63.5	1253	4	US-09-688-842-3	Sequence 3, Appli
44	32.5	62.5	62	4	US-09-621-976-4988	Sequence 4988, Ap
45	32	61.5	109	4	US-09-087-031E-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-499-215-5
; Sequence 5, Application US/08499215
; Patent No. 5612204
; GENERAL INFORMATION:
; APPLICANT: Saeki, Hisashi
; APPLICANT: Miura, Akira
; TITLE OF INVENTION: BIOLOGICAL DEGRADATIVE
; TITLE OF INVENTION: TREATMENT OF CHLORINE-SUBSTITUTED ETHYLENE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue
; CITY: N.W.
; STATE: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; SOFTWARE: & WordPerfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/499,215
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP Hei-6-179689
; FILING DATE: 08-JUL-1994
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-499-215-5

Query Match 78.8%; Score 41; DB 1; Length 342;
Best Local Similarity 77.8%; Pred. NO. 33;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9
DB 75 CASVPLEPC 83

RESULT 2
US-09-270-767-59896
; Sequence 59896, Application US/09270767

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; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59896
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-59896

Query Match          76.9%; Score 40; DB 4; Length 86;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1  CTSVPLVPC 9
Db      11 CLSVFPFPC 19
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RESULT 3
US-09-341-461-10
; Sequence 10, Application US/09341461
; Patent No. 6586389
; GENERAL INFORMATION:
; APPLICANT: Hammond, Timothy G.
; APPLICANT: Verroust, Pierre J.
; TITLE OF INVENTION: Cubilin Protein, DNA Sequences Encoding Cubilin
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: D6148
; CURRENT APPLICATION NUMBER: US/09/341,461
; CURRENT FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: PCT/US99/01259
; PRIOR FILING DATE: 1999-01-21
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 10
; LENGTH: 44
; TYPE: PRT
; ORGANISM: rat
; FEATURE:
; OTHER INFORMATION: amino acid sequence of rat cubilin EGP5 repeat
US-09-341-461-10

Query Match          73.1%; Score 38; DB 4; Length 44;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  CTSVPLVPC 9
Db      12 CSQAPLVPC 20
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RESULT 4
US-09-673-763-10
; Sequence 10, Application US/09673763
; Patent No. 6746676
; GENERAL INFORMATION:
; APPLICANT: Oregon State University
; TITLE OF INVENTION: Methods of use for infection-specific INCA, INCB, and
; TITLE OF INVENTION: INCC proteins of Chlamydia
; FILE REFERENCE: 52297
; CURRENT APPLICATION NUMBER: US/09/673,763
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/082,588
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082,438
; PRIOR FILING DATE: 1998-04-20
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; PRIOR APPLICATION NUMBER: 60/086,450
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Chlamydia psittaci
US-09-673-763-10

Query Match          73.1%; Score 38; DB 4; Length 198;
Best Local Similarity 55.6%; Pred. No. 58;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1  CTSVPLVPC 9
Db      157 CTSPLPISC 165
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RESULT 5
US-09-328-352-6901
; Sequence 6901, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6901
; LENGTH: 589
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6901

Query Match          73.1%; Score 38; DB 4; Length 589;
Best Local Similarity 77.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  CTSVPLVPC 9
Db      273 CTSVPLFHC 281
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RESULT 6
US-09-341-461-2
; Sequence 2, Application US/09341461
; Patent No. 6586389
; GENERAL INFORMATION:
; APPLICANT: Hammond, Timothy G.
; APPLICANT: Verroust, Pierre J.
; TITLE OF INVENTION: Cubilin Protein, DNA Sequences Encoding Cubilin
; TITLE OF INVENTION: and Uses thereof
; FILE REFERENCE: D6148
; CURRENT APPLICATION NUMBER: US/09/341,461
; CURRENT FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: PCT/US99/01259
; PRIOR FILING DATE: 1999-01-21
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 2
; LENGTH: 3623
; TYPE: PRT
; ORGANISM: rat
; FEATURE:
; OTHER INFORMATION: amino acid sequence of rat cubilin protein
US-09-341-461-2

Query Match          73.1%; Score 38; DB 4; Length 3623;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 C1SVPLVPC 9
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Db 313 CSOAPLVPC 321

RESULT 7
US-09-513-999C-4539
; Sequence 4539, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4539
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -19...-1
; OTHER INFORMATION: score 3.9
; OTHER INFORMATION: seq SVCLCPCLNKQGS/EN
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 37
; OTHER INFORMATION: Xaa = * or Trp
US-09-513-999C-4539

Query Match 71.2%; Score 37; DB 4; Length 64;
Best Local Similarity 77.8%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 C1SVPLVPC 9
| | | | |
Db 5 C1SVCLCPC 13

RESULT 8
US-09-252-991A-27872
; Sequence 27872, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27872
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27872

Query Match 71.2%; Score 37; DB 4; Length 168;
Best Local Similarity 55.6%; Pred. No. 71;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 C1SVPLVPC 9

Db 37 CTSIPGIPC 45
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RESULT 9
US-09-489-039A-13375
; Sequence 13375, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709-2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13375
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13375

Query Match 69.2%; Score 36; DB 4; Length 455;
Best Local Similarity 66.7%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 C1SVPLVPC 9
| | | | |
Db 8 CYYFPLVPC 16

RESULT 10
US-09-270-767-34100
; Sequence 34100, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34100
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-34100

Query Match 67.3%; Score 35; DB 4; Length 48;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 C1SVPLVPC 9
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Db 9 C1SMKVPVC 17

RESULT 11
US-09-270-767-49317
; Sequence 49317, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49317

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; LENGTH: 48
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-49317

Query Match      67.3%; Score 35; DB 4; Length 48;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 C1SVPLVPC 9
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Db 9 C1SMSKVP 17

RESULT 12
US-09-252-991A-20960
; Sequence 20960, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20960
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20960

Query Match      67.3%; Score 35; DB 4; Length 90;
Best Local Similarity 55.6%; Pred. No. 79;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 C1SVPLVPC 9
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Db 12 C1SCPVP 20

RESULT 13
US-09-640-211A-2187
; Sequence 2187, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2187
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-640-211A-2187

Query Match      67.3%; Score 35; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPLVPC 9
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Db 262 VPLVPC 267

RESULT 14
US-09-640-211A-823
; Sequence 823, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 823
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-640-211A-823

Query Match      67.3%; Score 35; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPLVPC 9
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Db 262 VPLVPC 267

RESULT 15
US-09-949-016-7027
; Sequence 7027, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7027
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7027

Query Match      67.3%; Score 35; DB 4; Length 556;
Best Local Similarity 85.7%; Pred. No. 5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SVPLVPC 9
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Db 121 SAPLVPC 127

Search completed: April 1, 2005, 09:36:20
Job time : 20.9726 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 07:04:23 ; Search time 22.1918 Seconds
(without alignments)
33.638 Million cell updates/sec

Title: US-09-761-636A-13

Perfect score: 56

Sequence: 1 CISVPLSVPC 10

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	71.4	198	4	US-09-270-767-44459
2	39	69.6	244	4	US-09-252-991A-32454
3	39	69.6	306	4	US-09-252-991A-23169
4	37	66.1	142	4	US-09-252-991A-23382
5	37	66.1	154	4	US-09-252-991A-18804
6	36	64.3	9	1	US-08-331-383-33
7	36	64.3	9	1	US-08-549-008-43
8	36	64.3	9	3	US-08-802-981-143
9	36	64.3	92	4	US-09-252-991A-29933
10	36	64.3	121	4	US-09-513-999C-8157
11	36	64.3	192	4	US-09-621-976-5605
12	36	64.3	341	4	US-09-252-991A-29740
13	36	64.3	510	4	US-09-252-991A-26663
14	36	64.3	581	4	US-09-538-092-383
15	36	64.3	700	4	US-09-252-991A-19384
16	35	62.5	178	4	US-09-902-540-10963
17	35	62.5	183	4	US-09-252-991A-30161
18	35	62.5	201	4	US-09-198-452A-145
19	35	62.5	760	4	US-09-438-185A-128
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21	34.5	61.6	72	4	US-09-334-951-58
22	34.5	61.6	72	4	US-09-334-923A-58
23	34.5	61.6	72	4	US-09-334-954A-58
24	34.5	61.6	73	3	US-08-722-719-26
25	34.5	61.6	73	3	US-08-722-719-57
26	34.5	61.6	73	4	US-09-334-951-26
27	34.5	61.6	73	4	US-09-334-951-57

28	34.5	61.6	73	4	US-09-334-923A-26	Sequence 26, Appl
29	34.5	61.6	73	4	US-09-334-923A-57	Sequence 57, Appl
30	34.5	61.6	73	4	US-09-689-693-26	Sequence 26, Appl
31	34.5	61.6	73	4	US-09-334-954A-26	Sequence 26, Appl
32	34.5	61.6	73	4	US-09-334-954A-57	Sequence 57, Appl
33	34.5	61.6	73	4	US-09-571-013-30	Sequence 30, Appl
34	34.5	61.6	74	4	US-09-689-693-39	Sequence 39, Appl
35	34.5	61.6	74	4	US-09-571-013-58	Sequence 58, Appl
36	34.5	61.6	75	3	US-08-722-719-55	Sequence 55, Appl
37	34.5	61.6	75	4	US-09-334-951-55	Sequence 55, Appl
38	34.5	61.6	75	4	US-09-334-923A-55	Sequence 55, Appl
39	34.5	61.6	75	4	US-09-334-954A-55	Sequence 55, Appl
40	34.5	61.6	76	3	US-08-722-719-24	Sequence 24, Appl
41	34.5	61.6	76	3	US-08-722-719-56	Sequence 56, Appl
42	34.5	61.6	76	3	US-08-722-719-59	Sequence 59, Appl
43	34.5	61.6	76	4	US-09-334-951-24	Sequence 24, Appl
44	34.5	61.6	76	4	US-09-334-951-56	Sequence 56, Appl
45	34.5	61.6	76	4	US-09-334-951-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1

US-09-270-767-44459
; Sequence 44459, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7325-034
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44459
; LENGTH: 198
; TYPE: PRT
; ORGANISM: *Drosophila melanogaster*
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-44459

Query Match 71.4%; Score 40; DB 4; Length 198;
Best Local Similarity 60.0%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY	1	CISVPLSVPC 10
DB	122	CLSVPFPXPC 131

RESULT 2

US-09-252-991A-32454
; Sequence 32454, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32454
; LENGTH: 244
; TYPE: PRT
; ORGANISM: *Pseudomonas aeruginosa*
US-09-252-991A-32454

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Query Match      69.6%; Score 39; DB 4; Length 244;
Best Local Similarity 60.0%; Pred. No. 61;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 C1SVPLSVPC 10
   |||:||||
Db 24 CCSRPMVAPC 33

RESULT 3
US-09-252-991A-23169
; Sequence 23169, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23169
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23169

Query Match      69.6%; Score 39; DB 4; Length 306;
Best Local Similarity 70.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 C1SVPLSVPC 10
   |||:||||
Db 7 CWSVPSSAPC 16

RESULT 4
US-09-252-991A-23382
; Sequence 23382, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23382
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23382

Query Match      66.1%; Score 37; DB 4; Length 142;
Best Local Similarity 50.0%; Pred. No. 72;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 C1SVPLSVPC 10
   |||:||||
Db 89 CLPPFISAPC 98

RESULT 5
```

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US-09-252-991A-18804
; Sequence 18804, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18804
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18804

Query Match      66.1%; Score 37; DB 4; Length 154;
Best Local Similarity 50.0%; Pred. No. 79;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 C1SVPLSVPC 10
   |||:||||
Db 137 CSSLPMLPC 146

RESULT 6
US-08-331-383-33
; Sequence 33, Application US/08331383
; Patent No. 5605809
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; TITLE OF INVENTION: Compositions for the Detection of
; TITLE OF INVENTION: Proteases in Biological Samples and Methods and Use
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331.383
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 16865-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-331-383-33
```



```
Query Match 64.3%; Score 36; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLSVPC 10
DB 2 AIPMSIPC 9

RESULT 7
US-08-549-008-43
; Sequence 43, Application US/08549008
; Patent No. 5714342
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of
; TITLE OF INVENTION: Protease in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/549,008
; FILING DATE: 27-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,383
; FILING DATE: 28-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 016865-0001100S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-549-008-43

Query Match 64.3%; Score 36; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLSVPC 10
DB 2 AIPMSIPC 9

RESULT 8
US-08-802-981-143
; Sequence 143, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-0003000S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 143:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-802-981-143

Query Match 64.3%; Score 36; DB 3; Length 9;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLSVPC 10
DB 2 AIPMSIPC 9

RESULT 9
US-09-252-991A-29933
; Sequence 29933, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29933
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29933

Query Match 64.3%; Score 36; DB 4; Length 92;
Best Local Similarity 55.6%; Pred. No. 67;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISVPLSVPC 10
DB 33 VEPVAVPC 41

RESULT 10
```

US-09-513-999C-8157
; Sequence 8157, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 8157
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 96
; OTHER INFORMATION: Xaa=Cys or Gly
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 113
; OTHER INFORMATION: Xaa=Gly or Val
US-09-513-999C-8157

Query Match 64.3%; Score 36; DB 4; Length 121;
Best Local Similarity 77.8%; Pred. No. 88;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTSVPLSV 9
DB 58 CTSVPLSPP 66

RESULT 11
US-09-621-976-5605
; Sequence 5605, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5605
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -25..-1
US-09-621-976-5605

Query Match 64.3%; Score 36; DB 4; Length 192;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTSVPLSVPC 10
DB 2 CMLSMTKVP 11

RESULT 12
US-09-252-991A-29740

; Sequence 29740, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29740
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29740

Query Match 64.3%; Score 36; DB 4; Length 341;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTSVPLSVPC 10
DB 294 CTSVSTLPC 303

RESULT 13
US-09-252-991A-26663
; Sequence 26663, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26663
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26663

Query Match 64.3%; Score 36; DB 4; Length 510;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTSVPLSVPC 10
DB 359 CIAVAAAI 368

RESULT 14
US-09-538-092-383
; Sequence 383, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01

; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurPatSeqFormatter Version 0.9
; SEQ ID NO 383
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YHR032W
US-09-538-092-383

Query Match 64.3%; Score 36; DB 4; Length 581;
Best Local Similarity 50.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVPLSVPC 10
Db 564 CVSIPVSGC 573

RESULT 15
US-09-252-991A-19384
; Sequence 19384, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19384
; LENGTH: 700
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19384

Query Match 64.3%; Score 36; DB 4; Length 700;
Best Local Similarity 75.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SVPLSVPC 10
Db 46 AAPLSVPC 53

Search completed: April 1, 2005, 09:36:19
Job time : 23.1918 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 06:17:29 ; Search time 13.0685 Seconds
(without alignments)
66.262 Million cell updates/sec

Title: US-09-761-636A-14

Perfect score: 52

Sequence: 1 CISVPLVPC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	39	75.0	297	2	T25817	hypothetical prote
2	39	75.0	347	2	A81988	probable N-acetyl-
3	39	75.0	347	2	D81043	N-acetyl-gamma-glu
4	39	75.0	416	2	A61404	keratin A type I
5	39	75.0	416	2	A46559	keratin, type I, h
6	38	73.1	154	2	D82795	phage-related endo
7	38	73.1	577	2	T00416	hypothetical prote
8	38	73.1	1015	2	C84918	probable ATP-depen
9	38	73.1	3623	2	T08618	intrinsic factor-B
10	37	71.2	287	2	H64690	type IIS restricti
11	37	71.2	407	2	T19895	hypothetical prote
12	36	69.2	1639	2	T50119	probable sensory t
13	35	67.3	61	2	JQ1086	nodulin-14 precurs
14	35	67.3	278	2	AF0936	probable Arac-fam
15	35	67.3	305	2	A82728	conserved hypothet
16	35	67.3	496	2	S51668	tyrosine kinase -
17	35	67.3	1210	2	D88013	protein K10B4.1 [i
18	35	67.3	1440	1	SYHQQT	multifunctional am
19	35	67.3	2240	2	T37057	probable multi-dom
20	34	65.4	397	2	AC1877	hypothetical prote
21	34	65.4	551	2	JC7562	glioblastoma RING
22	34	65.4	1876	2	T13801	phosphoinositide 3
23	33	63.5	339	2	AI3609	daunorubicin resis
24	33	63.5	370	2	T25627	hypothetical prote
25	33	63.5	434	2	T01390	hypothetical prote
26	33	63.5	491	2	T46915	hypothetical prote
27	33	63.5	497	1	S53834	NADH2 dehydrogenas
28	33	63.5	498	2	T45465	acetalate CoA-transf
29	33	63.5	725	2	JE0099	neural cell adhesi

30	33	63.5	771	2	F70757	probable cation tr
31	33	63.5	956	2	A65072	hypothetical prote
32	33	63.5	956	2	B91098	probable dehydroge
33	33	63.5	956	2	F85943	probable dehydroge
34	33	63.5	957	2	T41246	probable ribonucle
35	33	63.5	1021	2	S26985	probable DNA-direc
36	33	63.5	1046	2	A26838	prestalk protein p
37	33	63.5	1253	1	VHWV	structural polypro
38	33	63.5	1827	2	A35694	cutl protein - fis
39	33	63.5	1828	2	T41455	cutl protein - fis
40	32	61.5	58	2	A23101	lon protein - human
41	32	61.5	72	1	W5WL39	E5 protein - human
42	32	61.5	84	2	A61594	thrombospondin - b
43	32	61.5	115	2	D71541	probable inclusion
44	32	61.5	174	2	T02683	hypothetical prote
45	32	61.5	185	1	A47196	dual specificity p

ALIGNMENTS

RESULT 1

T25817
hypothetical protein K12D9.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25817
R:Graves, T.
submitted to the EMBL Data Library, November 1996
A:Description: The sequence of C. elegans cosmid K12D9.
A:Reference number: Z20093
A:Accession: T25817
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-297 <GRA>
A:Cross-references: UNIPROT:P91378; EMBL:U80030; PIDN:AAB37600.1; GSPDB:GN00023; CBSP:K12
A:Experimental source: strain Bristol N2; clone K12D9
C:Genetics:
A:Gene: CBSP:K12D9.3
A:Map position: 5
A:Introns: 165/3; 208/3

Query Match 75.0%; Score 39; DB 2; Length 297;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9
|||:|:|
Db 169 CISLPIVTC 177

RESULT 2

A81988
probable N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) NMA0676 [imported] - N
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C:Accession: A81988
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel;
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: A81988
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-347 <PAR>
A:Cross-references: UNIPROT:Q9JUV6; GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB8396;
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: argC; NMA0676
C:Superfamily: N-acetyl-gamma-glutamyl-phosphate reductase
C:Keywords: oxidoreductase

Query Match 75.0%; Score 39; DB 2; Length 347;
 Best Local Similarity 75.0%; Pred. No. 16;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 C1SVPLVP 8
 |:|:|:|:|
 Db 156 CVSPLPLVP 163

RESULT 3

D81043
 N-acetyl-gamma-glutamyl-phosphate reductase NMB1787 [imported] - Neisseria meningitidis
 C:Species: Neisseria meningitidis
 C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C:Accession: D81043
 R:Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
 xi, H.; Olin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
 Science 287, 1809-1815, 2000
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
 A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A:Reference number: A81000; MUID:20175755; PMID:10710307
 A:Accession: D81043
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-347 <TET>
 A:Cross-references: UNIPROT:Q9JY18; GB:AE002098; NID:g7227034; PIDN:AAF4212
 A:Experimental source: serogroup B, strain MC58
 C:Genetics:
 A:Gene: NMB1787
 C:Superfamily: N-acetyl-gamma-glutamyl-phosphate reductase

Query Match 75.0%; Score 39; DB 2; Length 347;
 Best Local Similarity 75.0%; Pred. No. 16;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 C1SVPLVP 8
 |:|:|:|:|
 Db 156 CVSPLPLVP 163

RESULT 4

A61404
 keratin A, type I - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 03-May-1996
 C:Accession: A61404
 R:Kaytes, P.S.; McNab, A.R.; Rea, T.J.; Groppi, V.; Kawabe, T.T.; Buhl, A.E.; Bertolino,
 J. Invest. Dermatol. 97, 835-842, 1991
 A:Title: Hair-specific keratins: characterization and expression of a mouse type I kerat
 A:Reference number: A61404; MUID:92013235; PMID:1717610
 A:Accession: A61404
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-416 <KAY>
 C:Superfamily: cytoskeletal keratin

Query Match 75.0%; Score 39; DB 2; Length 416;
 Best Local Similarity 66.7%; Pred. No. 19;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 C1SVPLVP 9
 |:|:|:|:|
 Db 385 CVSPLPLVP 393

RESULT 5

A46559
 keratin, type I, hair (clone MHKA-1) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
 C:Accession: A46559
 R:Bertolino, A.P.; Checkla, D.M.; Notterman, R.; Sklaver, I.; Schiff, T.A.; Freedberg, I

J. Invest. Dermatol. 91, 541-546, 1988
 A:Title: Cloning and characterization of a mouse type I hair keratin cDNA.
 A:Reference number: A46559; MUID:89054860; PMID:2461417
 A:Accession: A46559
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-416 <BER>
 A:Cross-references: UNIPROT:Q61765; GB:M27734; NID:g198585; PIDN:AAA39372.1; PID:g198586
 C:Superfamily: cytoskeletal keratin

Query Match 75.0%; Score 39; DB 2; Length 416;
 Best Local Similarity 66.7%; Pred. No. 19;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 C1SVPLVP 9
 |:|:|:|:|
 Db 385 CVSPLPLVP 393

RESULT 6

D82795
 phage-related endolysin XF0513 [imported] - Xylella fastidiosa (strain 9a5c)
 C:Species: Xylella fastidiosa
 C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C:Accession: D82795
 R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: A82515; MUID:20365717; PMID:10910347
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: D82795
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-154 <SIM>
 A:Cross-references: UNIPROT:Q9PFZ3; GB:AE003900; GB:AE003849; NID:g9105366; PIDN:AAF93332;
 A:Experimental source: strain 9a5c
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H.
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
 M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zz
 A:Reference number: A59328
 C:Genetics:
 A:Contents: annotation
 A:Gene: XF0513
 C:Superfamily: phage T4 lysozyme; phage T4 lysozyme homology

Query Match 73.1%; Score 38; DB 2; Length 154;
 Best Local Similarity 75.0%; Pred. No. 11;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 C1SVPLVP 8
 |:|:|:|:|
 Db 78 C1SVPLVP 85

RESULT 7

T00416
 hypothetical protein T30B22.1 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
 C:Accession: T00416
 R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Masor
 submitted to the EMBL Data Library, October 1998
 A:Description: Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence.
 A:Reference number: Z14149

A:Accession: T00416
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-577 <R0U>
A:CROSS-references: UNIPROT:O22243; EMBL:AC002535; NID:g2529657; PID:g2529658
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 2
A:Introns: 87/3; 126/3; 175/1; 264/3; 329/3; 507/3
C:Superfamily: Arabidopsis thaliana hypothetical protein T30B22.1

Query Match 73.1%; Score 38; DB 2; Length 577;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 C1SVPLVP 8
DB 238 C1SVPLVP 245
|:|||||

RESULT 8
C84918
probable ATP-dependent RNA helicase A [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: C84918
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: C84918
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1015 <STO>
A:CROSS-references: UNIPROT:O22243; GB:AE002093; NID:g3738282; PIDN:AAC63624.1; GSPDB:GN
C:Genetics:
A:Gene: At2g47680
A:Map position: 2

Query Match 73.1%; Score 38; DB 2; Length 1015;
Best Local Similarity 75.0%; Pred. No. 66;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 C1SVPLVP 8
DB 676 C1SVPLVP 683
|:|||||

RESULT 9
T08618
intrinsic factor-B12 receptor CUBILIN precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T08618
R:Moestrup, S.K.; Kozyraki, R.; Kristiansen, M.; Kayser, J.H.; Rasmussen, H.H.; Braut, J.
J. Biol. Chem. 273, 5235-5242, 1998
A:Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodies
A:Reference number: Z16459; MUID:98148073; PMID:9478979
A:Accession: T08618
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-3623 <MO>
A:CROSS-references: UNIPROT:O70244; EMBL:AF022247; NID:g3834379; PIDN:AAC71661.1; PID:g3
C:Genetics:
A:Gene: CUBILIN
C:Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
C:Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane;
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-3623/Product: intrinsic factor-B12 receptor CUBILIN #status predicted <MAT>
F:133-164/Domain: EGF homology <EGF>
F:436-467/Domain: EGF homology <EGF>

Query Match 73.1%; Score 38; DB 2; Length 3623;
Best Local Similarity 66.7%; Pred. No. 22e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 C1SVPLVPC 9
DB 313 C1SVPLVPC 321
|:|||||

RESULT 10
H64690
type IIS restriction enzyme M2 protein - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: H64690
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney,
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: H64690
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-287 <TOM>
A:CROSS-references: UNIPROT:O25921; GB:AE000637; GB:AE000511; NID:g2314536; PIDN:AAD0841;
C:Genetics:
A:Start codon: TTG
C:Superfamily: type II site-specific DNA-methyltransferase

Query Match 71.2%; Score 37; DB 2; Length 287;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 C1SVPLVP 8
DB 86 C1SVPLVP 93
|:|||||

RESULT 11
T19895
hypothetical protein C41G7.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19895
R:Steward, C.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19192
A:Accession: T19895
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-407 <WIL>
A:CROSS-references: UNIPROT:Q93368; EMBL:Z81048; PIDN:CAB02841.1; GSPDB:GN00019; CESP:C41
A:Experimental source: clone C41G7
C:Genetics:
A:Gene: CESP:C41G7.4
A:Map position: 1
A:Introns: 27/2; 107/3; 151/3; 333/3; 373/3

Query Match 71.2%; Score 37; DB 2; Length 407;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 C1SVPLVPC 9
DB 113 C1SVPLVPC 121
|:|||||

RESULT 12
TS0119
probable sensory transduction histidine kinase [imported] - fission yeast (Schizosacchar

C;Species: Schizosaccharomyces pombe
 C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
 C;Accession: T50119
 R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, February 2000
 A;Reference number: Z25039
 A;Accession: T50119
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1639 <SEE>
 A;Cross-references: UNIPROT:Q9P707; EMBL:AL157734; PIDN:CAB75776.1; GSPDB:GN00066; SPDB:
 A;Experimental source: strain 972h(-); cosmid c1834
 C;Genetics:
 A;Gene: SPDB:SPAC1834.08
 A;Map position: 1
 A;Introns: 23/3

Query Match 69.2%; Score 36; DB 2; Length 1639;
 Best Local Similarity 85.7%; Pred. No. 2.4e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLVPC 9
 |||||
 Db 557 SVPLVPC 563

RESULT 13

JQ1086
 nodulin-14 precursor - garden pea (fragment)
 C;Species: Pisum sativum (garden pea)
 C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 09-Jul-2004
 C;Accession: JQ1086
 R;Scheres, B.; van Engelen, F.; van der Knaap, E.; van de Wiel, C.; van Kammen, A.; Bise
 Plant Cell 2, 687-700, 1990
 A;Title: Sequential induction of nodulin gene expression in the developing pea nodule.
 A;Reference number: JQ1084; MUID:93005665; PMID:2152123
 A;Accession: JQ1086
 A;Molecule type: mRNA
 A;Residues: 1-61 <SCH>
 A;Cross-references: UNIPROT:P26415; GB:S45162; NID:g257036; PIDN:AAB23538.1; PID:g257037
 A;Experimental source: root nodule
 C;Comment: The gene encoding this protein is expressed in the second stage of root nodul
 C;Genetics:
 A;Gene: ENO14
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-61/Product: nodulin 14 #status predicted <MAT>

Query Match 67.3%; Score 35; DB 2; Length 61;
 Best Local Similarity 71.4%; Pred. No. 16;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLVPC 9
 :|||
 Db 21 NIPLVPC 27

RESULT 14

AF0936
 probable AraC-family transcription regulator STV3756 [imported] - Salmonella enterica su
 C;Species: Salmonella enterica subsp. enterica serovar Typhi
 A;Note: this species has also been called Salmonella typhi
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C;Accession: AF0936
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AF0936
 A;Status: preliminary
 A;Molecule type: DNA

A;Residues: 1-278 <PAR>
 A;Cross-references: GB:AL513382; PIDN:CAD09512.1; PID:g16504629; GSPDB:GN00176
 C;Genetics:
 A;Gene: STV3756
 C;Superfamily: hypothetical protein b2382

Query Match 67.3%; Score 35; DB 2; Length 278;
 Best Local Similarity 62.5%; Pred. No. 68;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISVPLVPC 9
 |::||
 Db 56 ITAPLIPC 63

RESULT 15

AB2728
 conserved hypothetical protein XF1068 [imported] - Xylella fastidiosa (strain 9a5c)
 C;Species: Xylella fastidiosa
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C;Accession: AB2728
 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
 Nature 406, 151-157, 2000
 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A;Reference number: AB2515; MUID:20365717; PMID:10910347
 A;Note: for a complete list of authors see reference number A59328 below
 A;Accession: AB2728
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-305 <SIM>
 A;Cross-references: UNIPROT:Q9PEG0; GB:AB003943; GB:AE003849; NID:g9106006; PIDN:AAF8387;
 A;Experimental source: strain 9a5c
 R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
 A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.A.;
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
 M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A;Reference number: A59328
 A;Contents: annotation
 C;Genetics:
 A;Gene: XF1068

Query Match 67.3%; Score 35; DB 2; Length 305;
 Best Local Similarity 57.1%; Pred. No. 74;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLVPC 9
 |::||
 Db 3 SIPIPC 9

Search completed: April 1, 2005, 09:33:30
 Job time : 14.0685 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 03:33:32 ; Search time 55.1096 Seconds

(without alignments)
83.628 Million cell updates/sec

Title: US-09-761-636A-14

Perfect score: 52

Sequence: 1 CISVPLVPC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_prot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	41	78.8	Q53028	Q53028 rhodococcus
2	40	76.9	Q7SG24	Q7SG24 neurospora
3	40	76.9	Q9MA88	Q9MA88 arabidopsis
4	40	76.9	Q6MVM6	Q6MVM6 neurospora
5	39	75.0	Q9JYU6	Q9JYU6 neisseria m
6	39	75.0	Q9JY18	Q9JY18 neisseria m
7	39	75.0	Q9JY18	Q9JY18 caenothabdi
8	39	75.0	Q9JY18	Q9JY18 mus musculus
9	38	73.1	Q9Z1Y6	Q9Z1Y6 borrelia bu
10	38	73.1	Q8N719	Q8N719 homo sapien
11	38	73.1	Q9PF23	Q9PF23 xylella fas
12	38	73.1	Q30782	Q30782 chlamydomo
13	38	73.1	Q9VW94	Q9VW94 drosophila
14	38	73.1	Q966C5	Q966C5 caenothabdi
15	38	73.1	Q22243	Q22243 arabidopsis
16	38	73.1	Q70244	Q70244 rattus norv
17	37	71.2	Q8N7H7	Q8N7H7 homo sapien
18	37	71.2	Q86SUS	Q86SUS homo sapien
19	37	71.2	Q25921	Q25921 helicobacte
20	37	71.2	Q8C244	Q8C244 mus musculus
21	37	71.2	Q9QY31	Q9QY31 mus musculus
22	37	71.2	Q93368	Q93368 caenothabdi
23	37	71.2	Q756M1	Q756M1 ashbya goss
24	37	71.2	Q7X9C0	Q7X9C0 lotus japon
25	37	71.2	Q7PRA2	Q7PRA2 anopheles g
26	36	69.2	Q96736	Q96736 avian adeno
27	36	69.2	Q6EN50	Q6EN50 oryza sativ
28	36	69.2	Q8BU71	Q8BU71 mus musculus
29	36	69.2	Q8R673	Q8R673 fusobacteri
30	36	69.2	Q99Y31	Q99Y31 streptococ
31	36	69.2	Q8NZF5	Q8NZF5 streptococ

32 36 69.2 186 2 Q7CMLS Q7CMLS streptococ
33 36 69.2 225 2 Q6YXS6 Q6YXS6 oryza sativ
34 36 69.2 309 2 Q87F37 Q87F37 xylella fas
35 36 69.2 442 2 Q8BN56 Q8BN56 mus musculu
36 36 69.2 556 2 Q15716 Q15716 dictyosteli
37 36 69.2 583 2 Q8N787 Q8N787 homo sapien
38 36 69.2 650 2 Q8TVZ0 Q8TVZ0 methanopyru
39 36 69.2 662 2 Q5ZS91 Q5ZS91 homo sapien
40 36 69.2 945 2 Q9M7A8 Q9M7A8 nicotiana t
41 36 69.2 1348 2 Q86KE8 Q86KE8 dictyosteli
42 36 69.2 1639 2 Q9P7Q7 Q9P7Q7 schizosacch
43 35 67.3 45 2 Q7RSW9 Q7RSW9 plasmodium
44 35 67.3 61 1 N014_PEA P26415 pisum sativ
45 35 67.3 78 1 VES_HP70 P50774 human papil

ALIGNMENTS

RESULT 1
Q53028 PRELIMINARY; PRT; 342 AA.
AC Q53028;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Reductase.
GN Name=amod;
OS Rhodococcus corallinus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Gordoniaceae; Gordonia.
OX NCBI_TaxID=36822;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B-276;
RA Sasaki H., Furuhashi K.;
RT "Cloning and characterization of a Nocardia corallina B-276 gene
cluster encoding alkene monooxygenase."
RL J. Ferment. Bioeng. 78:339-406 (1994).
DR EMBL; D37875; BAA07115.1; -;
DR HSSP; P23486; 1QFV.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006058; 2Fe2S_id_BS.
DR InterPro; IPR008333; FAD binding_6.
DR InterPro; IPR001041; Ferredoxin.
DR InterPro; IPR001709; FPN cyt redctse.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR InterPro; IPR001221; Phe_hydroxylase.
DR Pfam; PF00970; FAD binding_6; 1.
DR Pfam; PF00111; Fer2; 1.
DR Pfam; PF00175; NAD binding_1; 1.
DR PRINTS; PR00371; FENCR.
DR PRINTS; PR00410; PHEHYDRLASE.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
KW 2Fe-2S; Iron; Iron-sulfur; Metal-binding.
SQ SEQUENCE 342 AA; 37282 MW; 4651F38D116A8049 CRC64;

Query Match 78.8%; Score 41; DB 2; Length 342;
Best Local Similarity 77.8%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9
Db 75 CASVPLEPC 83

RESULT 2
Q7SGZ4 PRELIMINARY; PRT; 594 AA.
ID Q7SGZ4
AC Q7SGZ4;
DT 01-MAR-2004 (TREMBLrel. 26, Created)

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DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU03022.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysaelis M., Mauceli E., Bielke C., Rudd S., Frisman D.,
RA Kryzofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RA "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; ABAKX0100006; EAA36172.1; -
SQ SEQUENCE 594 AA; 67168 MW; 17B631E6D4695FAB CRC64;

Query Match 76.9%; Score 40; DB 2; Length 594;
Best Local Similarity 55.6%; Pred. No. 71;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9
DB 375 CTGIPVPC 383
| : : : |

RESULT 3
Q9MA88 PRELIMINARY; PRT; 648 AA.
ID AC Q9MA88;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE T12H1.28 protein.
GN Name=T12H1.28;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B., Wu D.,
RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Nierman W.C., Frazer C.M.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC009177; AAF27037.1; -
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR02048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; ehand; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN 2.
SQ SEQUENCE 648 AA; 73066 MW; D22FD23B724D8B7B CRC64;

Query Match 76.9%; Score 40; DB 2; Length 648;
Best Local Similarity 66.7%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 CISVPLVPC 9
DB 227 CFTPLVPC 235
| : : : |

RESULT 4
Q6MVM6 PRELIMINARY; PRT; 772 AA.
ID AC Q6MVM6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Hypothetical protein B18P24.130.
GN Name=B18P24.130;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX842626; CAE76271.1; -
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR Hypothetical protein.
SQ SEQUENCE 772 AA; 87442 MW; 76C8CDF43F94840B CRC64;

Query Match 76.9%; Score 40; DB 2; Length 772;
Best Local Similarity 55.6%; Pred. No. 92;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9
DB 454 CTGIPVPC 462
| : : : |

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RESULT 5
ARGC NEIMA STANDARD; PRT; 347 AA.
ID AC Q9JYU6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (AGPR) (N-
acetyl-L-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase).
GN Name=argC; OrderedLocNames=NMA0676;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / Serogroup A / Serotype 4B;
RX MEDLINE=2022555; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RL "Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis Z2491.";
RL Nature 404:502-506(2000).
CC -!- CATALYTIC ACTIVITY: N-acetyl-L-glutamate 5-semialdehyde + NADP(+)
+ phosphate = N-acetyl-5-glutamyl phosphate + NADPH.
CC -!- PATHWAY: Arginine biosynthesis; third step.

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CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the NAGSA dehydrogenase family. Subfamily
CC 1.
CC
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CC -----
CC EMBL; AL162753; CAB83963.1; -.
CC PIR; A81988; A81988.
CC HAMAP; MF_00150; -.
CC InterPro; IPR000706; AGPR_act_site.
CC InterPro; IPR011137; NAGSA_def.
CC Pfam; PF01118; Semialdehyde_dh; 1.
CC Pfam; PF02774; Semialdehyde_dhC; 1.
CC PIRSF; PIRSF000150; NAGSA_dh; 1.
CC ProDom; PD003765; AGPR_act_site; 1.
CC TIGRfam; TIGR01850; argC; 1.
CC PROSITE; PS01224; ARG_C; FALSE NEG.
KW Arginine biosynthesis; Complete proteome; NADP; Oxidoreductase.
FT ACT_SITE 152 152 By similarity.
SQ SEQUENCE 347 AA; 37227 MW; E1E8A19A2B9246 CRC64;

Query Match 75.0%; Score 39; DB 1; Length 347;
Best Local Similarity 75.0%; Pred. No. 64;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 C1SVPLVP 8
Db 156 C1SVPLVP 163

RESULT 6
ARGC_NEIMB STANDARD; PRT; 347 AA.
AC Q9JY18;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (AGPR) (N-
DE acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase).
GN Name=argC; OrderedLocNames=NM1787;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA Citterone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M.,
RA Qin H., Vanathavan J.J., Gill J., Scarlato V., Masiagnani V., Pizzo M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
CC -!- CATALYTIC ACTIVITY: N-acetyl-L-glutamate 5-semialdehyde + NADP(+)
CC + phosphate = N-acetyl-5-glutamyl phosphate + NADPH.
CC -!- PATHWAY: Arginine biosynthesis; third step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the NAGSA dehydrogenase family. Subfamily
CC 1.

```

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CC -----
CC EMBL; AE002528; AAF42126.1; -.
CC PIR; D81043; D81043.
CC TIGR; NMB1787; -.
CC HAMAP; MF_00150; -.
CC InterPro; IPR000706; AGPR_act_site.
CC InterPro; IPR011137; NAGSA_def.
CC Pfam; PF01118; Semialdehyde_dh; 1.
CC Pfam; PF02774; Semialdehyde_dhC; 1.
CC PIRSF; PIRSF000150; NAGSA_dh; 1.
CC ProDom; PD003765; AGPR_act_site; 1.
CC TIGRfam; TIGR01850; argC; 1.
CC PROSITE; PS01224; ARG_C; FALSE NEG.
KW Arginine biosynthesis; Complete proteome; NADP; Oxidoreductase.
FT ACT_SITE 152 152 By similarity.
SQ SEQUENCE 347 AA; 37213 MW; A927C570DB19ECD1 CRC64;

Query Match 75.0%; Score 39; DB 1; Length 347;
Best Local Similarity 75.0%; Pred. No. 64;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 C1SVPLVP 8
Db 156 C1SVPLVP 163

RESULT 7
P91378 PRELIMINARY; PRT; 362 AA.
ID P91378;
AC P91378;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Serpentine receptor, class w protein 121.
GN Name=srw-121; ORFNames=K12D9.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Graves T.;
RT "The sequence of C. elegans cosmid K12D9."
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [5]

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RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U80030; AAG24161.2; -.
DR PIR; T25817; T25817.
DR WormBase; WEGene0005868; K12D9.3.
DR WormPep; K12D9.3; CE34343.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR00276; GPCR Rhodopsin.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 362 AA; 41292 MW; F25CFD3B0E1D9435 CRC64;

Query Match 75.0%; Score 39; DB 2; Length 362;
Best Local Similarity 66.7%; Pred. No. 66;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9
|||:|:|
DB 233 CISLPIVTC 241

RESULT 8
ID K1H1 MOUSE STANDARD; PRT; 416 AA.
AC Q61765;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Keratin, type I cuticular HA1 (Hair keratin, type I HA1) (HKA-1).
GN Name=Krt1a1; Synonyms=Hk1a1, Krt1-1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hair;
RX MEDLINE=89054860; PubMed=2461417;
RA Bertolino A.P.; Checkla D.M.; Notterman R.; Sklaver I.; Schiff T.A.;
RA Freedberg I.M.; Didona G.J.;
RT "Cloning and characterization of a mouse type I hair keratin cDNA.";
RL J. Invest. Dermatol. 91:541-546(1988).
CC -!- MISCELLANEOUS: There are two types of hair/microfibrillar keratin,
CC -!- I (acidic) and II (neutral to basic).
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC
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CC
CC EMBL; M27734; AAA39372.1; -.
DR PIR; A46559; A46559.
DR HSSP; P08670; 1GK7.
DR MGD; MGI:130993; Krt1-1.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin I.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PROSITE; PS00226; IF; 1.

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KW Coiled coil; Intermediate filament; Keratin.
FT DOMAIN 2 56
FT DOMAIN 57 363 Head.
FT DOMAIN 364 416 Rod.
FT DOMAIN 57 91 Tail.
FT DOMAIN 92 102 Coil 1A.
FT DOMAIN 103 203 Linker 1.
FT DOMAIN 204 219 Coil 1B.
FT DOMAIN 220 363 Linker 12.
FT SITE 305 305 Coil 2.
FT SITE 305 305 Stutter.
SQ SEQUENCE 416 AA; 47112 MW; 9C3759CF4E3A3EF3 CRC64;

Query Match 75.0%; Score 39; DB 1; Length 416;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9
|||:|:|
DB 385 CVSNPCVPC 393

RESULT 9
Q92IY6 PRELIMINARY; PRT; 80 AA.
ID Q92IY6;
AC Q92IY6;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
DE Hypothetical protein.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N40;
RA Feng S.; Chen G.; Barthold S.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF005056; AADQ1230.1; -.
KW Hypothetical protein.
SQ SEQUENCE 80 AA; 9171 MW; C61A1E359DED8EA3 CRC64;

Query Match 73.1%; Score 38; DB 2; Length 80;
Best Local Similarity 87.5%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CISVPLVP 8
|||:|:|
DB 40 CISVPLVP 47

RESULT 10
Q8N7I9 PRELIMINARY; PRT; 134 AA.
ID Q8N7I9;
AC Q8N7I9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ25492.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Nishi T.; Ota T.; Nakagawa S.; Senoh A.; Mizuguchi H.; Inagaki H.;
RA Suzuki Y.; Hata H.; Nakagawa K.; Mizuno S.; Morinaga M.; Kawamura M.;
RA Sugiyama T.; Irie R.; Otsuki T.; Sato H.; Nishikawa T.; Sugiyama A.;
RA Kawakami B.; Nagai K.; Isogai T.; Sugano S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK098358; BAC05291.1; -.
SQ SEQUENCE 134 AA; 13911 MW; 9605A9F9912C2802 CRC64;

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```
Query Match 73.1%; Score 38; DB 2; Length 134;
Best Local Similarity 77.8%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9
   |||||
DB 94 CISVTLSPC 102

RESULT 11
ID Q9PF23 PRELIMINARY; PRT; 154 AA.
AC Q9PF23;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Phase-related endolysin.
GN OrderedLocusNames=Xf0513;
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9a5C;
RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.B., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krueger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406.151-159(2000).
CC -!- CATABOLIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between N-
acetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan
heteropolymers of the prokaryotes cell walls.
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 24 family.
DR EMBL; AF003900; AF83323.1; -.
DR PIR; D82795; D82795.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0003796; F:lysozyme activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0019835; P:cytolysis; IEA.
DR GO; GO:0042742; P:defense response to bacteria; IEA.
DR GO; GO:0009253; P:peptidoglycan catabolism; IEA.
DR InterPro; IPR002196; Glyco_Hydro_24.
DR Pfam; PF00959; Phage_lysozyme; 1.
KW Bacteriolytic enzyme; Complete proteome; Glycosidase; Hydrolase.
SQ SEQUENCE 154 AA; 16793 MW; 20A5570A19D715FD CRC64;

Query Match 73.1%; Score 38; DB 2; Length 154;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CISVPLVP 8
   |||||
DB 78 CISVDMPL 85

RESULT 12
ID O30782 PRELIMINARY; PRT; 198 AA.
AC O30782; Q7BYES;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Inclusion membrane protein B.
GN Name=IncB; Synonyms=incB; OrderedLocusNames=CCA00491;
OS Chlamydomonas reinhardtii.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83557;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GPIC;
RX MEDLINE=98326820; PubMed=9663687;
RA Bannantine J.P., Rockett D.D., Hackstadt T.;
RT "Tandem genes of Chlamydia psittaci that encode proteins localized to
the inclusion membrane.";
RL Mol. Microbiol. 28:1017-1026(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GPIC;
RX MEDLINE=22569155; PubMed=12682364; DOI=10.1093/nar/gkg321;
RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
RA Heidelberg J.F., Holtzapple E.K., Khouri H.M., Federova N.B.,
RA Carthy H.A., Unayam L.A., Haft D.H., Peterson J.D., Beanan M.J.,
RA White O., Salzberg S.L., Haia R.-C., McClarty G., Rank R.G.,
RA Bavoil P.M., Fraser C.M.;
RT "Genome sequence of Chlamydomonas reinhardtii (Chlamydia psittaci GPIC):
examining the role of niche-specific genes in the evolution of the
Chlamydiales.";
RL Nucleic Acids Res. 31:2134-2147(2003).
DR EMBL; AF017105; AAC46378.1; -.
DR EMBL; AE016995; AAP05235.1; -.
DR TIGR; CCA00491; -.
KW Complete proteome.
SQ SEQUENCE 198 AA; 20917 MW; 455E5EA09444FE29 CRC64;

Query Match 73.1%; Score 38; DB 2; Length 198;
Best Local Similarity 55.6%; Pred. No. 56;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9
   |||||
DB 157 CISLPIISC 165

RESULT 13
ID Q9VN94 PRELIMINARY; PRT; 562 AA.
AC Q9VN94;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE CG1113-PA.
GN ORFNames=CG1113;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
```

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.H., Blagej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Frannkoch C., Baldwin D.,
 RA Ballw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downs M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Gloddek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacלב J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J.J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zavari J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RT Science 287:2185-2195(2000).
 RN [2]
 RN [3]
 RN [4]
 RN [5]

RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RG WormBase Consortium;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Contains 1 SET domain.
 DR EMBL; AC006729; AAK84599.2; -.
 DR WormBase; WBGene00021282; Y24D9A.2.
 DR WormPep; Y24D9A.2; CE33849.
 DR InterPro; IPR001214; SET.
 DR Pfam; PF00856; SET; 1.
 DR SMART; SM00317; SET; 1.
 DR PROSITE; PS0280; SET; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 568 AA; 65908 MW; EE4299B1DCFB8E98D CRC64;

Query Match 73.1%; Score 38; DB 2; Length 568;
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9
 | | | | |
 DB 277 CSSKPIVPC 295

RESULT 15

O22243
 ID O22243 PRELIMINARY; PRT; 1015 AA.
 AC O22243;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative ATP-dependent RNA helicase A.
 GN Name:At2g47680;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rounsley S.D.; Lin X.; Kaul S.; Shea T.P.; Fujii C.Y.; Mason T.M.;
 RA Shen M.; Renning C.M.; Fraser C.M.; Somerville C.R.; Venter J.C.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Town C.D.; Kaul S.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC005309; AAC63624.1; -.
 DR PIR; C84918; C84918.
 DR PIR; T00416; T00416.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.

DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR011545; DEAD/DEAH_N.
 DR InterPro; IPR001650; Helicase_C.
 DR InterPro; IPR000571; Znf_CCH.

DR Pfam; PF00270; DEAD; 1. _CCH.
 DR Pfam; PF00271; Helicase_C; 1.
 DR Pfam; PF00642; zf-CCH; 2.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELIC; 1.
 DR SMART; SM00356; Znf_C3H1; 2.

KW ATP-binding; Helicase; Hydrolase.
 SQ SEQUENCE 1015 AA; 115083 MW; D1C342B338C561C9 CRC64;

Query Match 73.1%; Score 38; DB 2; Length 1015;
 Best Local Similarity 75.0%; Pred. No. 2.8e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CISVPLVP 8
 | | | | |
 DB 676 CVSVPFVP 683

Search completed: April 1, 2005, 09:26:09
 Job time : 57.1096 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 03:27:37 ; Search time 67.9315 Seconds
(without alignments)
51.240 Million cell updates/sec

Title: US-09-761-636A-14

Perfect score: 52

Sequence: 1 CISVPLVPC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	9	AAU04533	Aau04533 VEGF base
2	41.5	79.8	10	AAU04532	Aau04532 VEGF base
3	41	78.8	11	AAU04526	Aau04526 VEGF base
4	41	78.8	342	AAR66216	Aar66216 Nocardia
5	41	78.8	342	AAR81472	Aar81472 Nocardia
6	40	76.9	11	AAU04545	Aau04545 VEGF base
7	39	75.0	11	AAU04542	Aau04542 VEGF base
8	39	75.0	101	AAU06501	Aam06501 Human foe
9	39	75.0	102	ABG22400	Abg22400 Novel hum
10	39	75.0	347	ABP77742	Abp77742 N. gonorr
11	38	73.1	44	AAV27025	Aay27025 Amino aci
12	38	73.1	110	ADG22537	Adg22537 Cyanophag
13	38	73.1	198	AAV32174	Aay32174 Chlamydia
14	38	73.1	208	ADB64366	Adb64366 Human pro
15	38	73.1	413	ABM85368	Abm85368 Mouse pro
16	38	73.1	562	ABB57779	Abb57779 Drosophil
17	38	73.1	589	ADA35614	Ada35614 Acinetoba
18	38	73.1	3623	AAV27020	Aay27020 Rat cubil
19	37	71.2	64	AAG00458	Aag00458 Human sec
20	37	71.2	65	AAV12860	Aay12860 Human 5'
21	37	71.2	132	AAO16348	Aao16348 Zinc fing
22	37	71.2	168	ABO79126	AbO79126 Pseudomon
23	37	71.2	292	ABU96694	Abu96694 Human nuc
24	37	71.2	310	ADA55489	Ada55489 Human pro
25	37	71.2	320	ADR32240	Adr32240 Human tum

26	36	69.2	11	4	AAU04544	Aau04544 VEGF base
27	36	69.2	186	5	ABP28862	Abp28862 Streptoco
28	36	69.2	455	7	ABO66858	AbO66858 Klebsiell
29	36	69.2	650	7	ADM26642	Adm26642 Hyperther
30	36	69.2	662	8	ADR09403	Adr09403 Human pro
31	36	69.2	815	8	ADS44128	Ads44128 Bacterial
32	35	67.3	56	2	AAW85729	Aaw85729 Novel pro
33	35	67.3	56	7	ADC38773	Adc38773 Human sec
34	35	67.3	90	7	ABO72214	AbO72214 Pseudomon
35	35	67.3	120	4	AAW93613	Aam93613 Human pol
36	35	67.3	120	8	ADL31405	Adl31405 Human pro
37	35	67.3	200	4	ABG03676	Abg03676 Novel hum
38	35	67.3	249	2	AAW79090	Aaw79090 Human sec
39	35	67.3	249	4	AAU12226	Aau12226 Human PRO
40	35	67.3	249	4	AAU09180	Aau09180 Human PRO
41	35	67.3	249	5	AAW49039	Aam49039 Human tes
42	35	67.3	249	5	ABP61791	Abp61791 Human pol
43	35	67.3	249	6	ABO17670	AbO17670 Novel hum
44	35	67.3	249	6	ABU80924	Abu80924 Human PRO
45	35	67.3	249	6	ABU66624	Abu66624 Human PRO

ALIGNMENTS

RESULT 1
AAU04533
ID AAU04533 standard; peptide; 9 AA.
XX
AC AAU04533;
XX
DT 26-SEP-2001 (first entry)
XX
DE VEGF based monocyclic peptide 11.
XX
KW Human; VEGF: vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..9 /note= "This bond cyclises the peptide"
FT
XX
PN WO200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX
(LUDW-) LUDWIG INST CANCER RES.
XX
PI Achen MG, Hughes RA, Stackner S, Cendron A;
XX
DR WPI; 2001-442248/47.
XX
PT Novel monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.
XX
PS Claim 49; Page 32; 102pp; English.
XX
CC The sequence represents a monomeric monocyclic peptide of the invention,
CC whose 3-dimensional structure is modelled on the expose loop of human
CC VEGF (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CISVPLVPC 9
 |||||
 Db 1 CISVPLVPC 9

RESULT 2
 AAU04532
 ID AAU04532 standard; peptide; 10 AA.

XX
 AC AAU04532;
 DT 26-SEP-2001 (first entry)
 XX

DE VEGF based monocyclic peptide 10.

XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.

XX Synthetic.

XX Key Location/Qualifiers
 FH Disulfide-bond 1..10
 FT /note= "This bond cyclises the peptide"

XX WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

PR 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Hughes RA, Stacker S, Cendron A;

PI WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine

PT residues.
 XX Claim 49; Page 32; 102pp; English.
 XX
 CC The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the exposed loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 10 AA;

Query Match 79.8%; Score 41.5; DB 4; Length 10;
 Best Local Similarity 90.0%; Pred. No. 2.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 CISVPL-VPC 9
 |||||
 Db 1 CISVPLSVPC 10

RESULT 3

AAU04526

ID AAU04526 standard; peptide; 11 AA.

XX
 AC AAU04526;

XX 26-SEP-2001 (first entry)

XX VEGF based monocyclic peptide 3.

DE Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.

XX Synthetic.

XX Key Location/Qualifiers
 FH Disulfide-bond 1..11
 FT /note= "This bond cyclises the peptide"

XX WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

PR 16-MAY-2000; 2000US-0204590P.

XX

PA (LUDW-) LUDWIG INST CANCER RES.
 XX Achen MG, Hughes RA, Stacker S, Cendron A;
 XX WPI; 2001-442248/47.
 DR Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX Claim 49; Page 32; 102pp; English.
 PS The sequence represents a monomeric monocyclic peptide of the invention,
 XX whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGF (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis.
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX Sequence 11 AA;
 SQ Query Match 78.8%; Score 41; DB 4; Length 11;
 Best Local Similarity 81.8%; Pred. No. 3.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
 QY 1 C1SVPL--VPC 9
 DB 1 C1SVPLTSVPC 11
 RESULT 4
 AAR66216 ID AAR66216 standard; protein; 342 AA.
 XX AAR66216;
 XX 16-OCT-2003 (revised)
 DT 04-AUG-1995 (first entry)
 XX Nocardia corallina reductase (encoded by amod).
 DE alkene monooxygenase; reductase; epoxidation; amod.
 XX Gordononia rubripertinctus.
 OS JP06292571-A.
 XX 21-OCT-1994.
 PD 06-APR-1993; 93JP-00105171.
 XX

PR 06-APR-1993; 93JP-00105171.
 XX (NIHA) JAPAN ENERGY CORP.
 XX WPI; 1995-009069/02.
 DR N-PSDB; AAR79569.
 XX Alkene monooxygenase and corresp. gene - useful for the epoxidation of an
 PT alkene.
 XX Claim 2; Page 4-5; 30pp; Japanese.
 PS E.coli transformed with the DNA sequence AAR79569 are able to catalyse
 CC the epoxidation of alkenes. The DNA is derived from Nocardia corallina
 CC and comprises 4 open reading frames. ORFs amod and amoc encode subunits 1
 CC and 2 of the alkene monooxygenase enzyme and ORF amod encodes a reductase
 CC capable of transferring electrons from NADH coenzyme to a monooxygenase.
 CC (Updated on 16-OCT-2003 to standardise OS field)
 XX Sequence 342 AA;
 SQ Query Match 78.8%; Score 41; DB 2; Length 342;
 Best Local Similarity 77.8%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 C1SVPLVPC 9
 DB 75 CASVPLEPC 83
 RESULT 5
 AAR81472 ID AAR81472 standard; protein; 342 AA.
 XX AAR81472;
 XX 16-OCT-2003 (revised)
 DT 07-AUG-1996 (first entry)
 XX Nocardia corallina alkene mono-oxygenase gene product, amod.
 DE Alkene mono-oxygenase; indole; indigo production; biosynthesis;
 KW microbial oxidation; dye.
 XX Gordononia rubripertinctus; B-276.
 OS JP08023988-A.
 XX 30-JAN-1996.
 PD 08-JUL-1994; 94JP-00179688.
 PF 08-JUL-1994; 94JP-00179688.
 PR (NIHA) JAPAN ENERGY CORP.
 XX WPI; 1996-133426/14.
 DR N-PSDB; AAT17418.
 XX Prepn. of indigo by a microbiological method - by culturing a microbe
 PT having alkene monooxygenase activity to oxidise indole to indigo.
 XX Claim 5; Page 8-9; 11pp; Japanese.
 PS AAR81469-R81472 are protein products of the Nocardia corallina strain B-
 CC 276 alkene mono-oxygenase gene. The gene encodes 4 protein products amod,
 CC amob, amoc and amod derived from the 3 different reading frames of the
 CC operon. The gene is useful for the production of indigo via oxidation of
 CC indole. Nocardia corallina can be cultured in a medium contg. indole and
 CC will readily oxidise the indole yielding indigo into the culture medium.
 CC E. coli may also be transformed with the alkene mono-oxygenase gene and
 CC used as above to efficiently produce indigo by microbial oxidation.
 CC (Updated on 16-OCT-2003 to standardise OS field)

XX SQ Sequence 342 AA;
Query Match 78.8%; Score 41; DB 2; Length 342;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CTSVPLVPC 9
Db 75 CASVPLEPC 83

RESULT 6
AAU04545
ID AAU04545 standard; peptide; 11 AA.
XX AAU04545;
XX 26-SEP-2001 (first entry)
XX VEGF based monocyclic peptide 23.
DE Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX Synthetic.
OS Key Location/Qualifiers
FH Disulfide-bond 1..11 /note= "This bond cyclises the peptide"
FT WO200152875-A1.
XX 26-JUL-2001.
XX 18-JAN-2001; 2001WO-US001533.
XX 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX (LUDW-) LUDWIG INST CANCER RES.
PA Achen MG, Hughes RA, Stacker S, Cendron A;
XX WPI; 2001-442248/47.
XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
from an exposed loop of a growth factor protein by oxidizing the cysteine
residues.
XX Example 25; Page 47; 102pp; English.
PS The sequence represents a monomeric monocyclic peptide of the invention,
whose 3-dimensional structure is modelled on the expose loop of human
VEGFD (vascular endothelial growth factor). The invention relates to a
method of producing a monomeric monocyclic peptide by a measuring beta-
beta carbon separation distances on opposite antiparallel strands of a
peptide loop fragment from an exposed loop of a growth factor protein and
cyclising the peptide by oxidising the cysteine residues. The monocyclic
peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
peptides) and a cyclic peptide with at least one amino acid deleted prior
to cyclisation are used to interfere with angiogenesis.
CC neovascularisation or lymphangiogenesis in a mammal with a condition
characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC The condition is diabetic retinopathy, psoriasis, arthropathy,
CC hemangioma, vascularised malignant or benign tumour, post-recovery
CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC trauma, substance-induced neovascularisation of the liver, excessive
CC hormone-related angiogenic dysfunction, diabetes induced neovascular
sequelae, hypertension induced neovascular sequelae, or chronic liver

CC infection. The peptides are also used to modulate vascular permeability
in a mammal (the mammal has a condition characterised by fluid
accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
or brain. The peptides are used to image blood vessels and lymphatic
vasculature. The monomeric and bicyclic peptides are used to interfere
with at least one biological activity induced by VEGF, VEGF-C or -D and
are also used in combination with an anti-inflammatory agent, to treat a
chronic inflammation, especially rheumatoid arthritis, psoriasis and
diabetic retinopathy
XX XX
SQ Sequence 11 AA;
Query Match 76.9%; Score 40; DB 4; Length 11;
Best Local Similarity 72.7%; Pred. NO. 5.6;
Matches 8; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
QY 1 CTSVPL--VPC 9
Db 1 CVSVELTTVPC 11

RESULT 7
AAU04542
ID AAU04542 standard; peptide; 11 AA.
XX AAU04542;
XX 26-SEP-2001 (first entry)
XX VEGF based monocyclic peptide 20.
DE Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX Synthetic.
OS Key Location/Qualifiers
FH Disulfide-bond 1..11 /note= "This bond cyclises the peptide"
FT WO200152875-A1.
XX 26-JUL-2001.
XX 18-JAN-2001; 2001WO-US001533.
XX 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX (LUDW-) LUDWIG INST CANCER RES.
PA Achen MG, Hughes RA, Stacker S, Cendron A;
XX WPI; 2001-442248/47.
XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
from an exposed loop of a growth factor protein by oxidizing the cysteine
residues.
XX Example 25; Page 47; 102pp; English.
PS The sequence represents a monomeric monocyclic peptide of the invention,
whose 3-dimensional structure is modelled on the expose loop of human
VEGFD (vascular endothelial growth factor). The invention relates to a
method of producing a monomeric monocyclic peptide by a measuring beta-
beta carbon separation distances on opposite antiparallel strands of a
peptide loop fragment from an exposed loop of a growth factor protein and
cyclising the peptide by oxidising the cysteine residues. The monocyclic
peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
peptides) and a cyclic peptide with at least one amino acid deleted prior

CC to cyclisation are used to interfere with angiogenesis.
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 11 AA;

Query Match 75.0%; Score 39; DB 4; Length 11;
 Best Local Similarity 72.7%; Pred. No. 8.1;
 Matches 8; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 C1SVPL--VPC 9
 |:|||||
 Db 1 CLSVPLTSPVC 11

RESULT 8
 AAM06501
 ID AAM06501 standard; protein; 101 AA.

XX AC AAM06501;
 XX
 DT 05-OCT-2001 (first entry)
 XX
 DE Human foetal protein, SEQ ID NO: 232.
 XX
 KW Human; foetal protein; cytostatic; immunosuppressive; immunostimulant;
 KW neotropic; neuroprotective; thrombolytic; osteopathic; antiinflammatory;
 KW gene therapy; antisense therapy; cancer; immune disorder;
 KW growth disorder; osteoporosis; thrombolytic disorder;
 KW nervous system disorder; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200153339-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 25-JAN-2001; 2001WO-US002723.
 XX
 PR 25-JAN-2000; 2000US-00491404.
 PR 15-SEP-2000; 2000US-00663870.
 PR 06-NOV-2000; 2000US-00707351.
 XX
 PA (HYSE-) HYSEQ INC.

XX Yeung G, Ford JE, Boyle BJ, Arterburn MC, Drmanac RA, Tang YT;
 PI Liu C, Asundi V, Zhou P, Werhman T;
 XX
 DR WPI: 2001-465571/50.
 DR N-PSDB; AAH94176.
 XX
 PT Novel fetal proteins useful for the treatment and diagnosis of diseases
 PT associated with dysfunction of the protein e.g. cancers, immune
 PT disorders, growth disorders, thrombolytic disorders, nervous system
 PT disorders and inflammation.
 XX
 PS Claim 10; Page 264; 715pp; English.

CC The invention relates to novel foetal polypeptides encoded by
 CC polynucleotides comprising one of 477 sequences fully defined in the
 CC specification. The foetal polynucleotides and polypeptides are useful in
 CC the treatment and diagnosis of diseases such as cancers, immune
 CC disorders, growth disorders (e.g. osteoporosis), thrombolytic disorders,
 CC nervous system disorders and inflammation. The present sequence is a
 CC polypeptide encoded by a cDNA assembled using an expressed sequence tag
 CC (EST) found to be expressed in human foetal tissue cDNA libraries
 XX
 SQ Sequence 101 AA;

Query Match 75.0%; Score 39; DB 4; Length 101;
 Best Local Similarity 87.5%; Pred. No. 72;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 C1SVPLVP 8
 |||||
 Db 2 C1SVPLTP 9

RESULT 9
 AEG22400
 ID AEG22400 standard; protein; 102 AA.

XX AC AEG22400;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #22391.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 DR N-PSDB; AAS86587.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 52759; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping.
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 102 AA;

Query Match 75.0%; Score 39; DB 4; Length 102;
 Best Local Similarity 87.5%; Pred. No. 73;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CFSVPLVP 8
 DB 24 CFSVPLVP 31
 | | | | |

RESULT 10

ABP77742
 ID ABP77742 standard; protein; 347 AA.

AC ABP77742;

DT 07-MAR-2003 (first entry)

DE N. gonorrhoeae amino acid sequence SEQ ID 2014.

XX Antibacterial; infection; vaccine; gene therapy.

OS Neisseria gonorrhoeae.

XX WO200279243-A2.

XX 10-OCT-2002.

PF 12-FEB-2002; 2002WO-IB002069.

PR 12-FEB-2001; 2001GB-00003424.

XX (CHIR-) CHIRON SPA.

PI Fontana MR, Pizza M, Massignani V, Monaci E;

XX WPI; 2003-058415/05.

DR N-PSDB; AB238712.

PT New protein from Neisseria gonorrhoeae, useful for the manufacture of a
 PT medicament for treating or preventing N. gonorrhoeae infection.

XX Disclosure; Page 334; 815pp; English.

CC The present invention relates to proteins from Neisseria gonorrhoeae.
 CC Also disclosed are the nucleic acid molecules encoding the proteins and
 CC antibodies that specifically bind to the proteins. The composition
 CC comprising the protein, nucleic acid or antibody is useful for the
 CC manufacture of a medicament for treating or preventing N. gonorrhoeae
 CC infection, this may be in the form of a vaccine or gene therapy.

CC Sequences given in records ABP76736-ABP81046 represent nucleic acid
 CC molecules of the invention

XX Sequence 347 AA;

Query Match 75.0%; Score 39; DB 6; Length 347;
 Best Local Similarity 75.0%; Pred. No. 2,4e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFSVPLVP 8

DB 156 CFSVPLVP 163
 | | | | |

RESULT 11

ADG22537

ID ADG22537 standard; protein; 110 AA.

XX ADG22537;

XX 26-FEB-2004 (first entry)

DE Cyanophage S-2L encoded protein #282.

AAAY27025
 ID AAY27025 standard; protein; 44 AA.

XX AAY27025;

DT 08-OCT-1999 (first entry)

DE Amino acid sequence of rat cubilin EGF5 repeat.

XX Cubilin; epithelial glycoprotein receptor; vitamin B12; endocytosis;
 KW toxicity; kidney; spleen; brain; liver; heart; thyroid; abortion; rat;
 KW proteinuria; fetal malformation; fetal development; kidney damage; EGF.
 XX Rattus sp.

XX WO9937757-A1.

XX 29-JUL-1999.

PF 21-JAN-1999; 99WO-US001259.

PR 22-JAN-1998; 98US-0072197P.

XX (TULA) TULANE EDUCATIONAL FUND.

PA (INRM) INST NAT SANTE & RECH MEDICALE.

XX Hammond TG, Verroust PJ;

XX WPI; 1999-479045/40.

XX New DNA encoding cubilin, used for treating toxicity, particularly
 PT nephrotoxicity, and as marker of kidney damage.

XX Example 18; Fig 6A; 135pp; English.

CC The invention relates to a rat cubilin protein. Cubilin is a ligand-
 CC binding, epithelial glycoprotein receptor that facilitates uptake of
 CC intrinsic factor/vitamin B12 complexes in intestines and kidney. It is
 CC also involved in endocytosis and trafficking of light immunoglobulin
 CC chains in renal proximal tubule cells. Host cells containing a vector
 CC comprising the rat cubilin DNA sequence can be used for the recombinant
 CC expression of the protein. Cubilin, or its fragments, are used to treat
 CC or reduce toxicity, particularly in kidneys, spleen, brain, liver, heart
 CC and thyroid. Cubilin mutations may also be implicated in idiopathic
 CC proteinuria, fetal malformation, poor fetal development and spontaneous
 CC abortions. Cubilin may also be used to raise specific antibodies, used
 CC for its detection, or clones that express it, in standard immunoassays.
 CC Fragments of cubilin DNA can also be used to detect cubilin mRNA in cell
 CC and tissues, by hybridization. Abnormal levels of cubilin in the urine
 CC are indicative of kidney damage. Sequences AAY27021-35 represent EGF
 CC repeat sequences of rat cubilin and from homologous regions of other
 CC proteins

XX Sequence 44 AA;

Query Match 73.1%; Score 38; DB 2; Length 44;
 Best Local Similarity 66.7%; Pred. No. 46;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CFSVPLVPC 9

DB 12 CSQAPLVPC 20
 | | | | |

RESULT 12

ADG22537
 ID ADG22537 standard; protein; 110 AA.

XX ADG22537;

XX 26-FEB-2004 (first entry)

DE Cyanophage S-2L encoded protein #282.

```

XX genome; cyanophages; 2; 6-diaminopurine; chemotherapy; AIDS.
XX Cyanophage S-2L.
XX PR2839079-A1.
XX PN
XX 31-OCT-2003.
XX PD
XX 30-APR-2002; 2002PR-00005424.
XX PF
XX 30-APR-2002; 2002PR-00005424.
XX PR
XX (INSP ) INST PASTEUR.
XX PA (CNRS ) CNRS CENT NAT RECH SCI.
XX PA (GENO-) GENOSCOPE CENT NAT SEQUENCAGE GRP INTERE.
XX
XX Mariere P, Kaminski PA, Gallisson F, Bouzon M, Pochet S;
XX PI Weissenbach J, Saurin W, Robert C, Vico V;
XX
XX WPI; 2004-045746/05.
XX DR N-PSDB; ADG22255.
XX
XX New genomic sequence for cyanophage S-2L, useful for identifying genes
XX for synthesis of 2,6-diaminopurine bases or polynucleotides containing
XX them.
XX
XX Claim 6; SEQ ID NO 283; 423pp; French.
XX PS
XX
XX The invention relates to the entire genome of cyanophage S-2L, and to the
XX protein encoded by it. Genes isolated from the genome of S-2L are useful
XX for preparing enzymes for synthesis of D-bases, (D = 2,6-diaminopurine),
XX particularly D, dmp and dmp, or polynucleotides containing these bases,
XX polymerases involved in metabolism of D-bases and deoxynucleotide
XX analogs, for chemotherapy of AIDS. The genes, and encoded polypeptides,
XX can be used for detection and/or identification of S-2L, and for
XX identifying agents that modulate synthesis of D-bases or polynucleotides
XX containing them, and fusions of S-2L polypeptides with an antigen can be
XX used to raise specific antibodies, useful for detecting S-2L. This
XX sequence corresponds to one of the proteins encoded by the cyanophage S-
XX 2L genome.
XX
XX SQ Sequence 110 AA;
XX
XX Query Match 73.1%; Score 38; DB 8; Length 110;
XX Best Local Similarity 55.6%; Pred. No. 1.1e+02;
XX Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 C1SVPLVPC 9
XX | :||| :||
XX 50 CATVPTIPC 58
XX
XX
XX RESULT 13
XX AAY32174
XX ID AAY32174 standard; protein; 198 AA.
XX AC
XX AAY32174;
XX
XX 17-OCT-2003 (revised)
XX DT 01-FEB-2000 (first entry)
XX
XX Chlamydia psittaci infection-specific protein IncB.
XX DE
XX IncB; infection; vaccine; therapy; diagnosis.
XX KW
XX Chlamydomophila caviae.
XX OS
XX WO953948-A1.
XX PN
XX 28-OCT-1999.
XX PD
XX 20-APR-1999; 99WO-US008744.
XX PF

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XX 20-APR-1998; 98US-0082438P.
XX PR 21-APR-1998; 98US-0082588P.
XX PR 22-MAY-1998; 98US-0086450P.
XX
XX (UYOR-) UNIV OREGON STATE.
XX PA
XX Rocky DD, Bannantine JP;
XX PI
XX WPI; 1999-633904/54.
XX DR N-PSDB; AAZ34588.
XX
XX Novel bacterial infection specific proteins for treating and diagnosing
XX chlamydial infections.
XX PT
XX Claim 1; Page 41-42; 56pp; English.
XX PS
XX
XX This sequence represents novel infection-specific protein IncB of
XX Chlamydia psittaci strain GPIC. IncB is found in the inclusion membrane
XX of infected cells. It is associated primarily with the vegetative
XX reticulate body form of Chlamydia rather than with the refractile
XX elementary body form. The invention includes: a vaccine directed against
XX the reticulate body form of Chlamydia comprising 1 or more infection-
XX specific proteins (see AAY32170-78), including IncA, IncB and IncC;
XX methods of using and producing such a vaccine; methods for detection of
XX infection-specific antibodies or antigens in a biological specimen; and a
XX method of using therapeutic agents specifically directed against
XX infection-specific peptides, or the genes that code for such peptides, to
XX treat chlamydial infection. (Updated on 17-OCT-2003 to standardise OS
XX field)
XX CC
XX SQ Sequence 198 AA;
XX
XX Query Match 73.1%; Score 38; DB 2; Length 198;
XX Best Local Similarity 55.6%; Pred. No. 2e+02;
XX Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 C1SVPLVPC 9
XX | :||| :||
XX 157 C1SLPIISC 165
XX
XX
XX RESULT 14
XX ADB64366
XX ID ADB64366 standard; protein; 208 AA.
XX AC
XX ADB64366;
XX
XX 04-DEC-2003 (first entry)
XX DT
XX Human protein encoded by clone FCBBF30171230.
XX DE
XX Homo sapiens.
XX OS
XX EP1308459-A2.
XX PN
XX 07-MAY-2003.
XX PD
XX 28-MAR-2002; 2002EP-00007401.
XX PF
XX 05-NOV-2001; 2001JP-00379298.
XX PR 25-JAN-2002; 2002US-00350978.
XX
XX (HELI-) HELIX RES INST.
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
XX Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
XX

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PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX WPI; 2003-450961/43.

DR N-PSDB; ADB62396.

XX

PT New polynucleotides and polypeptides, useful for developing a diagnostic
PT marker or medicines for regulation of their expression and activity, or
PT as targets of gene therapy.

XX Claim 1; Page; 222pp; English.

XX The invention discloses a polynucleotide comprising a sequence selected
CC from 1970 fully defined nucleotide sequences which encode novel
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC or its partial peptide, an antibody binding to the polypeptide or peptide
CC of the polynucleotide, immunologically assaying the polypeptide or
CC peptide of the polynucleotide by contacting the polypeptide or peptide
CC with the antibody of the encoded protein, and observing the binding
CC between the two, a transformant carrying the polynucleotide in an
CC expressible manner and an antisense polynucleotide. The oligonucleotide
CC is useful as a primer for synthesizing the polynucleotide, or as a probe
CC for detecting the polynucleotide. The polynucleotides and encoded
CC proteins are useful as pharmaceutical agents and many disease-related
CC genes may be included in them, for developing a diagnostic marker or
CC medicines for regulation of their expression and activity, or as targets
CC of gene therapy. The genes are involved in tissue and/or cell
CC regeneration. Membrane proteins, signal transduction-related proteins,
CC transcription-related proteins, disease-related proteins and genes
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours. The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a protein of the invention. Note: Some of the
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office.

XX SQ Sequence 208 AA;

Query Match 73.1%; Score 38; DB 7; Length 208;

Best Local Similarity 66.7%; Pred. No. 2.2e+02;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9

Db 33 CASLPLSPC 41

RESULT 15

ABM85368
ID ABM85368 standard; protein; 413 AA.

XX AC ABM85368;

XX DT 18-NOV-2004 (first entry)

XX DE Mouse protein sequence mCP2310.

XX KW Cytostatic; carcinoma; lymphoma; cancer; murine.

XX OS Mus musculus.

XX PN WO2003073826-A2.

XX PD 12-SEP-2003.

XX PF 28-FEB-2003; 2003WO-US006235.

XX PR 01-MAR-2002; 2002US-00087192.

XX PA (SAGR-) SAGRES DISCOVERY.

XX PI Morris DW;

XX

DR WPI; 2003-328604/31.

XX Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
PT comprises a nucleotide sequence.

XX Claim 5; SEQ ID NO 519; Opp; English.

XX The present invention relates to novel DNA and protein sequences which
CC are associated with carcinomas. The sequences are useful for: (i) for
CC screening drug candidates; (ii) for screening of bioactive agent capable
CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
CC a bioactive agent capable of modulating the activity of CAP; (iv) for
CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcinoma Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CAP. Note:
CC This patent is an equivalent to basic patent US2002182586A1, for which no
CC sequence data was published

XX SQ Sequence 413 AA;

Query Match 73.1%; Score 38; DB 7; Length 413;

Best Local Similarity 66.7%; Pred. No. 4.2e+02;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9

Db 287 CSQAPLVPC 295

Search completed: April 1, 2005, 09:18:26

Job time : 69.9315 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 09:26:18 ; Search time 221.178 Seconds
(without alignments)
13.493 Million cell updates/sec

Title: US-09-761-636A-14

Perfect score: 52

Sequence: 1 CISVPLVPC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	9	US-09-761-636A-14	Sequence 14, Appl
2	41.5	79.8	10	US-09-761-636A-13	Sequence 13, Appl
3	41	78.8	11	US-09-761-636A-7	Sequence 7, Appl
4	40	76.9	11	US-09-761-636A-26	Sequence 26, Appl
5	39	75.0	11	US-09-761-636A-23	Sequence 23, Appl
6	39	75.0	71	US-10-437-963-181998	Sequence 181998,
7	38	73.1	208	US-10-104-047-2520	Sequence 2520, Ap
8	38	73.1	413	US-10-087-192-519	Sequence 519, App
9	37	71.2	80	US-10-767-701-56887	Sequence 56887, A
10	37	71.2	87	US-10-424-599-258586	Sequence 258586,
11	37	71.2	94	US-10-424-599-165772	Sequence 165772,
12	37	71.2	149	US-10-424-599-158427	Sequence 158427,
13	37	71.2	310	US-10-094-749-3057	Sequence 3057, Ap

14	37	71.2	320	16	US-10-467-506A-10	Sequence 10, Appl
15	36	69.2	11	9	US-09-761-636A-25	Sequence 25, Appl
16	36	69.2	53	16	US-10-437-963-148570	Sequence 148570,
17	36	69.2	60	15	US-10-424-599-279501	Sequence 279501,
18	36	69.2	216	16	US-10-437-963-159284	Sequence 159284,
19	36	69.2	689	16	US-10-437-963-176796	Sequence 176796,
20	36	69.2	725	16	US-10-437-963-187630	Sequence 187630,
21	36	69.2	815	15	US-10-369-493-22558	Sequence 22558, A
22	35.5	68.3	89	15	US-10-424-599-255153	Sequence 255153,
23	35	67.3	56	13	US-10-114-893-131	Sequence 131, App
24	35	67.3	56	16	US-10-767-701-47989	Sequence 47989, A
25	35	67.3	58	15	US-10-424-599-225406	Sequence 225406,
26	35	67.3	62	15	US-10-424-599-162402	Sequence 162402,
27	35	67.3	78	16	US-10-767-701-47752	Sequence 47752, A
28	35	67.3	92	16	US-10-437-963-162997	Sequence 162997,
29	35	67.3	93	15	US-10-424-599-267602	Sequence 267602,
30	35	67.3	233	15	US-10-425-114-43943	Sequence 43943, A
31	35	67.3	233	15	US-10-425-114-44103	Sequence 44103, A
32	35	67.3	242	15	US-10-425-114-43762	Sequence 43762, A
33	35	67.3	249	9	US-09-745-763-9	Sequence 9, Appl
34	35	67.3	249	14	US-10-028-072-110	Sequence 110, App
35	35	67.3	249	14	US-10-140-808-110	Sequence 110, App
36	35	67.3	249	14	US-10-121-049-110	Sequence 110, App
37	35	67.3	249	14	US-10-123-904-110	Sequence 110, App
38	35	67.3	249	14	US-10-140-470-110	Sequence 110, App
39	35	67.3	249	14	US-10-175-746-110	Sequence 110, App
40	35	67.3	249	14	US-10-176-918-110	Sequence 110, App
41	35	67.3	249	14	US-10-176-921-110	Sequence 110, App
42	35	67.3	249	14	US-10-137-865-110	Sequence 110, App
43	35	67.3	249	14	US-10-140-474-110	Sequence 110, App
44	35	67.3	249	14	US-10-142-431-110	Sequence 110, App
45	35	67.3	249	14	US-10-143-114-110	Sequence 110, App

ALIGNMENTS

RESULT 1
US-09-761-636A-14
; Sequence 14, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF-PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-14

Query Match 100.0%; Score 52; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9
Db 1 CISVPLVPC 9

RESULT 2
US-09-761-636A-13

; Sequence 13, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-13

Query Match 79.8%; Score 41.5; DB 9; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 C1SVPL-VPC 9
Db 1 C1SVPLSVPC 10

RESULT 3
US-09-761-636A-7
; Sequence 7, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-7

Query Match 78.8%; Score 41; DB 9; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1 C1SVPL-VPC 9
Db 1 C1SVPLTSVPC 11

RESULT 4
US-09-761-636A-26
; Sequence 26, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven

; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-26

Query Match 76.9%; Score 40; DB 9; Length 11;
Best Local Similarity 72.7%; Pred. No. 3.4;
Matches 8; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

Qy 1 C1SVPL-VPC 9
Db 1 C1SVPLTSVPC 11

RESULT 5
US-09-761-636A-23
; Sequence 23, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-23

Query Match 75.0%; Score 39; DB 9; Length 11;
Best Local Similarity 72.7%; Pred. No. 5;
Matches 8; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

Qy 1 C1SVPL-VPC 9
Db 1 C1SVPLTSVPC 11

RESULT 6
US-10-437-963-181998
; Sequence 181998, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad

```
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 181998
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_79226C.1.pap
US-10-437-963-181998

Query Match      75.0%; Score 39; DB 16; Length 71;
Best Local Similarity 62.5%; Pred. No. 31;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 C1SVPLVP 8
DB      57 C1SLPLIP 64

RESULT 7
US-10-104-047-2520
; Sequence 2520, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1el full length cdna
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2520
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2520

Query Match      73.1%; Score 38; DB 15; Length 208;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 C1SVPLVPC 9
DB      33 CASLPLSPC 41

RESULT 8
US-10-087-192-519
; Sequence 519, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 519
; LENGTH: 413
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; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(413)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-087-192-519

Query Match      73.1%; Score 38; DB 13; Length 413;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 C1SVPLVPC 9
DB      287 CSQAPLVPC 295

RESULT 9
US-10-767-701-56887
; Sequence 56887, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 56887
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 30950363.pap
US-10-767-701-56887

Query Match      71.2%; Score 37; DB 16; Length 80;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 C1SVPLVPC 9
DB      19 C1SPPAFC 27

RESULT 10
US-10-424-599-258586
; Sequence 258586, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 258586
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_75528C.1.pap
US-10-424-599-258586

Query Match      71.2%; Score 37; DB 15; Length 87;
Best Local Similarity 55.6%; Pred. No. 82;
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Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9
|:|:|

Db 69 CLSIQLTPC 77

RESULT 11
US-10-424-599-165772
; Sequence 165772, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285564
; SEQ ID NO 165772
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(94)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_120707C.1.pep
US-10-424-599-165772

Query Match 71.2%; Score 37; DB 15; Length 94;
Best Local Similarity 66.7%; Pred. No. 89;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9
|:|:|

Db 33 CVSKPGVPC 41

RESULT 12
US-10-424-599-158427
; Sequence 158427, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285564
; SEQ ID NO 158427
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(149)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_114078C.1.pep
US-10-424-599-158427

Query Match 71.2%; Score 37; DB 15; Length 149;
Best Local Similarity 66.7%; Pred. No. 14e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9
|:|:|

Db 21 CRSCPVPVC 29

RESULT 13
US-10-094-749-3057
; Sequence 3057, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YANAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTUYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3057
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-3057

Query Match 71.2%; Score 37; DB 15; Length 310;
Best Local Similarity 55.6%; Pred. No. 2.9e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVPLVPC 9
|:|:|

Db 202 CLSLPQAPC 210

RESULT 14
US-10-467-506A-10
; Sequence 10, Application US/10467506A
; Publication No. US20040170994A1
; GENERAL INFORMATION:
; APPLICANT: Callen, David Fredrick
; APPLICANT: Kremmidiotis, Gabriel
; APPLICANT: Whitmore, Scott
; APPLICANT: Gardner, Alison
; APPLICANT: Powell, Jason
; TITLE OF INVENTION: DNA SEQUENCES FOR HUMAN TUMOUR SUPPRESSOR GENES
; FILE REFERENCE: 1386-15
; CURRENT APPLICATION NUMBER: US/10/467,506A
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: PCT/AU02/00138
; PRIOR FILING DATE: 2002-02-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10

; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-467-506A-10

Query Match 71.2%; Score 37; DB 16; Length 320;
Best Local Similarity 75.0%; Pred. No. 3e+02; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CISVPLVP 8
Db 67 CISLPLLP 74

RESULT 15

US-09-761-636A-25
; Sequence 25, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-25

Query Match 69.2%; Score 36; DB 9; Length 11;
Best Local Similarity 63.6%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 1 CISVPL--VPC 9
Db 1 CISLPISSVPC 11

Search completed: April 1, 2005, 10:36:34
Job time : 221.178 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 07:04:23 ; Search time 13.3151 Seconds
(without alignments)
33.638 Million cell updates/sec

Title: US-09-761-636A-12
Perfect score: 38
Sequence: 1 CVPLTC 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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2: /cgn2_6/prodata/1/1aa/5B-COMB.pep:*
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5: /cgn2_6/prodata/1/1aa/PCTUS-COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	92.1	717	4	US-09-949-016-9436
2	34	89.5	289	4	US-09-902-540-12179
3	33	86.8	159	4	US-09-328-352-4708
4	33	86.8	549	1	US-08-325-071-61
5	33	86.8	549	3	US-08-461-004A-61
6	33	86.8	556	4	US-09-815-923-6
7	33	86.8	620	1	US-08-325-071-65
8	33	86.8	620	3	US-08-461-004A-65
9	33	86.8	650	1	US-08-325-071-56
10	33	86.8	650	1	US-08-325-071-59
11	33	86.8	650	1	US-08-325-071-63
12	33	86.8	650	1	US-08-325-071-67
13	33	86.8	650	3	US-08-461-004A-56
14	33	86.8	650	3	US-08-461-004A-59
15	33	86.8	650	3	US-08-461-004A-63
16	33	86.8	650	3	US-08-461-004A-67
17	33	86.8	688	1	US-08-325-071-57
18	33	86.8	688	3	US-08-461-004A-57
19	33	86.8	1897	4	US-09-845-583A-10
20	33	86.8	1587	4	US-09-561-709B-3
21	32	84.2	38	6	5208144-23
22	32	84.2	38	6	5208144-23
23	32	84.2	49	4	US-09-904-615-83
24	32	84.2	76	4	US-09-270-767-58544
25	32	84.2	338	4	US-09-248-796A-20392
26	32	84.2	473	4	US-09-270-767-44021
27	32	84.2	478	4	US-09-270-767-43204

28	32	84.2	726	6	5208144-37	Patent No. 5208144
29	32	84.2	726	6	5208144-37	Patent No. 5208144
30	32	84.2	1761	4	US-09-561-709B-1	Sequence 1, Appl
31	32	84.2	3571	4	US-09-911-842A-2	Sequence 2, Appl
32	32	84.2	4654	3	US-08-476-515A-84	Sequence 84, Appl
33	32	84.2	4655	3	US-08-652-877-84	Sequence 84, Appl
34	32	84.2	4655	3	US-08-652-877-86	Sequence 86, Appl
35	32	84.2	4655	3	US-08-652-877-88	Sequence 88, Appl
36	32	84.2	4655	3	US-08-652-877-90	Sequence 90, Appl
37	31	81.6	39	1	US-08-212-236-9	Sequence 9, Appl
38	31	81.6	40	1	US-08-033-873-5	Sequence 5, Appl
39	31	81.6	40	2	US-08-356-832-5	Sequence 5, Appl
40	31	81.6	40	3	US-08-988-705-5	Sequence 5, Appl
41	31	81.6	40	4	US-09-917-340-65	Sequence 65, Appl
42	31	81.6	62	4	US-09-270-767-34836	Sequence 34836, A
43	31	81.6	62	4	US-09-270-767-50053	Sequence 50053, A
44	31	81.6	162	4	US-09-270-767-33504	Sequence 33504, A
45	31	81.6	162	4	US-09-270-767-48721	Sequence 48721, A

ALIGNMENTS

RESULT 1
US-09-949-016-9436
; Sequence 9436, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9436
; LENGTH: 717
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9436

Query Match 92.1%; Score 35; DB 4; Length 717;
Best Local Similarity 83.3%; Pred. No. 3.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6
DB 500 CVPVTC 505

RESULT 2
US-09-902-540-12179
; Sequence 12179, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825

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; SEQ ID NO 12179
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-12179

Query Match      89.5%; Score 34; DB 4; Length 289;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CVPLTC 6
DB      229 CTPLTC 234

RESULT 3
US-09-328-352-4708
; Sequence 4708, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4708
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4708

Query Match      86.8%; Score 33; DB 4; Length 159;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CVPLTC 6
DB      113 CVPLAC 118

RESULT 4
US-08-325-071-61
; Sequence 61, Application US/08325071
; Patent No. 5587311
; GENERAL INFORMATION:
; APPLICANT: COBON, Stewart Gary
; APPLICANT: MOORE, Joanna Terry
; APPLICANT: JOHNSON, Law Anthony York
; APPLICANT: WILLADSEN, Peter
; APPLICANT: KEMP, David Harold
; APPLICANT: SRISKANTHA, Alegeacone
; APPLICANT: RIDING, George Alfred
; APPLICANT: RAND, Keith No. 5587311man
; TITLE OF INVENTION: DNA Encoding A Cell Membrane
; TITLE OF INVENTION: Glycoprotein Of A Tick Gut
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,071
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/062,109
; FILING DATE: 17-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,368
; FILING DATE: 07-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/242,196
; FILING DATE: 06-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU87/00401
; FILING DATE: 27-NOV-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PI4912
; FILING DATE: 16-OCT-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PI2570
; FILING DATE: 19-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PH9196
; FILING DATE: 27-NOV-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 60042/111 BIAU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 672 5300
; TELEFAX: 202 672 5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 549 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-325-071-61

Query Match      86.8%; Score 33; DB 1; Length 549;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CVPLTC 6
DB      66 CVPTTC 71

RESULT 5
US-08-461-004A-61
; Sequence 61, Application US/08461004A
; Patent No. 6235283
; GENERAL INFORMATION:
; APPLICANT: COBON, Stewart Gary
; APPLICANT: MOORE, Joanna Terry
; APPLICANT: JOHNSON, Law Anthony York
; APPLICANT: WILLADSEN, Peter
; APPLICANT: KEMP, David Harold
; APPLICANT: SRISKANTHA, Alegeacone
; APPLICANT: RIDING, George Alfred
; APPLICANT: RAND, Keith No. 6235283man
; TITLE OF INVENTION: DNA Encoding A Cell Membrane
; TITLE OF INVENTION: Glycoprotein Of A Tick Gut
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/461,004A
FILING DATE: 04-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/325,071
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: 07/242,196
FILING DATE: 06-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU87/00401
FILING DATE: 27-NOV-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P14912
FILING DATE: 16-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P12570
FILING DATE: 19-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PH9196
FILING DATE: 27-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 60042/152
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 549 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-004A-61

Query Match 86.8%; Score 33; DB 3; Length 549;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTC 6
DB 66 CVPTTC 71

RESULT 6
US-09-815-923-6
Sequence 6, Application US/09815923
Patent No. 6787642
GENERAL INFORMATION:
APPLICANT: Gill, Sarjeet S.
APPLICANT: Ross, Linda S.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Use of Insect Cell Membrane Transporters as No. 6787642el
FILE REFERENCE: 023070-093800US
CURRENT APPLICATION NUMBER: US/09/815,923
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 556
TYPE: PRT
ORGANISM: Manduca sexta
FEATURE:
OTHER INFORMATION: proline transporter
US-09-815-923-6

Query Match 86.8%; Score 33; DB 4; Length 556;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTC 6
DB 423 CVPLVC 428

RESULT 7
US-08-325-071-65
Sequence 65, Application US/08325071
Patent No. 5587311
GENERAL INFORMATION:
APPLICANT: COBON, Stewart Gary
APPLICANT: MOORE, Joanna Terry
APPLICANT: JOHNSON, Law Anthony York
APPLICANT: WILLADSEN, Peter
APPLICANT: KEMP, David Harold
APPLICANT: SRISKANTHA, Alagacone
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 5587311man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,071
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/242,196
FILING DATE: 06-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU87/00401
FILING DATE: 27-NOV-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P14912
FILING DATE: 16-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P12570
FILING DATE: 19-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PH9196
FILING DATE: 27-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 60042/111 BIAU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 amino acids
TYPE: amino acid

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/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-325-071-65

Query Match      86.8%; Score 33; DB 1; Length 620;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CVPLTC 6
Db      117 CVPTTC 122

RESULT 8
US-08-461-004A-65
; Sequence 65, Application US/08461004A
; Patent No. 6235283
; GENERAL INFORMATION:
; APPLICANT: COBON, Stewart Gary
; APPLICANT: MOORE, Joanna Terry
; APPLICANT: JOHNSON, Law Anthony York
; APPLICANT: WILLADSEN, Peter
; APPLICANT: KEMP, David Harold
; APPLICANT: SRISKANTHA, Alagacone
; APPLICANT: RIDING, George Alfred
; APPLICANT: RAND, Keith No. 6235283man
; TITLE OF INVENTION: DNA Encoding A Cell Membrane
; TITLE OF INVENTION: Glycoprotein Of A Tick Gut
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,004A
; FILING DATE: 04-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/325,071
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/062,109
; FILING DATE: 17-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,368
; FILING DATE: 07-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/242,196
; FILING DATE: 06-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU87/00401
; FILING DATE: 27-NOV-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PI4912
; FILING DATE: 16-OCT-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PI2570
; FILING DATE: 19-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PH9196
; FILING DATE: 27-NOV-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 60042/152
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 672 5300
```

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/ TELEFAX: 202 672 5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 65:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 620 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-461-004A-65

Query Match      86.8%; Score 33; DB 3; Length 620;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CVPLTC 6
Db      117 CVPTTC 122

RESULT 9
US-08-325-071-56
; Sequence 56, Application US/08325071
; Patent No. 5587311
; GENERAL INFORMATION:
; APPLICANT: COBON, Stewart Gary
; APPLICANT: MOORE, Joanna Terry
; APPLICANT: JOHNSON, Law Anthony York
; APPLICANT: WILLADSEN, Peter
; APPLICANT: KEMP, David Harold
; APPLICANT: SRISKANTHA, Alagacone
; APPLICANT: RIDING, George Alfred
; APPLICANT: RAND, Keith No. 5587311man
; TITLE OF INVENTION: DNA Encoding A Cell Membrane
; TITLE OF INVENTION: Glycoprotein Of A Tick Gut
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,071
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/062,109
; FILING DATE: 17-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,368
; FILING DATE: 07-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/242,196
; FILING DATE: 06-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU87/00401
; FILING DATE: 27-NOV-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PI4912
; FILING DATE: 16-OCT-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PI2570
; FILING DATE: 19-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PH9196
; FILING DATE: 27-NOV-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 672 5300
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; REFERENCE/DOCKET NUMBER: 60042/111 BIAU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 672 5300
; TELEFAX: 202 672 5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 650 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-325-071-56

Query Match 86.8%; Score 33; DB 1; Length 650;
Best Local Similarity 83.3%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 147 CVPTTC 152

RESULT 10
US-08-325-071-59
; Sequence 59, Application US/08325071
; Patent No. 5587311
; GENERAL INFORMATION:
; APPLICANT: COBON, Stewart Gary
; APPLICANT: MOORE, Joanna Terry
; APPLICANT: JOHNSON, Law Anthony York
; APPLICANT: WILLADSEN, Peter
; APPLICANT: KEMP, David Harold
; APPLICANT: SRISKANTHA, Alagacone
; APPLICANT: RIDING, George Alfred
; APPLICANT: RAND, Keith No. 5587311man
; TITLE OF INVENTION: DNA Encoding A Cell Membrane
; TITLE OF INVENTION: Glycoprotein Of A Tick Gut
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,071
; FILING DATE: 17-MAY-1993
; APPLICATION NUMBER: US 08/062,109
; FILING DATE: 07-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/242,196
; FILING DATE: 06-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU87/00401
; FILING DATE: 27-NOV-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU P4912
; FILING DATE: 16-OCT-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU P12570
; FILING DATE: 19-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PH9196
; FILING DATE: 27-NOV-1986

; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 60042/111 BIAU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 672 5300
; TELEFAX: 202 672 5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 650 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-325-071-59

Query Match 86.8%; Score 33; DB 1; Length 650;
Best Local Similarity 83.3%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 147 CVPTTC 152

RESULT 11
US-08-325-071-63
; Sequence 63, Application US/08325071
; Patent No. 5587311
; GENERAL INFORMATION:
; APPLICANT: COBON, Stewart Gary
; APPLICANT: MOORE, Joanna Terry
; APPLICANT: JOHNSON, Law Anthony York
; APPLICANT: WILLADSEN, Peter
; APPLICANT: KEMP, David Harold
; APPLICANT: SRISKANTHA, Alagacone
; APPLICANT: RIDING, George Alfred
; APPLICANT: RAND, Keith No. 5587311man
; TITLE OF INVENTION: DNA Encoding A Cell Membrane
; TITLE OF INVENTION: Glycoprotein Of A Tick Gut
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,071
; FILING DATE: 17-MAY-1993
; APPLICATION NUMBER: US 08/062,109
; FILING DATE: 07-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/242,196
; FILING DATE: 06-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU87/00401
; FILING DATE: 27-NOV-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU P4912
; FILING DATE: 16-OCT-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU P12570
; FILING DATE: 19-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PH12570
; FILING DATE: 19-JUN-1987
```

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: AU PH9196
;; FILING DATE: 27-NOV-1986
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BENT, Stephen A.
;; REGISTRATION NUMBER: 29,768
;; REFERENCE/DOCKET NUMBER: 60042/111 BIAU
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202 672 5300
;; TELEFAX: 202 672 5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 63:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 650 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-325-071-63

Query Match 86.8%; Score 33; DB 1; Length 650;
Best Local Similarity 83.3%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 147 CVPTTC 152

RESULT 12
US-08-325-071-67
; Sequence 67, Application US/08325071
; Patent No. 5587311
; GENERAL INFORMATION:
; APPLICANT: COBON, Stewart Gary
; APPLICANT: MOORE, Joanna Terry
; APPLICANT: JOHNSON, Law Anthony York
; APPLICANT: WILLADSEN, Peter
; APPLICANT: KEMP, David Harold
; APPLICANT: SRISKANTHA, Alagacone
; APPLICANT: RIDING, George Alfred
; APPLICANT: RAND, Keith No. 5587311man
; TITLE OF INVENTION: DNA Encoding A Cell Membrane
; TITLE OF INVENTION: Glycoprotein Of A Tick Gut
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,071
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/062,109
; FILING DATE: 17-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,368
; FILING DATE: 07-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/242,196
; FILING DATE: 06-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU87/00401
; FILING DATE: 27-NOV-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU P4912
; FILING DATE: 16-OCT-1987

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: AU P12570
;; FILING DATE: 19-JUN-1987
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: AU PH9196
;; FILING DATE: 27-NOV-1986
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BENT, Stephen A.
;; REGISTRATION NUMBER: 29,768
;; REFERENCE/DOCKET NUMBER: 60042/111 BIAU
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202 672 5300
;; TELEFAX: 202 672 5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 67:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 650 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-325-071-67

Query Match 86.8%; Score 33; DB 1; Length 650;
Best Local Similarity 83.3%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 147 CVPTTC 152

RESULT 13
US-08-461-004A-56
; Sequence 56, Application US/08461004A
; Patent No. 6235283
; GENERAL INFORMATION:
; APPLICANT: COBON, Stewart Gary
; APPLICANT: MOORE, Joanna Terry
; APPLICANT: JOHNSON, Law Anthony York
; APPLICANT: WILLADSEN, Peter
; APPLICANT: KEMP, David Harold
; APPLICANT: SRISKANTHA, Alagacone
; APPLICANT: RIDING, George Alfred
; APPLICANT: RAND, Keith No. 6235283man
; TITLE OF INVENTION: DNA Encoding A Cell Membrane
; TITLE OF INVENTION: Glycoprotein Of A Tick Gut
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,004A
; FILING DATE: 04-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/325,071
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/062,109
; FILING DATE: 17-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,368
; FILING DATE: 07-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/242,196
; FILING DATE: 06-JUL-1988

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/AU87/00401
;; FILING DATE: 27-NOV-1987
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: AU P14912
;; FILING DATE: 16-OCT-1987
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: AU P12570
;; FILING DATE: 19-JUN-1987
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: AU PH9196
;; FILING DATE: 27-NOV-1986
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BENT, Stephen A.
;; REGISTRATION NUMBER: 29,768
;; REFERENCE/DOCKET NUMBER: 60042/152
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202 672 5300
;; TELEFAX: 202 672 5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 56:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 650 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-461-004A-56

Query Match 86.8%; Score 33; DB 3; Length 650;
Best Local Similarity 83.3%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 147 CVPTTC 152

RESULT 14
US-08-461-004A-59
; Sequence 59, Application US/08461004A
; Patent No. 6235283
; GENERAL INFORMATION:
; APPLICANT: COBON, Stewart Gary
; APPLICANT: MOORE, Joanna Terry
; APPLICANT: JOHNSON, Law Anthony York
; APPLICANT: WILLADSEN, Peter
; APPLICANT: KEMP, David Harold
; APPLICANT: SRISKANTHA, Alagacone
; APPLICANT: RIDING, George Alfred
; TITLE OF INVENTION: DNA Encoding A Cell Membrane
; TITLE OF INVENTION: Glycoprotein Of A Tick Gut
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,004A
; FILING DATE: 04-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/325,071
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/062,109
; FILING DATE: 17-MAY-1993

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/926,368
;; FILING DATE: 07-AUG-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/242,196
;; FILING DATE: 06-JUL-1988
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/AU87/00401
;; FILING DATE: 27-NOV-1987
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: AU P14912
;; FILING DATE: 16-OCT-1987
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: AU P12570
;; FILING DATE: 19-JUN-1987
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: AU PH9196
;; FILING DATE: 27-NOV-1986
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BENT, Stephen A.
;; REGISTRATION NUMBER: 29,768
;; REFERENCE/DOCKET NUMBER: 60042/152
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202 672 5300
;; TELEFAX: 202 672 5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 59:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 650 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-461-004A-59

Query Match 86.8%; Score 33; DB 3; Length 650;
Best Local Similarity 83.3%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 147 CVPTTC 152

RESULT 15
US-08-461-004A-63
; Sequence 63, Application US/08461004A
; Patent No. 6235283
; GENERAL INFORMATION:
; APPLICANT: COBON, Stewart Gary
; APPLICANT: MOORE, Joanna Terry
; APPLICANT: JOHNSON, Law Anthony York
; APPLICANT: WILLADSEN, Peter
; APPLICANT: KEMP, David Harold
; APPLICANT: SRISKANTHA, Alagacone
; APPLICANT: RIDING, George Alfred
; APPLICANT: RAND, Keith No. 6235283man
; TITLE OF INVENTION: DNA Encoding A Cell Membrane
; TITLE OF INVENTION: Glycoprotein Of A Tick Gut
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,004A
; FILING DATE: 04-JUN-1995

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/325,071
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/062,109
; FILING DATE: 17-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,368
; FILING DATE: 07-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/242,196
; FILING DATE: 06-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU87/00401
; FILING DATE: 27-NOV-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PI4912
; FILING DATE: 16-OCT-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PI2570
; FILING DATE: 19-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PH9196
; FILING DATE: 27-NOV-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 60042/152
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 672 5300
; TELEFAX: 202 672 5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 650 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-461-004A-63

```

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Query Match      86.8%; Score 33; DB 3; Length 650;
Best Local Similarity 83.3%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 CVPLTC 6
Db      147 CVPTTC 152

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Search completed: April 1, 2005, 09:36:18
Job time : 14.3151 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 06:17:29 ; Search time 14.5205 Seconds
(without alignments)
66.262 Million cell updates/sec

Title: US-09-761-636A-13

Perfect score: 56

Sequence: 1 CISVPLSVPC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	69.6	85	2 T44555	hypothetical prote
2	39	69.6	148	2 G82599	hypothetical prote
3	38	67.9	502	2 F86298	IMP dehydrogenase
4	38	67.9	503	1 JC4999	IMP dehydrogenase
5	38	67.9	616	2 D71864	hypothetical prote
6	37	66.1	89	2 F82521	hypothetical prote
7	37	66.1	485	2 A33647	sulfated surface g
8	36	64.3	134	2 D45835	Ly6 homolog RK3 pr
9	36	64.3	207	2 B86781	hypothetical prote
10	36	64.3	256	2 G75515	conserved hypothet
11	36	64.3	496	2 G83136	probable amino aci
12	36	64.3	512	2 H96759	hypothetical prote
13	36	64.3	581	2 S46742	probable steroid 2
14	36	64.3	669	2 T08827	hypothetical prote
15	35	62.5	100	2 F72751	hypothetical prote
16	35	62.5	255	2 JC7593	SH2 domain-contain
17	35	62.5	323	2 I49529	transcription fact
18	35	62.5	372	2 A83171	masC protein - Myc
19	35	62.5	382	2 T15039	probable aminotran
20	35	62.5	438	2 T50982	omega-3 fatty acid
21	35	62.5	468	2 T50982	origin recognition
22	35	62.5	503	2 D75437	DNA repair protein
23	35	62.5	578	2 A70877	probable acyl-coas
24	35	62.5	579	2 B86926	acyl-CoA synthetas
25	35	62.5	579	2 D87063	probable acyl-CoA
26	35	62.5	580	2 B70668	probable Acyl-CoA
27	35	62.5	706	2 D71289	probable single-st
28	35	62.5	759	2 G85506	hypothetical prote
29	35	62.5	759	2 G72115	hypothetical prote

30	35	62.5	1162	2 B97852	hypothetical prote
31	34	60.7	38	2 C54471	agitoxin 3 - scorp
32	34	60.7	77	2 D97718	acetate kinase (Ac
33	34	60.7	156	2 H71023	hypothetical prote
34	34	60.7	249	2 AD0966	probable PTS syste
35	34	60.7	250	2 S06314	regulatory protein
36	34	60.7	252	2 B33538	regulatory protein
37	34	60.7	328	2 F89914	hypothetical prote
38	34	60.7	387	2 T44873	probable secreted
39	34	60.7	399	2 AD2559	hypothetical prote
40	34	60.7	410	2 I38502	gene Brn-3b protel
41	34	60.7	440	2 I48291	transcription fact
42	34	60.7	461	1 KXHU	protein C (activat
43	34	60.7	502	2 C55349	hypothetical prote
44	34	60.7	527	2 H85135	hypothetical prote
45	34	60.7	554	2 A56111	propanediol dehydr

ALIGNMENTS

RESULT 1

T44555

hypothetical protein PA0631 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004

C:Accession: T44555; E83568

R:Nakayama, K.; Takashima, K.; Ishihara, H.; Shinomiya, T.; Kageyama, M.; Kanaya, S.; Oh
submitted to the EMBL Data Library, August 1999

A:Description: Genetic relationship between bacteriociens and bacteriophages.

A:Reference number: Z22790

A:Accession: T44555

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-85 <NAK>

A:Cross-references: UNIPROT:Q9S564; EMBL:AB030825; PIDN:BA083170.1

A:Experimental source: strain PA01

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: E83568

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-85 <STO>

A:Cross-references: GB:AE004498; GB:AE004091; NID:G9946491; PIDN:AAG04020.1; GSPDB:GN0013

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA0631

Query Match 69.6%; Score 39; DB 2; Length 85;

Best Local Similarity 66.7%; Pred. No. 6.1;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISVPLSVPC 10

: |||: |||

Db 27 VEVPLAVPC 35

RESULT 2

G82599

hypothetical protein XF2118 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C:Accession: G82599

R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A>Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A>Note: for a complete list of authors see reference number A59328 below

A:Accession: G82599

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-148 <SIM>
A:Cross-references: UNIPROT:Q9PBM2; GB:AE004026; GB:AE003849; NID:g9107228; PIDN:AAF8491
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, P.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorray, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Teshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF2118

Query Match 69.6%; Score 39; DB 2; Length 148;
Best Local Similarity 50.0%; Pred. No. 10;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTSVPLSVPC 10
|:|:|:|
Db 8 CCAVPMNAPC 17

RESULT 3
F86298
IMP dehydrogenase (EC 1.1.1.205) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: F86298
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huiizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ket, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F86298
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-502 <STO>
A:Cross-references: UNIPROT:Q9SA34; GB:AE005172; NID:g496356; PIDN:AAD34687.1; GSPDB:GN
C:Genetics:
A:Map position: 1
C:Superfamily: inosine-5'-monophosphate dehydrogenase; CBS homology; IMP dehydrogenase a
C:Keywords: GMP biosynthesis; NAD; oxidoreductase

Query Match 67.9%; Score 38; DB 2; Length 502;
Best Local Similarity 85.7%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPLSVPC 10
|:|:|:|
Db 49 VPLSIPC 55

RESULT 4
JC4999
IMP dehydrogenase (EC 1.1.1.205) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: JC4999

R;Collart, F.R.; Osipiuk, J.; Trent, J.; Olsen, G.J.; Huberman, E.
Gene 174, 217-220, 1996
A:Title: Cloning and characterization of the gene encoding IMP dehydrogenase from Arabid
A:Reference number: JC4999; MUID:97045815; PMID:8890737
A:Accession: JC4999
A:Molecule type: DNA
A:Residues: 1-503 <COL>
A:Cross-references: UNIPROT:P47996; GB:L34684; NID:g1100062; PIDN:AAB41940.1; PID:g110006
C:Genetics:
A:Gene: impdh
A:Introns: 135/1; 334/3; 404/3; 490/3
C:Complex: homotetramer
C:Function:
A:Description: provides precursors for DNA and RNA biosynthesis; it catalyzes the conver
C:Superfamily: inosine-5'-monophosphate dehydrogenase; CBS homology; IMP dehydrogenase an
C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
F;20-86/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F;172-220/Domain: CBS homology <CBS2>
F;221-465/Domain: IMP dehydrogenase catalytic homology <IMP>
F;322/Active site: Cys #status predicted

Query Match 67.9%; Score 38; DB 1; Length 503;
Best Local Similarity 85.7%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPLSVPC 10
|:|:|:|
Db 49 VPLSIPC 55

RESULT 5
D71864
hypothetical protein jhp0985 - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; J
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: D71864
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-616 <ARN>
A:Cross-references: UNIPROT:Q9ZKF3; GB:AE001527; GB:AE001439; NID:g4155558; PIDN:AAD0656
A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp0985

Query Match 67.9%; Score 38; DB 2; Length 616;
Best Local Similarity 77.8%; Pred. No. 61;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTSVPLSVPC 9
|:|:|:|
Db 253 CLSNPLSVPC 261

RESULT 6
F82521
hypothetical protein XF2736 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: F82521
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: For a complete list of authors see reference number A59328 below
A:Accession: F82521
A>Status: preliminary

A:Molecule type: DNA
A:Residues: 1-89 <SIM>
A:Cross-references: UNIPROT:Q9P9V4; GB:AE004080; GB:AE003849; NID:g9107971; PIDN:AAF8552
A:Experimental source: strain 9a5c
C:Species: *Rattus norvegicus* (Norway rat)
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir M.; Tsuchiaki, M.H.; Vailada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF2736

Query Match 66.1%; Score 37; DB 2; Length 89;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISVPLSVPC 10
: || || || ||
Db 19 VSAPLRVPC 27
: || || || ||

RESULT 7
A33647
sulfated surface glycoprotein 185 - Volvox carteri
C:Species: *Volvox carteri*
C:Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 09-Jul-2004
C:Accession: A33647
R:Erl, H.; Mengelle, R.; Wenzl, S.; Engel, J.; Sumper, M.
J. Cell Biol. 109, 3493-3501, 1999
A:Title: The extracellular matrix of *Volvox carteri*: molecular structure of the cellular A:Reference number: A33647; MUID:90094551; PMID:2689458
A:Accession: A33647
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-485 <ERT>
A:Cross-references: UNIPROT:P21997; GB:X51616; NID:g21999; PIDN:CAA35953.1; PID:g1405821
C:Keywords: glycoprotein

Query Match 66.1%; Score 37; DB 2; Length 485;
Best Local Similarity 60.0%; Pred. No. 72;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVPLSVPC 10
: || || || ||
Db 83 CQTPLTEPC 92
: || || || ||

RESULT 8
D45835
Ly6 homolog RK3 precursor - rat
C:Species: *Rattus norvegicus* (Norway rat)
C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C:Accession: D45835; C45835
R:Friedman, S.; Palfrey, R.G.E.; Sirlin, S.; Haemmerling, U.
Immunogenetics 31, 104-111, 1990
A:Title: Analysis of three distinct Ly6-A-related cDNA sequences isolated from rat kidney A:Reference number: A45835; MUID:190152758; PMID:2154400
A:Accession: D45835
A:Molecule type: mRNA
A:Residues: 1-134 <FRI>
A:Cross-references: UNIPROT:O63318; GB:M30690; NID:g205249; PIDN:AAA41547.1; PID:g205250
A:Experimental source: clone RK3
A:Accession: C45835
A:Molecule type: mRNA

A:Residues: 2-134 <FR2>
A:Cross-references: GB:M30691; NID:g205251; PIDN:AAA41548.1; PID:g205252
A:Experimental source: clone RK11
C:Superfamily: Ly-6 antigen; Ly-6 homology
C:Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkage F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-105/Product: Ly6 homolog RK3 #status predicted <MAT>
F:106-134/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:105/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature form)

Query Match 64.3%; Score 36; DB 2; Length 134;
Best Local Similarity 60.0%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CISVPLSVPC 10
: || || || ||
Db 32 CIEVPLNANC 41
: || || || ||

RESULT 9
B86781
hypothetical protein ymhC [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL1403)
C:Species: *Lactococcus lactis* subsp. *lactis*
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: B86781
R:Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ssi A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: B86781
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-207 <STO>
A:Cross-references: UNIPROT:Q9CG60; GB:AE005176; PID:g12724223; PIDN:AAK05348.1; GSPDB:IG A:Experimental source: strain IL1403
C:Genetics:
A:Gene: ymhC

Query Match 64.3%; Score 36; DB 2; Length 207;
Best Local Similarity 55.6%; Pred. No. 48;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CISVPLSVPC 9
: || || || ||
Db 128 CINPLQIP 136
: || || || ||

RESULT 10
G75515
conserved hypothetical protein - *Deinococcus radiodurans* (strain R1)
C:Species: *Deinococcus radiodurans*
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: G75515
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1. A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: G75515
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-256 <WHI>
A:Cross-references: UNIPROT:Q9RX44; GB:AE001906; GB:AE000513; NID:g6458151; PIDN:AAF1005 C:Genetics:
A:Experimental source: strain R1
A:Gene: DR0471
A:Map position: 1

Query Match 64.3%; Score 36; DB 2; Length 256;
Best Local Similarity 50.0%; Pred. No. 58;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CISVPLSVPC 10
|:|:|:|:
Db 4 CVPAPRSAPC 13

RESULT 11

G83136
probable amino acid permease PA4072 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: G83136
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: G83136
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-496 <STO>
A:Cross-references: UNIPROT:Q9HWV6; GB:AE004823; GB:AE004091; NID:g950265; PIDN:AAG0745
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA4072

Query Match 64.3%; Score 36; DB 2; Length 496;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVPLSVPC 10
|:|:|:|:
Db 345 CIAVAAAIIPC 354

RESULT 12

H96759
probable steroid 22-alpha-hydroxylase T9L24.44 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H96759
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.; Mansueti, N.F.; Hughes, B.; Huizlar, L.
A:Title: The Arabidopsis genome
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H96759
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-512 <STO>
A:Cross-references: UNIPROT:Q9FX29; GB:AE005173; NID:g11120803; PIDN:AAG30983.1; GSPDB:G000000000
C:Genetics:
A:Gene: T9L24.44
A:Map position: 1
C:Superfamily: Synchocystis cytochrome P450 slr0574; cytochrome P450 homology
C:Keywords: heme; iron; metalloprotein
F:455/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 64.3%; Score 36; DB 2; Length 512;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CISVPLSVPC 9
|:|:|:|:
Db 244 CLSVBIDLP 252

RESULT 13

S46742
hypothetical protein YHR032w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein H8179.15
C:Species: Saccharomyces cerevisiae
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C:Accession: S46742

R:Du, Z.
A:Submitted to the EMBL Data Library, May 1994
A:Description: The sequence of S. cerevisiae cosmid 8179.

A:Reference number: S46732
A:Accession: S46742
A:Molecule type: DNA
A:Residues: 1-581 <DUZ>
A:Cross-references: UNIPROT:P38767; EMBL:U00062; NID:g488162; PIDN:AAB68911.1; PID:g488162
C:Genetics:
A:Cross-references: SGD:S0001074
A:Map position: 8R
C:Keywords: transmembrane protein

Query Match 64.3%; Score 36; DB 2; Length 581;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVPLSVPC 10
|:|:|:|:
Db 564 CVSIPVSSGC 573

RESULT 14

T08827
hypothetical protein cotel - human
C:Species: Homo sapiens (man)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T08827
R:Winfield, S.L.; Tayebi, N.; Martin, B.M.; Ginns, E.I.; Sidransky, E.
A:Title: Identification of three additional genes contiguous to the glucocerebrosidase 1 gene
A:Reference number: Z16482; MUID:97474796; PMID:9331372
A:Accession: T08827
A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-669 <WIN>
A:Cross-references: UNIPROT:P81408; EMBL:AF023268; NID:g2564910; PIDN:AAC51822.1; PID:g2564910
C:Genetics:
A:Gene: cotel
A:Map position: 1
A:Introns: 75/3; 94/3; 131/3; 171/3; 207/3; 266/2; 299/3; 323/1; 505/1; 528/1; 612/3

Query Match 64.3%; Score 36; DB 2; Length 669;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CISVPLSVPC 10
|:|:|:|:
Db 139 CPSVPLLRPC 148

RESULT 15

F72751
hypothetical protein APE0003 - Aeropyrum pernix (strain KL)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: F72751

R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahashi, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kikuchi, T.
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: F72751
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-100 <KAW>

A:Cross-references: UNIPROT:Q9YVG98; DDBJ:AP000058; NID:G5103388; PIDN:BAA78912.1; PID:G5103388

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE0003

C:Superfamily: Aeropyrum pernix hypothetical protein APE0003

Query Match 62.5%; Score 35; DB 2; Length 100;

Best Local Similarity 71.4%; Pred. No. 35;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPLSVPC 10

:||:||||

Db 57 IPLTVPC 63

Search completed: April 1, 2005, 09:33:29

Job time : 15.5205 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 03:33:32 ; Search time 61.2329 Seconds
(without alignments)
83.628 Million cell updates/sec

Title: US-09-761-636A-13
Perfect score: 56
Sequence: 1 CISVPLSVPC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	75.0	569	1 MAMC_PIRSP	P55298 piromyces s
2	42	75.0	571	1 MAMC_PIRSP	P55297 piromyces s
3	40	71.4	109	2 Q9L4Y0	Q9L4Y0 streptomyce
4	39	69.6	85	2 Q9S556	Q9S556 pseudomonas
5	39	69.6	85	2 Q9S564	Q9S564 pseudomonas
6	39	69.6	148	2 Q9PBM2	Q9PBM2 xylella fas
7	39	69.6	620	2 Q89893	Q89893 human herpe
8	38	67.9	144	2 Q8TGP8	Q8TGP8 saccharomyc
9	38	67.9	402	2 Q6C595	Q6C595 yarrowia li
10	38	67.9	502	2 IMH2_ARATH	Q9SA34 arabidopsis
11	38	67.9	503	1 IMH1_ARATH	P47996 arabidopsis
12	38	67.9	503	2 Q8L8U2	Q8L8U2 arabidopsis
13	38	67.9	528	2 Q89D16	Q89D16 bradyrhizob
14	38	67.9	563	1 ADEC_LACPL	Q888r1 lactobacill
15	38	67.9	616	2 Q9P9Y4	Q9Zkf3 helicobacte
16	38	67.9	630	2 Q7R1J7	Q7R1J7 giardia lam
17	38	67.9	982	2 Q6CGV5	Q6CGV5 yarrowia li
18	37	66.1	86	2 Q9MC88	Q9MC88 bacterioph
19	37	66.1	89	2 Q9P9Y4	Q9P9Y4 xylella fas
20	37	66.1	121	2 Q6CFG3	Q6CFG3 yarrowia li
21	37	66.1	129	2 Q8BWA6	Q8BWA6 mus musculu
22	37	66.1	134	2 Q8N7T2	Q8N7T2 homo sapien
23	37	66.1	155	2 Q8DMP5	Q8DMP5 synecococc
24	37	66.1	236	2 Q87XN8	Q87XN8 pseudomonas
25	37	66.1	284	2 Q92RN5	Q92RN5 rhizobium m
26	37	66.1	316	2 Q9V743	Q9V743 drosophila
27	37	66.1	343	2 Q6NNX6	Q6NNX6 drosophila
28	37	66.1	355	2 Q9LGY9	Q9LGY9 oryza sativ
29	37	66.1	370	2 Q9VNA4	Q9VNA4 drosophila
30	37	66.1	405	2 Q7PJ04	Q7PJ04 fusbacteri
31	37	66.1	420	1 CG2A_CHLVR	P51986 chlorohydra

32	37	66.1	471	2 Q6QTA0	Q6QTA0 trypanosoma
33	37	66.1	480	2 Q8SPG1	Q8SPG1 leishmania
34	37	66.1	485	1 SSGP_VOLCA	P21997 volvox cart
35	37	66.1	501	2 Q9AY75	Q9AY75 oryza sativ
36	37	66.1	525	2 Q7Q011	Q7Q011 anopheles g
37	37	66.1	525	2 Q7QLB8	Q7QLB8 anopheles g
38	37	66.1	725	2 Q9N8V1	Q9N8V1 trypanosoma
39	36	64.3	58	2 Q7URUS	Q7URUS rhodopirell
40	36	64.3	93	2 Q64MV0	Q64MV0 bacteroides
41	36	64.3	112	2 Q14634	Q14634 homo sapien
42	36	64.3	133	2 Q78EE7	Q78EE7 rattus norv
43	36	64.3	134	2 Q63318	Q63318 rattus norv
44	36	64.3	207	2 Q9CG60	Q9CG60 lactococcus
45	36	64.3	208	2 Q9NF93	Q9NF93 leishmania

ALIGNMENTS

RESULT 1

ID	MAMC_PIRSP	STANDARD	PRT	569 AA
AC	P55298			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Mannan endo-1,4-beta-mannosidase C precursor (EC 3.2.1.78) (Beta-mannanase C) (1,4-beta-D-mannan mannanohydrolase C).			
GN	Name=MAMC;			
OS	Piromyces sp.			
OC	Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;			
OC	Neocallimastaceae; Piromyces.			
OX	NCBI_TaxID=45796;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9631314; PubMed=8768520; DOI=10.1016/0378-1097(96)00219-4;			
RA	Millward-Sadler S.J., Hall J., Black G.W., Hazlewood G.P.,			
RA	Gilbert H.J.;			
RT	"Evidence that the Piromyces gene family encoding endo-1,4-mannanases arose through gene duplication."			
RL	FEMS Microbiol. Lett. 141:183-188(1996).			
CC	!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-beta-D-mannosidic linkages in mannan, galactomannans, glucomannans, and galactoglucomannans.			
CC	!- SIMILARITY: Belongs to the glycosyl hydrolase 26 family.			
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CC	EMBL; X97520; CAA66134.1; -.			
DR	InterPro; IPR005084; CBM 6.			
DR	InterPro; IPR002883; Dockering CBD 5.			
DR	InterPro; IPR009034; Dockering CBD.			
DR	InterPro; IPR008979; Gal bind-like.			
DR	InterPro; IPR008005; Glyco_hydro_26.			
DR	Pfam; PF02013; CBM_10; 2.			
DR	Pfam; PF03422; CBM_6; 1.			
DR	Pfam; PF02156; Glyco_hydro_26; 1.			
DR	PRINTS; PR00739; GLHYDRLASE26.			
KW	Glycosidase; Hydrolase; Multigene family; Repeat; Signal.			
FT	SIGNAL 1 18			
FT	CHAIN 19 569			
FT	DOMAIN 490 569			
FT	REPEAT 488 525			
FT	REPEAT 531 569			
FT	DOMAIN 473 477			
FT	Poly-Asn.			
FT	Poly-Asn.			
FT	SEQUENCE 569 AA; 64115 MW; 19277764E18328B5 CRC64;			

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Query Match      75.0%; Score 42; DB 1; Length 569;
Best Local Similarity 60.0%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CISVPLSVPC 10
Db 490 CFSIPLGYPC 499

RESULT 2
MANB_PIRSB
ID MANB_PIRSB STANDARD; PRT; 571 AA.
AC P55297;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Mannan endo-1,4-beta-mannosidase B precursor (EC 3.2.1.78) (Beta-
DE mannase MANB) (1,4-beta-D-mannan mannanohydrolase B).
GN Name=MANB;
GN Piromyces sp.
OS Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;
OC Neocallimastacaceae; Piromyces.
OX NCBI_TaxID=45796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96313314; PubMed=8768520; DOI=10.1016/0378-1097(96)00219-4;
RA Millward-Sadler S.J., Hall J., Black G.W., Hazlewood G.P.,
RA Gilbert H.J.;
RT "Evidence that the Piromyces gene family encoding endo-1,4-mannanases
RT arose through gene duplication.";
RL FEMS Microbiol. Lett. 141:183-188(1996).
CC -1- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-beta-D-mannosidic
CC linkages in mannans, galactomannans, glucomannans, and
CC galactoglucumannans.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 26 family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC ENBL; X97408; CAA66061.1; --
CC InterPro; IPR005084; CBM 6.
CC InterPro; IPR009034; Dockerling CDD.
CC InterPro; IPR002883; Dockerling CBD_5.
CC InterPro; IPR008979; Gal_bind like.
CC InterPro; IPR000805; Glyco_hydro_26.
CC Pfam; PF02013; CBM 10; 2.
CC Pfam; PF03422; CBM 6; 1.
CC Pfam; PF02156; Glyco_hydro_26; 1.
CC PRINTS; PR00739; GLHYDRLASE26.
KW Glycosidase; Hydrolase; Multigene family; Repeat; Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 571 Mannan endo-1,4-beta-mannosidase B.
FT DOMAIN 490 571 2 X 39 AA approximate repeats.
FT REPEAT 490 527 1.
FT REPEAT 533 571 2.
FT DOMAIN 475 479 Poly-Asn.
FT DOMAIN 482 488 Poly-Asn.
SQ SEQUENCE 571 AA; 64397 MW; B13E44581FAA9DAA CRC64;

Query Match      75.0%; Score 42; DB 1; Length 571;
Best Local Similarity 60.0%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CISVPLSVPC 10
Db 492 CFSIPLGYPC 501

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Db          : |||:|
27 VEVPLAVPC 35

RESULT 5
Q9S564      PRELIMINARY;      PRT;      85 AA.
AC Q9S564; Q7DCJ0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=PA0631;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PA01, and SLME6;
RX MEDLINE=20521925; PubMed=11069649;
RA Nakayama K., Takashima K., Ishihara H., Shinomiya T., Kageyama M.,
RA Kanaya S., Ohnishi M., Murata T., Mori H., Hayashi T.;
RT "The R-type pyocin of Pseudomonas aeruginosa is related to P2 phage,
RT and the F-type is related to lambda phage.";
RL Mol. Microbiol. 38:213-231(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AB030825; BAA83170.1; -.
DR EMBL; AB045308; BAA97449.1; -.
DR EMBL; AE004498; AAG04020.1; -.
DR PIR; T44555; T44555.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 85 AA; 9222 MW; F2267D9C542C7F48 CRC64;

Query Match 69.6%; Score 39; DB 2; Length 85;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy          2 ISVPLSVPC 10
Db          : |||:|
27 VEVPLAVPC 35

RESULT 6
Q9PBM2      PRELIMINARY;      PRT;      148 AA.
AC Q9PBM2;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=Xf2118;
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9a5C;
RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,

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RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Pacincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.R.,
RA Praga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miraca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A.Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuchiko M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AE004026; AAF84917.1; -.
DR PIR; G82599; G82599.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 148 AA; 15990 MW; B78D2FAE68929260 CRC64;

Query Match 69.6%; Score 39; DB 2; Length 148;
Best Local Similarity 50.0%; Pred. No. 49;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy          1 CISVPLSVPC 10
Db          8 CCAVPMNAPC 17

RESULT 7
Q98993      PRELIMINARY;      PRT;      620 AA.
ID Q98993
AC Q98993;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE DR2.
GN Name=DR2;
OS Human herpesvirus 6.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
OX NCBI_TaxID=10368;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102;
RX MEDLINE=90112641; PubMed=2153237;
RA Littler E., Lawrence G., Liu M.Y., Barrell B.G., Arrand J.R.;
RT "Identification, cloning, and expression of the major capsid protein
RT gene of human herpesvirus 6.";
RL J. Virol. 64:714-722(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102;
RX MEDLINE=90080132; PubMed=2152817;
RA Lawrence G.L., Chee M., Craxton M.A., Gompels U.A., Honess R.W.,
RA Barrell B.G.;
RT "Human herpesvirus 6 is closely related to human cytomegalovirus.";
RL J. Virol. 64:287-299(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102;

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RX MEDLINE=91226542; PubMed=1851252; DOI=10.1038/351078a0;
RA Thomson B.J., Efsthathiou S., Honess R.W.;
RT "Acquisition of the human adeno-associated virus type-2 rep gene by
RT human herpesvirus type-6.";
RL Nature 351:78-80(1991).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102;
RX MEDLINE=91333007; PubMed=1651403;
RA Teo I.A., Griffin B.E., Jones M.D.;
RT "Characterization of the DNA polymerase gene of human herpesvirus 6.";
RL J. Virol. 65:4670-4680(1991).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102;
RX MEDLINE=91374590; PubMed=1654446;
RA Martin M.E.D., Nicholas J., Thomson B.J., Newman C., Honess R.W.;
RT "Identification of a transactivating function mapping to the putative
RT immediate-early locus of human herpesvirus 6.";
RL J. Virol. 65:5381-5390(1991).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102;
RX MEDLINE=91237802; PubMed=1851860;
RA Chang C.K., Balachandran N.;
RT "Identification, characterization, and sequence analysis of a cDNA
RT encoding a phosphoprotein of human herpesvirus 6.";
RL J. Virol. 65:2884-2894(1991).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102;
RX MEDLINE=92148942; PubMed=1310766;
RA Geng Y., Chandran B., Josephs S.F., Wood C.;
RT "Identification and characterization of a human herpesvirus 6 gene
RT segment that trans activates the human immunodeficiency virus type 1
RT promoter.";
RL J. Virol. 66:1564-1570(1992).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102;
RX MEDLINE=92260671; PubMed=1374813;
RA Neipel F., Ellinger K., Fleckenstein B.;
RT "Gene for the major antigenic structural protein (p100) of human
RT herpesvirus 6.";
RL J. Virol. 66:3918-3924(1992).
RN [9]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102;
RX MEDLINE=9233249; PubMed=1321206;
RA Efsthathiou S., Lawrence G.L., Brown C.M., Barrell B.G.;
RT "Identification of homologs to the human cytomegalovirus US22 gene
RT family in human herpesvirus-6.";
RL J. Gen. Virol. 73:1661-1671(1992).
RN [10]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102;
RX MEDLINE=93187613; PubMed=8383182;
RA Ellinger K., Neipel F., Foa-Tomasi L., Campadelli-Fiume G.,
RA Fleckenstein B.;
RT "The glycoprotein B homologue of human herpesvirus 6.";
RL J. Gen. Virol. 74:495-500(1993).
RN [11]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102;
RX MEDLINE=9233248; PubMed=1321205;
RA Thomson B.J., Honess R.W.;
RT "The right end of the unique region of the genome of human herpesvirus
RT 6 U102 contains a candidate immediate early gene enhancer and a
RT homologue of the human cytomegalovirus US22 gene family.";
RL J. Gen. Virol. 73:1649-1660(1992).
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102;

RX MEDLINE=93091236; PubMed=133836;
RA Gompels U.A., Carss A.L., Sun N., Arrand J.R.;
RT "Infectivity determinants encoded in a conserved gene block of human
RT herpesvirus-6.";
RL DNA Seq. 3:25-39(1992).
RN [13]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102;
RX MEDLINE=94181269; PubMed=8134119;
RA Thompson J., Choudhury S., Kashanchi F., Doniger J., Berneman Z.,
RA Frenkel N., Rosenthal L.J.;
RT "A transforming fragment within the direct repeat region of human
RT herpesvirus type 6 that transactivates HIV-1.";
RL Oncogene 9:1167-1175(1994).
RN [14]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102;
RX MEDLINE=93224882; PubMed=8385692;
RA Gompels U.A., Carrigan D.R., Carss A.L., Arno J.;
RT "Two groups of human herpesvirus 6 identified by sequence analyses of
RT laboratory strains and variants from Hodgkin's lymphoma and bone
RT marrow transplant patients.";
RL J. Gen. Virol. 74:613-622(1993).
RN [15]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102;
RX MEDLINE=93323202; PubMed=7687301;
RA Pfeiffer B., Berneman Z.N., Neipel F., Chang C.K., Tirwatnapong S.,
RA Chandran B.;
RT "Identification and mapping of the gene encoding the glycoprotein
RT complex gp82-gp105 of human herpesvirus 6 and mapping of the
RT neutralizing epitope recognized by monoclonal antibodies.";
RL J. Virol. 67:4611-4620(1993).
RN [16]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102;
RX MEDLINE=93331710; PubMed=7687803;
RA Pellett P.E., Sanchez-Martinez D., Dominguez G., Black J.B., Anton E.,
RA Greenamoyer C., Dambaugh T.R.;
RT "A strongly immunoreactive virion protein of human herpesvirus 6
RT variant B strain Z29: identification and characterization of the gene
RT and mapping of a variant-specific monoclonal antibody reactive
RT epitope.";
RL Virology 195:521-531(1993).
RN [17]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102;
RX MEDLINE=94025598; PubMed=8212582;
RA Jones M., Teo I.;
RT "Identification and analysis of the transport/capsid assembly protein
RT (tp/cap) gene of human herpesvirus-6 (HHV-6).";
RL Virology 197:449-454(1993).
RN [18]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102;
RX MEDLINE=93389439; PubMed=8397282;
RA Liu D.X., Gompels U.A., Nicholas J., Lelliott C.;
RT "Identification and expression of the human herpesvirus 6 glycoprotein
RT H and interaction with an accessory 40K glycoprotein.";
RL J. Gen. Virol. 74:1847-1857(1993).
RN [19]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102;
RX MEDLINE=94118404; PubMed=8289364;
RA Nicholas J., Martin M.;
RT "Nucleotide sequence analysis of a 38.5-kilobase-pair region of the
RT genome of human herpesvirus 6 encoding human cytomegalovirus
RT immediate-early gene homologs and transactivating functions.";
RL J. Virol. 68:597-610(1994).
RN [20]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102;
RX MEDLINE=94167865; PubMed=8123264;


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RA Zhou Y., Chang C.K., Qian G., Chandran B., Wood C.;
RT "trans-activation of the HIV promoter by a cDNA and its genomic clones
RL of human herpesvirus-6.";
RN Virology 199:311-322(1994).
RP [21]
RC SEQUENCE FROM N.A.
RX STRAIN=U1102;
RX MEDLINE=95146989; PubMed=7844567;
RA Gompels U.A., Macaulay H.A.;
RT "Characterisation of human telomeric repeat sequences from human
RT herpesvirus-6 and relationship to replication.";
RL J. Gen. Virol. 76:451-458(1995).
RN [22]
RC SEQUENCE FROM N.A.
RX STRAIN=U1102;
RX MEDLINE=94202288; PubMed=8151770;
RA Thomson B.J., Dewhurst S., Gray D.;
RT "Structure and heterogeneity of the a sequences of human herpesvirus 6
RT strain variants U1102 and Z29 and identification of human telomeric
RT repeat sequences at the genomic termini.";
RL J. Virol. 68:3007-3014(1994).
RN [23]
RC SEQUENCE FROM N.A.
RX STRAIN=U1102;

Query Match 69.6%; Score 39; DB 2; Length 620;
Best Local Similarity 77.8%; Pred. No. 2.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CUSVPLSVP 9
DB 439 CPSIPLSVP 447

RESULT 8
Q8TGP8 PRELIMINARY; PRT; 144 AA.
AC Q8TGP8;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein YD1086C-A.
GN Name=YD1086C-A;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=21624570; PubMed=11753363;
RA Kumar A., Harrison P.M., Cheung K.H., Lan N., Echols N., Bertone P.,
RA Miller P., Gerstein M.B., Snyder M.;
RT "An integrated approach for finding overlooked genes in yeast.";
RL Nat. Biotechnol. 20:58-63(2002).
DR EMBL; AF479940; AAL79253.1; -.
KW Hypothetical protein.
SQ SEQUENCE 144 AA; 16381 MW; 43F0BFCF4F5B1BFA CRC64;

Query Match 67.9%; Score 38; DB 2; Length 144;
Best Local Similarity 75.0%; Pred. No. 72;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLSVP 10
DB 135 SLPISVP 142

RESULT 9
Q6C595 PRELIMINARY; PRT; 402 AA.
AC Q6C595;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)

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DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Similarity.
GN ORFNames=YALI0E19965g;
OS Yarrowia lipolytica CLIB99.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=CLIB99;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Falla E.,
RA Goffard N., Frangeul L., Aigle M., Anhouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Botsrame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RC SEQUENCE FROM N.A.
RX STRAIN=CLIB99;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382131; CAG79762.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf_C2H2; 1.
DR SMART; SM00355; Znf_C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
SQ SEQUENCE 402 AA; 43889 MW; 0BAC7170D0EAE444 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 402;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SVPLSVP 10
DB 43 SVPLDIPC 50

RESULT 10
IMH2 ARATH
ID IMH2 ARATH STANDARD; PRT; 502 AA.
AC Q9SA34;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Probable inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN OrderedLocNames=At1g16350; ORFNames=F309.15;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712; DOI=10.1038/35048500;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

```

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Miltischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana";
RL Nature 408:816-820(2000).
CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -!- PATHWAY: GMP biosynthesis from IMP; first step.
CC -!- SIMILARITY: Belongs to the IMPDH/GMPR family.
CC -!- SIMILARITY: Contains 1 CBS domain.
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AC006341; AAD34687.1; -.
DR PIR; F86298; F86298.
DR HSP; P12268; 1B30.
DR InterPro; IPR003009; FMN enzyme.
DR InterPro; IPR005990; IMP dehyd.
DR InterPro; IPR001093; IMPDH/GMPRTase.
DR TIGRfam; TIGR01302; IMP dehydrog; 1.
DR PROSITE; PS00487; IMP DH GMP RED; 1.
DR CBS domain; GMP biosynthesis; NAD; Oxidoreductase;
KW Purine biosynthesis; Repeat.
FT DOMAIN 157 219 CBS.
FT BINDING 243 266 NAD (ADP part) (By similarity).
FT ACT SITE 321 321 Thioimide intermediate (By similarity).
FT BINDING 266 266 Inhibitor (By similarity).
FT METAL 316 316 Potassium (via carbonyl oxygen) (By
FT METAL 318 318 Potassium (via carbonyl oxygen) (By
FT BINDING 323 323 Inhibitor (By similarity).
FT BINDING 354 354 IMP (ribose moiety) (By similarity).
FT BINDING 401 401 IMP (phosphate group) (By similarity).
SQ SEQUENCE 502 AA; 54051 MW; FB87D84160818310 CRC64;
Query Match 67.9%; Score 38; DB 1; Length 502;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 VPLSVPC 10
DB 49 VPLSIFC 55
RESULT 11
ID IMH1_ARATH
AC P47996;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).

GN Name=IMPDH; OrderedLocusNames=Atlg79470; ORFNames=T8K14.11;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=97045815; PubMed=8890737; DOI=10.1016/0378-1119(96)00045-5;
Collart F.R., Osipuk J., Trent J., Olsen G.J., Huberman E.;
RT "Cloning and characterization of the gene encoding IMP dehydrogenase
RT from Arabidopsis thaliana";
RL Gene 174:217-220(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712; DOI=10.1038/35048500;
Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Miltischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana";
RL Nature 408:816-820(2000).
CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -!- PATHWAY: GMP biosynthesis from IMP; first step.
CC -!- SIMILARITY: Belongs to the IMPDH/GMPR family.
CC -!- SIMILARITY: Contains 2 CBS domains.
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CC
DR EMBL; L34684; AAB41940.1; -.
DR PIR; J4999; J4999.
DR HSP; P12268; 1B30.
DR InterPro; IPR003009; FMN enzyme.
DR InterPro; IPR005990; IMP dehyd.
DR InterPro; IPR001093; IMPDH/GMPRTase.
DR Pfam; PF00478; IMPDH; 1.
DR TIGRfam; TIGR01302; IMP dehydrog; 1.
DR PROSITE; PS00487; IMP DH GMP RED; 1.
KW CBS domain; GMP biosynthesis; NAD; Oxidoreductase;
FT BIND 244 267 NAD (ADP part) (By similarity).
FT ACT SITE 322 322 Thioimide intermediate (By similarity).
FT BINDING 267 267 Inhibitor (By similarity).
FT METAL 317 317 Potassium (via carbonyl oxygen) (By
FT METAL 319 319 Potassium (via carbonyl oxygen) (By
FT BINDING 324 324 Inhibitor (By similarity).
FT BINDING 355 355 IMP (ribose moiety) (By similarity).
FT BINDING 402 402 IMP (phosphate group) (By similarity).

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SQ SEQUENCE 503 AA; 54194 MW; ADDDAF9C3A697A9A CRC64;
Query Match 67.9%; Score 38; DB 1; Length 503;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPLSVPC 10
DB 49 VPLSIPC 55

RESULT 12
Q8L8U2 PRELIMINARY; PRT; 503 AA.
AC Q8L8U2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase, putative.
OS Arabidopsis thaliana (Mouse-ear Cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22088475; PubMed=12093376;
RA Haas B.J., Voifovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -!- PATHWAY: GMP biosynthesis from IMP; first step.
CC -!- SIMILARITY: Belongs to the IMPDH/GMPR family.
DR EMBL; AY088810; AAM67120.1; -.
DR HSSP; P12268; 1B30.
DR GO; GO:0003938; F:IMP dehydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006177; P:GMP biosynthesis; IEA.
DR InterPro; IPR003009; FMN enzyme.
DR InterPro; IPR001093; IMPDH/GMPrtase.
DR InterPro; IPR005990; IMP_dehyd.
DR Pfam; PF00478; IMPDH; 1.
DR TIGRFAMs; TIGR01302; IMP dehydrog; 1.
DR PROSITE; PS00487; IMP_DH_GMP_RSD; 1.
KW GMP biosynthesis; NAD; Oxidoreductase; Purine biosynthesis.
SQ SEQUENCE 503 AA; 54218 MW; 99D478F48E4E649C CRC64;

Query Match 67.9%; Score 38; DB 2; Length 503;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPLSVPC 10
DB 49 VPLSIPC 55

RESULT 13
Q89D16 PRELIMINARY; PRT; 528 AA.
AC Q89D16;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Blr7629 protein.
GN OrderedLocusNames=blr7629;

OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiyama T.,
RA Sasamoto S., Watanabe A., Idegawa K., Iritiguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; AP005962; BACS2894.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003678; F:DNA helicase activity; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR InterPro; IPR002830; carboxylase.
DR InterPro; IPR007693; DnaB_N.
DR InterPro; IPR000585; Hemopexin.
DR Pfam; PF01977; UbiD; 1.
DR TIGRFAMs; TIGR00148; carboxylase; 1.
DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
KW COMPLETE proteome.
SQ SEQUENCE 528 AA; 58441 MW; 4A1DB04BD1B08546 CRC64;

Query Match 67.9%; Score 38; DB 2; Length 528;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CISVPLSVP 9
DB 284 CLTVPLEVP 292

RESULT 14
ADEC LACPL STANDARD; PRT; 563 AA.
AC Q88SR1;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Adenine deaminase (EC 3.5.4.2) (Adenase) (Adenine aminase).
GN Name=ade; Synonyms=adeC; OrderedLocusNames=lp_3334;
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8826 / WCFS1;
RX MEDLINE=22480296; PubMed=12566566; DOI=10.1073/pnas.0337704100;
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Siezen R.J.;
RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
CC -!- CATALYTIC ACTIVITY: Adenine + H(2)O = hypoxanthine + NH(3).
CC -!- COFACTOR: Manganese (By similarity).
CC -!- SIMILARITY: Belongs to the adenine deaminase family.
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DR EMBL; AL935261; CAD65449.1; -.
DR HAMAP; MF_01518; -; 1.
DR InterPro; IPR006679; Adenine deam.
DR InterPro; IPR006680; Amidohydro 1.
DR InterPro; IPR011059; Metallo hydrolase.
DR Pfam; PF01979; Amidohydro 1; 1.
DR PRODOM; PD001248; Amidohydro-like; 1.
DR TIGRFAMs; TIGR01178; ade; 1.
DR Complete proteome; Hydrolase; Manganese.
SQ SEQUENCE 563 AA; 60927 MW; A4B5159C11718FA7 CRC64;

Query Match 67.9%; Score 38; DB 1; Length 563;
Best Local Similarity 60.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CISVPLSVPC 10
DB 120 CFMLPSSVPC 129

RESULT 15
Y396 HELPJ
ID Y396 HELPU STANDARD; PRT; 616 AA.
AC Q92KF3,
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical protein JHP0985.
GN OrderedLocustNames=JHP0985;
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RA "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori."
RL Nature 397:176-180(1999).
CC -!- SIMILARITY: Belongs to the ubiD family.
-----
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-----
CC EMBL; AE001527; RAD06568.1; -.
DR PIR; D71864; D71864.
DR InterPro; IPR002830; carboxylase.
DR Pfam; PF01977; UbiD; 1.
DR TIGRFAMs; TIGR00148; carboxylase; 1.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 616 AA; 70989 MW; C219E1DCE4C8BDD5 CRC64;

Query Match 67.9%; Score 38; DB 1; Length 616;
Best Local Similarity 77.8%; Pred. No. 3.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CISVPLSV 9
DB 253 CLSNPLSV 261

Search completed: April 1, 2005, 09:26:07
Job time : 63.2329 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 03:27:37 ; Search time 75.4794 Seconds
(without alignments)
51.240 Million cell updates/sec

Title: US-09-761-636a-13

Perfect score: 56

Sequence: 1 CISVPLSVPC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 385760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	10	AAU04532	AAU04532 VEGF base
2	45.5	81.2	11	AAU04526	AAU04526 VEGF base
3	45	80.4	141	AAR66394	AAR66394 Human psy
4	43.5	77.7	11	AAU04542	AAU04542 VEGF base
5	41.5	74.1	9	AAU04533	AAU04533 VEGF base
6	41.5	74.1	11	AAU04545	AAU04545 VEGF base
7	40.5	72.3	11	AAU04544	AAU04544 VEGF base
8	39	69.6	77	AAM95534	AAM95534 Human rep
9	39	69.6	77	ABB96216	ABB96216 Human tes
10	39	69.6	108	AAM95827	AAM95827 Human rep
11	39	69.6	108	ABB96358	ABB96358 Human tes
12	39	69.6	193	ADJ92263	ADJ92263 Mouse hai
13	39	69.6	244	ABO83708	ABO83708 Pseudomon
14	39	69.6	306	ABO74423	ABO74423 Pseudomon
15	38.5	68.8	11	AAU04543	AAU04543 VEGF base
16	38	67.9	59	ABG12542	ABG12542 Novel hum
17	38	67.9	59	ABG12530	ABG12530 Novel hum
18	38	67.9	71	AAMI6003	AAMI6003 Peptide #
19	38	67.9	71	ABE20407	ABE20407 Protein #
20	38	67.9	71	ABG37710	ABG37710 Human pep
21	38	67.9	217	ADB64084	ADB64084 Human pro
22	38	67.9	502	AAQ30888	AAQ30888 Arabidops
23	38	67.9	503	AAQ20989	AAQ20989 Arabidops
24	38	67.9	503	AAQ43108	AAQ43108 Arabidops
25	37	66.1	108	ABB15040	ABB15040 Human ner

26	37	66.1	134	7	ADM05846	Adm05846 Human pro
27	37	66.1	142	7	ABO74636	ABO74636 Pseudomon
28	37	66.1	154	7	ABO70058	ABO70058 Pseudomon
29	37	66.1	316	4	ABB67498	ABB67498 Drosophil
30	37	66.1	368	4	ABG21894	ABG21894 Novel hum
31	37	66.1	370	4	ABB56535	ABB56535 Drosophil
32	37	66.1	438	4	ABG20151	ABG20151 Novel hum
33	37	66.1	875	6	ABG71244	ABG71244 Guinea pi
34	36	64.3	9	2	AAR96138	AAR96138 Protease
35	36	64.3	9	2	AAM82212	AAM82212 D-NoxFES-
36	36	64.3	9	2	AAW46562	AAW46562 Peptide b
37	36	64.3	63	4	AAU58478	AAU58478 Propionib
38	36	64.3	63	6	ABM54997	ABM54997 Propionib
39	36	64.3	64	5	ABP64007	ABP64007 Human ORF
40	36	64.3	65	3	AAAB45459	AAAB45459 Human sec
41	36	64.3	65	3	AAAB45460	AAAB45460 Human sec
42	36	64.3	70	8	ABO56191	ABO56191 Human gen
43	36	64.3	76	4	AAG89148	AAG89148 Human sec
44	36	64.3	83	3	AAAB45461	AAAB45461 Human sec
45	36	64.3	85	3	AAAB45462	AAAB45462 Human sec

ALIGNMENTS

RESULT 1
AAU04532
ID AAU04532 standard; peptide; 10 AA.
XX
AC AAU04532;
XX
DT 26-SEP-2001 (first entry)
XX
DE VEGF based monocyclic peptide 10.
XX
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..10
FT /note= "This bond cyclises the peptide"
XX
PN WO200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR WPI; 2001-442248/47.
XX
PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.
XX
PS Claim 49; Page 32; 102pp; English.
XX
CC The sequence represents a monomeric monocyclic peptide of the invention,
CC whose 3-dimensional structure is modelled on the exposed loop of human
CC VEGF (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclizing the peptide by oxidizing the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 56; DB 4; Length 10;
 AAU04526 100.0%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTSVPLSVPC 10
 |||||
 DB 1 CTSVPLSVPC 10

RESULT 2
 AAU04526
 ID AAU04526 standard; peptide; 11 AA.

XX AC AAU04526;
 XX 26-SEP-2001 (first entry)
 DE VEGF based monocyclic peptide 3.
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX Synthetic.

XX Key Location/Qualifiers
 FH Disulfide-bond 1..11
 FT /note= "This bond cyclises the peptide"

XX WO200152875-A1.
 PD 26-JUL-2001.
 XX 18-JAN-2001; 2001WO-US001533.
 PF 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Hughes RA, Stacker S, Cendron A;
 PI WPI; 2001-442248/47.
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine

PT residues.

XX Claim 49; Page 32; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the exposed loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclizing the peptide by oxidizing the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 11 AA;

Query Match 81.2%; Score 45.5; DB 4; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.73;
 Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CTSVPL-SVPC 10
 |||||
 DB 1 CTSVPLTSVPC 11

RESULT 3
 AAR66394
 ID AAR66394 standard; peptide; 141 AA.

XX AC AAR66394;
 XX 25-MAR-2003 (revised)
 DT 11-AUG-1995 (first entry)
 XX Human psychosis protecting peptide encoded by reading frame 1.
 DE Psychosis protecting peptide.
 XX Homo sapiens.
 OS Key Location/Qualifiers
 FH Misc-difference 1..141
 FT /note= "X corresp. to translated stop codon"

XX WO9426107-A1.
 PD 24-NOV-1994.
 XX 13-MAY-1994; 94WO-US005445.
 PF 13-MAY-1993; 93US-00060560.
 PR (UINY) UNIV NEW YORK STATE.
 XX Friedhoff AJ, Basham DA, Miller JC;

XX WPI: 1995-006234/01.
 DR N-PSDB; AAQ75090.
 XX
 PT New nucleic acids encoding psychosis protecting peptide and antibodies -
 PT for the treatment, diagnosis and research of psychotic disorders, such as
 PT schizophrenia.
 XX
 PS Claim 1; Page 56; 87pp; English.
 XX
 CC Psychosis protecting peptide (PP peptide) can be obtd. initially by
 CC using the sequence in AAQ75090 as a basis for designing polynucleotide
 CC probes to clone, sequence and express or synthesize PP related protein
 CC and peptides occurring in normal individuals, and to a substantially
 CC lesser degree in individuals with psychotic disorders. The PP encoding
 CC gene was discovered using the subtraction cloning of cDNA from mRNA obtd.
 CC from monozygotic twins discordant for schizophrenia and assaying for
 CC clones in which expression is greatest in the 'well' twin. A nt sequence
 CC substantially corresp. to AAQ75090 is claimed, which comprises 30-X nts,
 CC where X=80, 95, 158, 222, 243, 249, 260, 295, 407 or 423. A PP peptide of
 CC 10-141 AAs is also claimed. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 141 AA;
 Query Match 80.4%; Score 45; DB 2; Length 141;
 Best Local Similarity 77.8%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 C1SVPLSPV 9
 |||||
 DB 28 C1SIPLSIP 36
 |||||
 RESULT 4
 AAU04542
 ID AAU04542 standard; peptide; 11 AA.
 XX
 AC AAU04542;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE VEGF based monocyclic peptide 20.
 XX
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..11
 FT /note= "This bond cyclises the peptide"
 XX
 PN WO200152875-A1.
 XX
 PD 26-JUL-2001.
 XX
 XX 18-JAN-2001; 2001WO-US001533.
 PF
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Achen MG, Hughes RA, Stackler S, Cendron A;
 XX
 DR WPI; 2001-442248/47.
 XX
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.

XX Example 25; Page 47; 102pp; English.
 XX
 CC The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 11 AA;
 Query Match 77.7%; Score 43.5; DB 4; Length 11;
 Best Local Similarity 81.8%; Pred. No. 1.6;
 Matches 9; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
 QY 1 C1SVPL-SVPC 10
 |||||
 DB 1 C1SVPLTSVPC 11
 |||||
 RESULT 5
 AAU04533
 ID AAU04533 standard; peptide; 9 AA.
 XX
 AC AAU04533;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE VEGF based monocyclic peptide 11.
 XX
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..9
 FT /note= "This bond cyclises the peptide"
 XX
 PN WO200152875-A1.
 XX
 PD 26-JUL-2001.
 XX
 XX 18-JAN-2001; 2001WO-US001533.
 PF
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX

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XX PI Achen MG, Hughes RA, Stacker S, Cendron A;
XX DR WPI; 2001-442248/47.
XX
XX PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
XX FT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
XX FT from an exposed loop of a growth factor protein by oxidizing the cysteine
XX FT residues.
XX
XX PS Claim 49; Page 32; 102pp; English.
XX
XX CC The sequence represents a monomeric monocyclic peptide of the invention,
XX CC whose 3-dimensional structure is modelled on the expose loop of human
XX CC VEGF (vascular endothelial growth factor). The invention relates to a
XX CC method of producing a monomeric monocyclic peptide by a measuring beta-
XX CC beta carbon separation distances on opposite antiparallel strands of a
XX CC peptide loop fragment from an exposed loop of a growth factor protein and
XX CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
XX CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
XX CC peptides) and a cyclic peptide with at least one amino acid deleted prior
XX CC to cyclisation are used to interfere with angiogenesis,
XX CC neovascularisation or lymphangiogenesis in a mammal with a condition
XX CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
XX CC The condition is diabetic retinopathy, psoriasis, arthropathy,
XX CC hemangioma, vascularised malignant or benign tumour, post-recovery
XX CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
XX CC trauma, substance-induced neovascularisation of the liver, excessive
XX CC hormone-related angiogenic dysfunction, diabetes induced neovascular
XX CC sequelae, hypertension induced neovascular sequelae, or chronic liver
XX CC infection. The peptides are also used to modulate vascular permeability
XX CC in a mammal (the mammal has a condition characterised by fluid
XX CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
XX CC or brain. The peptides are used to image blood vessels and lymphatic
XX CC vasculature. The monomeric and bicyclic peptides are used to interfere
XX CC with at least one biological activity induced by VEGF, VEGF-C or -D and
XX CC are also used in combination with an anti-inflammatory agent, to treat a
XX CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
XX CC diabetic retinopathy
XX
XX SQ Sequence 9 AA;
XX
XX Query Match 74.1%; Score 41.5; DB 4; Length 9;
XX Best Local Similarity 90.0%; Pred. No. 1.8e-06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
XX QY 1 CTSVPLSVPC 10
XX |||||
XX Db 1 CTSVPL-VPC 9
XX
XX RESULT 6
XX AAU04545
XX ID AAU04545 standard; peptide; 11 AA.
XX
XX AC AAU04545;
XX
XX DT 26-SEP-2001 (first entry)
XX
XX DE VEGF based monocyclic peptide 23.
XX
XX KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
XX KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
XX KW diabetes induced neovascular sequelae; rheumatoid arthritis;
XX KW diabetic retinopathy; chronic inflammation; cyclic.
XX
XX OS Synthetic.
XX
XX FH Key
XX FT Disulfide-bond 1..11
XX FT Location/Qualifiers
XX FT /note= "This bond cyclises the peptide"
XX
XX PN WO200152875-A1.
XX

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XX PD 26-JUL-2001.
XX PF 18-JAN-2001; 2001WO-US001533.
XX PR 18-JAN-2000; 2000US-0176293P.
XX PR 16-MAY-2000; 2000US-0204590P.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX
XX PI Achen MG, Hughes RA, Stacker S, Cendron A;
XX DR WPI; 2001-442248/47.
XX
XX PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
XX FT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
XX FT from an exposed loop of a growth factor protein by oxidizing the cysteine
XX FT residues.
XX
XX PS Example 25; Page 47; 102pp; English.
XX
XX CC The sequence represents a monomeric monocyclic peptide of the invention,
XX CC whose 3-dimensional structure is modelled on the expose loop of human
XX CC VEGF (vascular endothelial growth factor). The invention relates to a
XX CC method of producing a monomeric monocyclic peptide by a measuring beta-
XX CC beta carbon separation distances on opposite antiparallel strands of a
XX CC peptide loop fragment from an exposed loop of a growth factor protein and
XX CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
XX CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
XX CC peptides) and a cyclic peptide with at least one amino acid deleted prior
XX CC to cyclisation are used to interfere with angiogenesis,
XX CC neovascularisation or lymphangiogenesis in a mammal with a condition
XX CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
XX CC The condition is diabetic retinopathy, psoriasis, arthropathy,
XX CC hemangioma, vascularised malignant or benign tumour, post-recovery
XX CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
XX CC trauma, substance-induced neovascularisation of the liver, excessive
XX CC hormone-related angiogenic dysfunction, diabetes induced neovascular
XX CC sequelae, hypertension induced neovascular sequelae, or chronic liver
XX CC infection. The peptides are also used to modulate vascular permeability
XX CC in a mammal (the mammal has a condition characterised by fluid
XX CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
XX CC or brain. The peptides are used to image blood vessels and lymphatic
XX CC vasculature. The monomeric and bicyclic peptides are used to interfere
XX CC with at least one biological activity induced by VEGF, VEGF-C or -D and
XX CC are also used in combination with an anti-inflammatory agent, to treat a
XX CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
XX CC diabetic retinopathy
XX
XX SQ Sequence 11 AA;
XX
XX Query Match 74.1%; Score 41.5; DB 4; Length 11;
XX Best Local Similarity 72.7%; Pred. No. 3.3;
XX Matches 8; Conservative 2; Mismatches 0; Indels 1; Gaps 1;
XX
XX QY 1 CTSVPL-SVPC 10
XX |||||
XX Db 1 CTSVPLTTVPC 11
XX
XX RESULT 7
XX AAU04544
XX ID AAU04544 standard; peptide; 11 AA.
XX
XX AC AAU04544;
XX
XX DT 26-SEP-2001 (first entry)
XX
XX DE VEGF based monocyclic peptide 22.
XX
XX KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
XX KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
XX KW diabetes induced neovascular sequelae; rheumatoid arthritis;

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KW diabetic retinopathy; chronic inflammation; cyclic.

OS Synthetic.

XX Key Location/Qualifiers

XX Disulfide-bond 1..11

XX FT /note= "This bond cyclises the peptide"

XX WO200152875-A1.

XX PD 26-JUL-2001.

XX PF 18-JAN-2001; 2001WO-US001533.

XX PR 18-JAN-2000; 2000US-0176293P.

XX PR 16-MAY-2000; 2000US-0204590P.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Achen MG, Hughes RA, Stacker S, Cendron A;

XX DR WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

XX Example 25; Page 47; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the exposed loop of human VEGF (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis,

XX neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain). The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy

XX Sequence 11 AA;

Query Match 72.3%; Score 40.5; DB 4; Length 11;

Best Local Similarity 72.7%; Pred. No. 4.8;

Matches 8; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

Oy 1 CISVPL-SVPC 10

Db 1 CISLFISSVPC 11

RESULT 8

AA095534

ID AA095534 standard; protein; 77 AA.

XX

AC AA095534;

XX 21-NOV-2001 (first entry)

XX Human reproductive system related antigen SEQ ID NO: 4192.

XX Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy.

XX Homo sapiens.

XX WO200155320-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US001339.

XX 31-JAN-2000; 2000US-0179065P.

XX 04-FEB-2000; 2000US-0180628P.

XX 24-FEB-2000; 2000US-0184664P.

XX 02-MAR-2000; 2000US-0186350P.

XX 16-MAR-2000; 2000US-0189874P.

XX 17-MAR-2000; 2000US-0190076P.

XX 18-APR-2000; 2000US-0198123P.

XX 19-MAY-2000; 2000US-0205515P.

XX 07-JUN-2000; 2000US-0209467P.

XX 28-JUN-2000; 2000US-0214886P.

XX 30-JUN-2000; 2000US-0215135P.

XX 07-JUL-2000; 2000US-0216647P.

XX 07-JUL-2000; 2000US-0216800P.

XX 11-JUL-2000; 2000US-0217487P.

XX 11-JUL-2000; 2000US-0217496P.

XX 14-JUL-2000; 2000US-0218290P.

XX 26-JUL-2000; 2000US-0220963P.

XX 26-JUL-2000; 2000US-0220964P.

XX 14-AUG-2000; 2000US-0224518P.

XX 14-AUG-2000; 2000US-0224519P.

XX 14-AUG-2000; 2000US-0225213P.

XX 14-AUG-2000; 2000US-0225214P.

XX 14-AUG-2000; 2000US-0225266P.

XX 14-AUG-2000; 2000US-0225267P.

XX 14-AUG-2000; 2000US-0225268P.

XX 14-AUG-2000; 2000US-0225270P.

XX 14-AUG-2000; 2000US-0225447P.

XX 14-AUG-2000; 2000US-0225757P.

XX 14-AUG-2000; 2000US-0225758P.

XX 18-AUG-2000; 2000US-0225759P.

XX 22-AUG-2000; 2000US-0226279P.

XX 22-AUG-2000; 2000US-0226681P.

XX 22-AUG-2000; 2000US-0226868P.

XX 22-AUG-2000; 2000US-0227182P.

XX 23-AUG-2000; 2000US-0227009P.

XX 30-AUG-2000; 2000US-0228924P.

XX 01-SEP-2000; 2000US-0229287P.

XX 01-SEP-2000; 2000US-0229343P.

XX 01-SEP-2000; 2000US-0229344P.

XX 01-SEP-2000; 2000US-0229345P.

XX 05-SEP-2000; 2000US-0229509P.

XX 05-SEP-2000; 2000US-0229513P.

XX 06-SEP-2000; 2000US-0230437P.

XX 06-SEP-2000; 2000US-0230438P.

XX 08-SEP-2000; 2000US-0231242P.

XX 08-SEP-2000; 2000US-0231243P.

XX 08-SEP-2000; 2000US-0231244P.

XX 08-SEP-2000; 2000US-0231413P.

XX 08-SEP-2000; 2000US-0231414P.

XX 08-SEP-2000; 2000US-0232080P.

XX 08-SEP-2000; 2000US-0232081P.

XX 12-SEP-2000; 2000US-0231968P.

XX 14-SEP-2000; 2000US-0232397P.

XX 14-SEP-2000; 2000US-0232398P.

XX 14-SEP-2000; 2000US-0232399P.

XX 14-SEP-2000; 2000US-0232400P.

PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246529P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
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 PR 17-NOV-2000; 2000US-0249244P.
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 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0255179P.

PR 08-DEC-2000; 2000US-0251856P.
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 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-465570/50.
 DR N-PSDB; AAL01504.
 XX
 PT Isolated nucleic acid molecule encoding a reproductive system antigen is
 used in preventing, treating or ameliorating a medical condition.
 XX
 PS Claim 11; SEQ ID NO 4192; 1297pp + Sequence Listing; English.
 XX
 CC The present invention provides the protein and coding sequences of a
 number of human reproductive system related antigens. These can be used
 in the prevention and treatment of reproductive system disorders,
 CC including cancer. The present sequence is a protein of the invention
 CC
 SQ Sequence 77 AA;
 Query Match 69.6%; Score 39; DB 4; Length 77;
 Best Local Similarity 40.0%; Pred. No. 63;
 Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 C1SVPLSVPC 10
 Db 47 CLNAPIRIPC 56
 RESULT 9
 ABB96216
 ID ABB96216 standard; protein; 77 AA.
 XX ABB96216;
 AC
 XX 21-JUN-2002 (first entry)
 DT Human testicular antigen SEQ ID NO: 1600.
 DE Human; testicular antigen; testes; cancer; metastasis; immune disorder;
 KW reproductive system disorder; urinary system disorder; gene therapy;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disease; infection; cytostatic.
 XX Homo sapiens.
 OS
 XX WO200155317-A2.
 PN
 XX 02-AUG-2001.
 PD
 XX 17-JAN-2001; 2001WO-US001329.
 PF
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
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 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
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 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.


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PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-465570/50.
DR N-PSDB; AAL01797.
XX
XX Isolated nucleic acid molecule encoding a reproductive system antigen is
PT used in preventing, treating or ameliorating a medical condition.
XX
XX Claim 11; SEQ ID NO 4485; 1297pp + Sequence Listing; English.
XX
XX The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a protein of the invention
XX
XX SQ Sequence 108 AA;

Query Match          69.6%; Score 39; DB 4; Length 108;
Best Local Similarity 77.8%; Pred. No. 89;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 ISVPLSVPC 10
Db      :|||||
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RESULT 11
ABB96358
ID ABB96358 standard; protein; 108 AA.
XX
XX ABB96358;
XX
XX
XX 21-JUN-2002 (first entry)
DT
XX
DE Human testicular antigen SEQ ID NO: 1742.
XX
XX Human; testicular antigen; testes; cancer; metastasis; immune disorder;
KW reproductive system disorder; urinary system disorder; gene therapy;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disease; infection; cytostatic.
XX
XX Homo sapiens.
XX
XX WO200155317-A2.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001329.
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XX 31-JAN-2000; 2000US-0179065P.
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PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
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PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
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PR 14-AUG-2000; 2000US-0224518P.
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PR 12-SEP-2000; 2000US-0231968P.
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PR 21-SEP-2000; 2000US-0234223P.
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PR 25-SEP-2000; 2000US-0234997P.
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PR 26-SEP-2000; 2000US-0235484P.
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PR 27-SEP-2000; 2000US-0235836P.
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PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
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PR 02-OCT-2000; 2000US-0237039P.
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02-OCT-2000; 2000US-0237040P.
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 PR 17-NOV-2000; 2000US-0249265P.
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 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254057P.
 PR 05-JAN-2001; 2001US-0259678P.
 PR XX
 FA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 XX WPT; 2001-483232/52.
 XX
 PT Nucleic acids encoding 973 human testicular antigen polypeptides, useful
 PT for preventing, diagnosing and/or treating testicular cancer.
 XX
 XX
 PS Claim 11; SEQ ID NO 1742; 766pp; English.
 CC
 CC The present invention provides the protein and coding sequences of 973

CC partial peptides or (I) or (II), expression vectors for them, or host
 CC cells transformed by these vectors. KAP sequences can be used as hair
 CC growth promoters. The KAPs are useful as active ingredients in toiletry
 CC compositions (such as hair and beard growth improvers, hair colourants
 CC and hair conditioners) and in therapeutic compositions for hair
 CC disorders. The present sequence is used in the exemplification of the
 CC present invention.

XX Sequence 193 AA;

Query Match 69.6%; Score 39; DB 7; Length 193;
 Best Local Similarity 60.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTSVPLSVPC 10
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 Db 91 CWSNPCTPC 100

RESULT 13

ABO83708
 ID ABO83708 standard; protein; 244 AA.

XX AC ABO83708;

DT 29-JUL-2004 (first entry)

XX Pseudomonas aeruginosa polypeptide #15883.

DE Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX OS Pseudomonas aeruginosa.

XX PN US6551795-B1.

XX PD 22-APR-2003.

XX PF 18-FEB-1999; 99US-00252991.

XX PR 18-FEB-1998; 98US-0074788P.

XX PR 27-JUL-1998; 98US-0094190P.

XX PA (GENO-) GENOME THERAPEUTICS CORP.

XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX DR WPI; 2003-615309/58.

XX DR N-PSDB; ABD17279.

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.

XX Disclosure; SEQ ID NO 32454; 455pp; English.

CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biotech technology. Sequences ABO67826-
 CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html

XX Sequence 244 AA;

Query Match 69.6%; Score 39; DB 7; Length 244;
 Best Local Similarity 60.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTSVPLSVPC 10
 | : | | | |
 Db 24 CCSRPMAVPC 33

RESULT 14

ABO74423
 ID ABO74423 standard; protein; 306 AA.

XX AC ABO74423;

DT 29-JUL-2004 (first entry)

XX Pseudomonas aeruginosa polypeptide #6598.

DE Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX OS Pseudomonas aeruginosa.

XX PN US6551795-B1.

XX PD 22-APR-2003.

XX PF 18-FEB-1999; 99US-00252991.

XX PR 18-FEB-1998; 98US-0074788P.

XX PR 27-JUL-1998; 98US-0094190P.

XX PA (GENO-) GENOME THERAPEUTICS CORP.

XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX DR WPI; 2003-615309/58.

XX DR N-PSDB; ABD07994.

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.

XX Disclosure; SEQ ID NO 23169; 455pp; English.

CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biotech technology. Sequences ABO67826-
 CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html

XX Sequence 306 AA;

Query Match 69.6%; Score 39; DB 7; Length 306;
 Best Local Similarity 70.0%; Pred. No. 2.6e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTSVPLSVPC 10
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 Db 7 CWSVPSSAPC 16

RESULT 15
AAU04543
ID AAU04543 standard; peptide, 11 AA.
XX
XX AC AAU04543;
XX 26-SEP-2001 (first entry)
XX
XX VEGF based monocyclic peptide 21.
DE
XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Disulfide-bond 1..11
FT /note= "This bond cyclises the peptide"
FT
XX WO200152875-A1.
PN
XX 26-JUL-2001.
PD
XX 18-JAN-2001; 2001WO-US001533.
PF
XX 18-JAN-2000; 2000US-0176293P.
PR
XX 16-MAY-2000; 2000US-0204590P.
XX
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX
XX PI Achen MG, Hughes RA, Stacker S, Cendron A;
XX WPI; 2001-442248/47.
XX
XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.
XX
XX Example 25; Page 47; 102pp; English.
XX
XX The sequence represents a monomeric monocyclic peptide of the invention,
CC whose 3-dimensional structure is modelled on the expose loop of human
CC VEGF (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a
CC peptide loop fragment from an exposed loop of a growth factor protein and
CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC peptides) and a cyclic peptide with at least one amino acid deleted prior
CC to cyclisation are used to interfere with angiogenesis,
CC neovascularisation or lymphangiogenesis in a mammal with a condition
CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC The condition is diabetic retinopathy, psoriasis, arthropathy,
CC hemangioma, vascularised malignant or benign tumour, post-recovery
CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC trauma, substance-induced neovascularisation of the liver, excessive
CC hormone-related angiogenic dysfunction, diabetes induced neovascular
CC sequelae, hypertension induced neovascular sequelae, or chronic liver
CC infection. The peptides are also used to modulate vascular permeability
CC in a mammal (the mammal has a condition characterised by fluid
CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC or brain. The peptides are used to image blood vessels and lymphatic
CC vasculature. The monomeric and bicyclic peptides are used to interfere
CC with at least one biological activity induced by VEGF, VEGF-C or -D and
CC are also used in combination with an anti-inflammatory agent, to treat a
CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC diabetic retinopathy
XX
SQ Sequence 11 AA;

Query Match 68.8%; Score 38.5; DB 4; Length 11;
Best Local Similarity 63.6%; Pred. No. 10;
Matches 7; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CTSVPL-SVPC 10
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Db 1 CITIPLTSLPC 11

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Job time : 77.4794 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 09:26:18 ; Search time 245.753 Seconds
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Title: US-09-761-636A-13

Perfect score: 56

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Total number of hits satisfying chosen parameters: 1413372

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Listing first 45 summaries

Database : Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	45.5	81.2	11	9 US-09-761-636A-7	Sequence 7, Appl
3	43.5	77.7	11	9 US-09-761-636A-23	Sequence 23, Appl
4	43	76.8	140	16 US-10-437-963-174203	Sequence 174203
5	41.5	74.1	9	9 US-09-761-636A-14	Sequence 14, Appl
6	41.5	74.1	11	9 US-09-761-636A-26	Sequence 26, Appl
7	41	73.2	84	15 US-10-424-599-264847	Sequence 264847
8	40.5	72.3	11	9 US-09-761-636A-25	Sequence 25, Appl
9	40	71.4	279	16 US-10-437-963-167987	Sequence 167987
10	39	69.6	77	10 US-09-764-891-4192	Sequence 4192, Ap
11	39	69.6	83	15 US-10-425-114-58210	Sequence 58210, A
12	39	69.6	108	10 US-09-764-891-4485	Sequence 4485, Ap
13	39	69.6	190	15 US-10-425-114-50298	Sequence 50298, A

14	38.5	68.8	11	9 US-09-761-636A-24	Sequence 24, Appl
15	38	67.9	71	9 US-09-864-761-35705	Sequence 35705, A
16	38	67.9	142	15 US-10-424-599-220123	Sequence 220123, A
17	38	67.9	202	16 US-10-437-963-140110	Sequence 140110, A
18	38	67.9	217	15 US-10-104-047-2238	Sequence 2238, Ap
19	38	67.9	465	15 US-10-335-977-7910	Sequence 7910, Ap
20	38	67.9	578	15 US-10-335-977-7911	Sequence 7911, Ap
21	38	67.9	616	15 US-10-335-977-7912	Sequence 7912, Ap
22	38	67.9	1590	16 US-10-437-963-106960	Sequence 106960, A
23	37	66.1	92	16 US-10-767-701-60298	Sequence 60298, A
24	37	66.1	134	15 US-10-108-260A-4531	Sequence 4531, Ap
25	37	66.1	355	16 US-10-437-963-125857	Sequence 125857, A
26	37	66.1	420	16 US-10-437-963-142446	Sequence 142446, A
27	37	66.1	769	13 US-10-087-110-6	Sequence 6, Appli
28	37	66.1	875	13 US-10-087-110-2	Sequence 2, Appli
29	36	64.3	46	15 US-10-424-599-284943	Sequence 284943, A
30	36	64.3	59	16 US-10-437-963-199587	Sequence 199587, A
31	36	64.3	64	9 US-09-867-550-754	Sequence 754, App
32	36	64.3	70	14 US-10-029-386-29825	Sequence 29825, A
33	36	64.3	76	9 US-09-731-872-268	Sequence 268, App
34	36	64.3	76	10 US-09-876-997-268	Sequence 268, App
35	36	64.3	82	16 US-10-437-963-106647	Sequence 106647, A
36	36	64.3	108	15 US-10-424-599-184465	Sequence 184465, A
37	36	64.3	113	9 US-09-815-248-2	Sequence 2, Appli
38	36	64.3	170	16 US-10-787-701-59682	Sequence 59682, A
39	36	64.3	217	15 US-10-424-599-198582	Sequence 198582, A
40	36	64.3	230	15 US-10-104-047-3554	Sequence 3554, Ap
41	36	64.3	241	15 US-10-425-114-60080	Sequence 60080, A
42	36	64.3	381	15 US-10-369-493-7846	Sequence 7846, Ap
43	36	64.3	669	10 US-09-790-852-7	Sequence 7, Appli
44	36	64.3	836	16 US-10-437-963-119123	Sequence 119123, A
45	35.5	63.4	80	13 US-10-052-586-576	Sequence 576, App

ALIGNMENTS

RESULT 1

US-09-761-636A-13
; Sequence 13, Application US/09761636A
; Patent No. US2002005218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-13

Query Match 100.0%; Score 56; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.017; 0; Indels 0; Gaps 0;
Matches 10; Mismatches 0;

Qy 1 CISVPLSVPC 10
Db 1 CISVPLSVPC 10

RESULT 2

US-09-761-636A-7

; Sequence 7, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-7

Query Match 81.2%; Score 45.5; DB 9; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.88;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CISVPL-SVPC 10
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Db 1 CISVPLTSVPC 11

RESULT 3

US-09-761-636A-23
; Sequence 23, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-23

Query Match 77.7%; Score 43.5; DB 9; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.8;
Matches 9; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 CISVPL-SVPC 10
|||||
Db 1 CLSVPLTSVPC 11

RESULT 4

US-10-437-963-174203
; Sequence 174203, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 174203
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Oryza sativa
; NAME/KEY: unsure
; LOCATION: (1)..(140)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_72167C.1.pep
US-10-437-963-174203

Query Match 76.8%; Score 43; DB 16; Length 140;
Best Local Similarity 70.0%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVPLSVPC 10
|||||
Db 115 CSSTPLTVPC 124

RESULT 5

US-09-761-636A-14
; Sequence 14, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-14

Query Match 74.1%; Score 41.5; DB 9; Length 9;
Best Local Similarity 90.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CISVPLSVPC 10
|||||
Db 1 CISVPL-VPC 9

RESULT 6

US-09-761-636A-26
; Sequence 26, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc

APPLICANT: STACKER, Steven
APPLICANT: HUGHES, Richard
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2001-01-18

PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn version 3.0

SEQ ID NO 26

LENGTH: 11

TYPE: PRT

ORGANISM: synthetic construct

US-09-761-636A-26

Query Match 74.1%; Score 41.5; DB 9; Length 11;
Best Local Similarity 72.7%; Pred. No. 3.8;
Matches 8; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CISVPL-SVPC 10

Db 1 CVSPLTTVPC 11

RESULT 7

US-10-424-599-264847
Sequence 264847, Application US/10424599
Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 264847

LENGTH: 84

TYPE: PRT

ORGANISM: Glycine max

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_81177C.1.pap

US-10-424-599-264847

Query Match 73.2%; Score 41; DB 15; Length 84;
Best Local Similarity 70.0%; Pred. No. 34;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CISVPLSVPC 10

Db 24 CVSPLTTVPC 33

RESULT 8

US-09-761-636A-25

Sequence 25, Application US/09761636A

Patent No. US20020065218A1

GENERAL INFORMATION:

APPLICANT: ACHEN, Marc

APPLICANT: STACKER, Steven

APPLICANT: HUGHES, Richard

APPLICANT: CENDRON, Angela

TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/48505 Achen et al

CURRENT APPLICATION NUMBER: US/09/761,636A

CURRENT FILING DATE: 2001-01-18

PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn version 3.0

SEQ ID NO 25

LENGTH: 11

TYPE: PRT

ORGANISM: synthetic construct

US-09-761-636A-25

Query Match 72.3%; Score 40.5; DB 9; Length 11;
Best Local Similarity 72.7%; Pred. No. 5.4;
Matches 8; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CISVPL-SVPC 10

Db 1 CISPLISSVPC 11

RESULT 9

US-10-437-963-167987

Sequence 167987, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 167987

LENGTH: 279

TYPE: PRT

ORGANISM: Oryza sativa

FEATURE:

NAME/KEY: unsure

LOCATION: (1)-(279)

OTHER INFORMATION: unsure at all Xaa locations

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT4530_66546C.1.pap

US-10-437-963-167987

Query Match 71.4%; Score 40; DB 16; Length 279;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CISVPLSVPC 9

Db 175 CINVPFSVP 183

RESULT 10

US-09-764-891-4192

Sequence 4192, Application US/09764891

Publication No. US20030077808A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC006

CURRENT APPLICATION NUMBER: US/09/764,891

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 10231

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4192
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (49)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (51)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (73)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (93)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-764-891-4485

Query Match          69.6%; Score 39; DB 10; Length 77;
Best Local Similarity 40.0%; Pred. No. 64;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 C1SVPLSVPC 10
   : : : : :
Db 47 CLNADIRIPC 56

RESULT 11
US-10-425-114-58210
; Sequence 58210, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 58210
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB84-029-E3_FLI.pgp
US-10-425-114-58210

Query Match          69.6%; Score 39; DB 15; Length 83;
Best Local Similarity 75.0%; Pred. No. 69;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVPLSVPC 10
   : : : : :
Db 68 TVPLSIPC 75

RESULT 12
US-09-764-891-4485
; Sequence 4485, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4485
; LENGTH: 108
; TYPE: PRT

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (49)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (51)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (73)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (93)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-764-891-4485

Query Match          69.6%; Score 39; DB 10; Length 108;
Best Local Similarity 77.8%; Pred. No. 89;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 1SVPLSVPC 10
   : : : : :
Db 33 VSVPLSHPC 41

RESULT 13
US-10-425-114-50298
; Sequence 50298, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 50298
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB189-012-E9_FLI.pgp
US-10-425-114-50298

Query Match          69.6%; Score 39; DB 15; Length 190;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVPLSVPC 10
   : : : : :
Db 175 TVPLSIPC 182

RESULT 14
US-09-761-636A-24
; Sequence 24, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
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; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636a-24

Query Match 68.8%; Score 38.5; DB 9; Length 11;
Best Local Similarity 63.6%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 CISVPL-SVPC 10
||:|||||
Db 1 CITIPLTSLPC 11

RESULT 15

US-09-864-761-35705
; Sequence 35705, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aomic-a-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35705

; LENGTH: 71
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL078621.19
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.91
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.94
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.7
; OTHER INFORMATION: EST_HUMAN HIT: BF125501.1, EVALUATE 1.70e+00
; OTHER INFORMATION: SWISSPROT HIT: P11992, EVALUATE 2.20e-01
US-09-864-761-35705

Query Match 67.9%; Score 38; DB 9; Length 71;
Best Local Similarity 77.8%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVPLSVP 9
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Db 51 CISVPLPTP 59

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Title: US-09-761-636A-12

Perfect score: 38

Sequence: 1 CVPLTC 6

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- 10: /cgn2_6/prodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
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- 14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/prodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	100.0	6	9 US-09-761-636A-12	Sequence 12, Appl
2	38	100.0	45	15 US-10-424-599-164353	Sequence 164353,
3	36	94.7	175	10 US-09-826-734-122	Sequence 128, Appl
4	36	94.7	613	9 US-09-799-514-9	Sequence 9, Appl
5	36	94.7	3104	15 US-10-016-248-2	Sequence 2, Appl
6	36	94.7	3389	15 US-10-016-248-47	Sequence 47, Appl
7	36	94.7	3389	16 US-10-408-765A-2286	Sequence 2286, Ap
8	36	94.7	3508	15 US-10-016-248-45	Sequence 46, Appl
9	36	94.7	3564	15 US-10-016-248-45	Sequence 45, Appl
10	35	92.1	127	15 US-10-424-599-198429	Sequence 198429,
11	35	92.1	310	15 US-10-094-749-3057	Sequence 3057, Ap
12	35	92.1	1232	17 US-10-741-600-1404	Sequence 1404, Ap
13	35	92.1	1420	17 US-10-741-600-1403	Sequence 1403, Ap

14	35	92.1	1420	17	US-10-741-600-1405	Sequence 1405, Ap
15	35	92.1	1547	17	US-10-783-311-2	Sequence 2, Appl
16	35	92.1	1627	10	US-09-983-025-25	Sequence 25, Appl
17	35	92.1	1627	15	US-10-295-027-663	Sequence 663, App
18	35	92.1	1627	17	US-10-783-311-1	Sequence 1, Appl
19	35	92.1	1627	17	US-10-741-600-1406	Sequence 1406, Ap
20	34	89.5	80	15	US-10-424-599-272858	Sequence 272858,
21	34	89.5	570	15	US-10-104-047-3842	Sequence 3842, Ap
22	33	86.8	52	16	US-10-437-963-190243	Sequence 190243,
23	33	86.8	58	15	US-10-424-599-252356	Sequence 252356,
24	33	86.8	60	15	US-10-424-599-198470	Sequence 198470,
25	33	86.8	62	15	US-10-424-599-170802	Sequence 170802,
26	33	86.8	69	15	US-10-424-599-145317	Sequence 145317,
27	33	86.8	103	15	US-10-424-599-21717	Sequence 21717,
28	33	86.8	149	15	US-10-425-114-60690	Sequence 60690, A
29	33	86.8	158	15	US-10-282-122A-44515	Sequence 44515, A
30	33	86.8	162	15	US-10-425-114-50640	Sequence 50640, A
31	33	86.8	187	15	US-10-425-114-50780	Sequence 50780, A
32	33	86.8	556	9	US-09-815-923-6	Sequence 6, Appl
33	33	86.8	1575	15	US-10-262-839-212	Sequence 212, App
34	33	86.8	1587	9	US-09-845-583-10	Sequence 10, Appl
35	33	86.8	1587	15	US-10-262-839-210	Sequence 210, App
36	32	84.2	34	16	US-10-437-963-200127	Sequence 200127,
37	32	84.2	49	9	US-09-739-254-83	Sequence 83, Appl
38	32	84.2	49	9	US-09-904-615-83	Sequence 83, Appl
39	32	84.2	49	14	US-10-054-988-83	Sequence 83, Appl
40	32	84.2	55	15	US-10-424-599-207242	Sequence 207242,
41	32	84.2	57	15	US-10-424-599-240922	Sequence 240922,
42	32	84.2	64	16	US-10-767-701-49761	Sequence 49761, A
43	32	84.2	113	16	US-10-767-701-56027	Sequence 56027, A
44	32	84.2	117	15	US-10-424-599-274520	Sequence 274520,
45	32	84.2	125	9	US-09-864-761-46679	Sequence 46679, A

ALIGNMENTS

RESULT 1
US-09-761-636A-12
; Sequence 12, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-12

Query Match 100.0%; Score 38; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVPLTC 6

Db 1 CVPLTC 6

RESULT 2

US-10-424-599-164353

; Sequence 164353, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 164353
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_119429C.1.pep
US-10-424-599-164353

Query Match 100.0%; Score 38; DB 15; Length 45;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 34 CVPLTC 39

RESULT 3
US-09-826-734-122
; Sequence 122, Application US/09826734
; Publication No. US20030017457A1
; GENERAL INFORMATION:
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Vernhet, Corine A.M.
; APPLICANT: Mishra, Vishnu S.
; APPLICANT: Leach, Martin D.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Kekuda, Ramesha
; TITLE OF INVENTION: Novel Polynucleotides and Polypeptides Encoded Thereby
; FILE REFERENCE: 15966-754
; CURRENT APPLICATION NUMBER: US/09/826,734
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,576
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 270
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122
; LENGTH: 175
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-826-734-122

Query Match 94.7%; Score 36; DB 10; Length 175;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 117 CVPLTC 122

RESULT 4
US-09-799-514-9
; Sequence 9, Application US/09799514
; Patent No. US20020065220A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and Ar
; FILE REFERENCE: PT015P1

; CURRENT APPLICATION NUMBER: US/09/799,514
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT/US00/23662
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: 60/152,248
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-514-9

Query Match 94.7%; Score 36; DB 9; Length 613;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 264 CVPLTC 269

RESULT 5
US-10-016-248-2
; Sequence 2, Application US/10016248
; Publication No. US20040033491A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-218
; CURRENT APPLICATION NUMBER: US/10/016,248
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315,639
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 3104
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-248-2

Query Match 94.7%; Score 36; DB 15; Length 3104;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 2486 CVPLTC 2491

RESULT 6
US-10-016-248-47
; Sequence 47, Application US/10016248
; Publication No. US20040033491A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-218
; CURRENT APPLICATION NUMBER: US/10/016,248


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; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315,639
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 3389
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-248-47

Query Match          94.7%; Score 36; DB 15; Length 3389;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 2677 CVPITC 2682

RESULT 7
US-10-408-765A-2286
; Sequence 2286, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale B.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2286
; LENGTH: 3389
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2286

Query Match          94.7%; Score 36; DB 16; Length 3389;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 2677 CVPITC 2682

RESULT 8
US-10-016-248-46
; Sequence 46, Application US/10016248
; Publication No. US20040033491A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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; FILE REFERENCE: 21402-218
; CURRENT APPLICATION NUMBER: US/10/016,248
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315,639
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 3508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-248-46

Query Match          94.7%; Score 36; DB 15; Length 3508;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 2677 CVPITC 2682

RESULT 9
US-10-016-248-45
; Sequence 45, Application US/10016248
; Publication No. US20040033491A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-218
; CURRENT APPLICATION NUMBER: US/10/016,248
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315,639
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 3564
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-016-248-45

Query Match          94.7%; Score 36; DB 15; Length 3564;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 2733 CVPITC 2738
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-3057

Query Match      92.1%; Score 35; DB 15; Length 310;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CVPLTC 6
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Db      262 CLPLTC 267

RESULT 12
US-10-741-600-1404
; Sequence 1404, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1404
; LENGTH: 1232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1404

Query Match      92.1%; Score 35; DB 17; Length 1232;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CVPLTC 6
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Db      1203 CVPVTC 1208

RESULT 13
US-10-741-600-1403
; Sequence 1403, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1403
; LENGTH: 1420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1403

Query Match      92.1%; Score 35; DB 17; Length 1420;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CVPLTC 6
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Db      1203 CVPVTC 1208

RESULT 14
US-10-741-600-1405
; Sequence 1405, Application US/10741600
; Publication No. US20050026169A1
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RESULT 10
US-10-424-599-198429
; Sequence 198429, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 198429
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(127)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_21205C.1.pap
US-10-424-599-198429

Query Match      92.1%; Score 35; DB 15; Length 127;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CVPLTC 6
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Db      116 CLPLTC 121

RESULT 11
US-10-094-749-3057
; Sequence 3057, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3057
; LENGTH: 310
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; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1405
; LENGTH: 1420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1405

Query Match 92.1%; Score 35; DB 17; Length 1420;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVP LTC 6
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RESULT 15
US-10-783-311-2
; Sequence 2, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1547
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-783-311-2

Query Match 92.1%; Score 35; DB 17; Length 1547;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVP LTC 6
Db 1330 CVPVTC 1335

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Title: US-09-761-636A-11

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- 3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/PCITUS_COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	88.1	616	4	US-09-134-000C-6380
2	35	83.3	627	4	US-10-246-658-4
3	35	83.3	585	4	US-10-246-658-2
4	34	81.0	394	4	US-09-252-991A-29358
5	34	81.0	2476	2	US-08-276-967-2
6	34	81.0	2594	3	US-08-718-388-7
7	34	81.0	5405	3	US-08-718-388-9
8	33	78.6	280	2	US-08-969-106-11
9	33	78.6	280	4	US-09-338-125-11
10	33	78.6	376	2	US-08-875-972-2
11	33	78.6	5179	4	US-09-538-092-1258
12	32	76.2	68	4	US-09-904-615-92
13	32	76.2	71	4	US-09-270-767-36833
14	32	76.2	71	4	US-09-270-767-52050
15	32	76.2	142	4	US-09-252-991A-22994
16	32	76.2	150	4	US-09-252-991A-33012
17	32	76.2	382	4	US-09-252-991A-29595
18	32	76.2	432	4	US-09-248-796A-24125
19	32	76.2	460	4	US-09-949-016-8029
20	32	76.2	661	2	US-08-417-174-27
21	32	76.2	661	2	US-08-417-174-121
22	32	76.2	661	2	US-08-231-565A-27
23	32	76.2	661	2	US-09-007-961-27
24	32	76.2	661	3	US-09-267-439-27
25	32	76.2	661	3	US-09-267-439-121
26	32	76.2	661	4	US-08-388-852B-2
27	32	76.2	661	4	US-09-073-138-27

28	32	76.2	661	4	US-09-073-138-121	Sequence 121, Appl
29	32	76.2	668	1	US-07-891-942G-6	Sequence 6, Appli
30	32	76.2	710	4	US-09-134-000C-6451	Sequence 6451, Ap
31	31	73.8	7	1	US-08-526-710-21	Sequence 21, Appl
32	31	73.8	7	3	US-08-862-855-21	Sequence 21, Appl
33	31	73.8	7	3	US-09-226-985-21	Sequence 21, Appl
34	31	73.8	7	3	US-09-227-906-21	Sequence 21, Appl
35	31	73.8	7	4	US-09-228-865-21	Sequence 21, Appl
36	31	73.8	12	3	US-08-742-243-35	Sequence 35, Appl
37	31	73.8	12	3	US-08-742-243-36	Sequence 36, Appl
38	31	73.8	12	3	US-08-742-243-37	Sequence 37, Appl
39	31	73.8	12	3	US-08-742-243-38	Sequence 38, Appl
40	31	73.8	17	3	US-08-807-992B-23	Sequence 23, Appl
41	31	73.8	45	4	US-09-716-129-94	Sequence 94, Appl
42	31	73.8	65	4	US-09-244-583-12	Sequence 12, Appl
43	31	73.8	97	4	US-09-270-767-42215	Sequence 42215, A
44	31	73.8	109	3	US-08-691-794-3	Sequence 3, Appli
45	31	73.8	110	3	US-09-392-932-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-134-000C-6380
; Sequence 6380, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patent version 3.1
; SEQ ID NO 6380
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6380

Query Match 88.1%; Score 37; DB 4; Length 616;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 CVPLTSC 7
DB 507 CLPMTSC 513

RESULT 2
US-10-246-658-4
; Sequence 4, Application US/10246658
; Patent No. 6790660
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Scoville, John
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Nguyen, Nghi D.
; TITLE OF INVENTION: No. 6790660eol Human Kielin-Like Proteins and Polynucleotides Encod
; FILE REFERENCE: LEX-0376-USA
; CURRENT APPLICATION NUMBER: US/10/246,658
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/323,068
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 627
; TYPE: PRT

; ORGANISM: homo sapiens
US-10-246-658-4

Query Match 83.3%; Score 35; DB 4; Length 627;
Best Local Similarity 57.1%; Pred. No. 2.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
|:|:|
Db 336 CIPISSC 342

RESULT 3

US-10-246-658-2
; Sequence 2, Application US/10246658
; Patent No. 6790660

; GENERAL INFORMATION:

; APPLICANT: Yu, Xuanchuan

; APPLICANT: Scoville, John

; APPLICANT: Wilganowski, Nathaniel L.

; APPLICANT: Nguyen, Nghi D.

; TITLE OF INVENTION: NO. 6790660el Human Kiellin-Like Proteins and Polynucleotides Encod

; FILE REFERENCE: LEX-0376-USA

; CURRENT APPLICATION NUMBER: US/10/246,658

; CURRENT FILING DATE: 2002-09-18

; PRIOR APPLICATION NUMBER: US 60/323,068

; PRIOR FILING DATE: 2001-09-18

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 685

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-246-658-2

Query Match 83.3%; Score 35; DB 4; Length 685;
Best Local Similarity 57.1%; Pred. No. 2.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
|:|:|
Db 336 CIPISSC 342

RESULT 4

US-09-252-991A-29358

; Sequence 29358, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 29358

; LENGTH: 394

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-29358

Query Match 81.0%; Score 34; DB 4; Length 394;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
|:|:|
Db 169 CMPTSC 175

RESULT 5

US-08-276-967-2

; Sequence 2, Application US/08276967

; Patent No. 5851817

; GENERAL INFORMATION:

; APPLICANT: Hardy, Daniel M.

; APPLICANT: Garbers, David L.

; TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of

; TITLE OF INVENTION: Sperm

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P. O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA: US/08/276,967

; APPLICATION NUMBER: US/08/276,967

; FILING DATE: Submitted Herewith

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Kitchell, Barbara S.

; REGISTRATION NUMBER: 33,928

; REFERENCE/DOCKET NUMBER: UTSD:418\KIT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 713-787-1400

; TELEFAX: 713-789-2679

; TELEX: 79-0924

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2476 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-276-967-2

Query Match 81.0%; Score 34; DB 2; Length 2476;
Best Local Similarity 71.4%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
|:|:|
Db 1505 CVPLSQC 1511

RESULT 6

US-08-718-388-7

; Sequence 7, Application US/08718388

; Patent No. 6271362

; GENERAL INFORMATION:

; APPLICANT: MORIKAWA, MINORU

; APPLICANT: HARADA, NAOKI

; TITLE OF INVENTION: GENE ENCODING IGG Fc REGION-BINDING

; TITLE OF INVENTION: PROTEIN

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH

; STREET: PO BOX 747

; CITY: FALLS CHURCH

; STATE: VA

; COUNTRY: USA

; ZIP: 22040-0747

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/718,388
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 0230-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2594 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-718-388-7

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Query Match 81.0%; Score 34; DB 3; Length 2594;
Best Local Similarity 71.4%; Pred. NO. 1.4e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	1	CVPLTSC	7
		:	
Db	1183	CLPLASC	1189

RESULT 7
US-08-718-388-9
; Sequence 9, Application US/08718388
; Patent No. 6271362
; GENERAL INFORMATION:

/ APPLICANT: MORIKAWA, MINORU
 / APPLICANT: HARADA, NAOKI
 / TITLE OF INVENTION: GENE ENCODING IgG Fc REGION-BINDING
 / TITLE OF INVENTION: PROTEIN
 / NUMBER OF SEQUENCES: 29
 / CORRESPONDENCE ADDRESS:

ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA

COUNTRY: USA

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/ ZIP: 22040-0747
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0,
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/718,388
/ FILING DATE:
/

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CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0230-111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000

```

; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5405 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-08-718-388-9

Query Match 81.0%; Score 34; DB 3; Length 5405;

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Best Local Similarity 71.4%; Pred. No. 2.8e+03;
Matches 5; Conservative 1; Mismatches 1

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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,106
FILING DATE: 13-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-057
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 FENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-969-106-11

Query Match 78.6%; Score 33; DB 2; Length 280;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels

Qy 1 CVPLTSC 7
Dp 227 CVPATEC 233

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RESULT 9
US-09-338-125-11
; Sequence 11, Application US/09338125
; Patent No. 6521412
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas

```

;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10036
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/338.125
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/969.106
;; FILING DATE: 13-NOV-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Misrock, S. Leslie
;; REGISTRATION NUMBER: 18.872
;; REFERENCE/DOCKET NUMBER: 7934-057
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-790-9090
;; TELEFAX: 212-869-9741
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 280 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; US-09-338-125-11

Query Match 78.6%; Score 33; DB 4; Length 280;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
Db 227 CVPATEC 233

RESULT 10
US-08-875-972-2
; Sequence 2, Application US/08875972
; Patent No. 5985564
; GENERAL INFORMATION:
; APPLICANT: Huntington Potter and Jinhue Li
; TITLE OF INVENTION: ASSAY FOR IDENTIFYING GENES CAUSING
; TITLE OF INVENTION: CHROMOSOME NON-DISJUNCTION
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875.972
; FILING DATE: 08-AUG-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/002.448
; FILING DATE: 16-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan Esq., Patricia
; REGISTRATION NUMBER: 32,227

;; REFERENCE/DOCKET NUMBER: HU95-03PA
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (781) 861-6240
;; TELEFAX: (781) 861-9540
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 376 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-875-972-2

Query Match 78.6%; Score 33; DB 2; Length 376;
Best Local Similarity 71.4%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
Db 26 CVPVTL 32

RESULT 11
US-09-538-092-1258
; Sequence 1258, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538.092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurafatSeqformatter Version 0.9
; SEQ ID NO 1258
; LENGTH: 5179
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q02817
; US-09-538-092-1258

Query Match 78.6%; Score 33; DB 4; Length 5179;
Best Local Similarity 71.4%; Pred. No. 4e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
Db 712 CVPLAKC 718

RESULT 12
US-09-904-615-92
; Sequence 92, Application US/09904615
; Patent No. 6566325
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: PZ032P1
; CURRENT APPLICATION NUMBER: US/09/904.615
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/511,554
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/097,917
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 60/098,634
; PRIOR FILING DATE: 1998-08-31

; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (68)
; OTHER INFORMATION: Xaa equals stop translation
US-09-904-615-92

Query Match 76.2%; Score 32; DB 4; Length 68;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VPLTSC 7
:|||||
Db 38 IPLTSC 43

RESULT 13
US-09-270-767-36833
; Sequence 36833, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36833
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-36833

Query Match 76.2%; Score 32; DB 4; Length 71;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
:|||||
Db 45 CLPNTSC 51

RESULT 14
US-09-270-767-52050
; Sequence 52050, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52050
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-52050

Query Match 76.2%; Score 32; DB 4; Length 71;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
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Db 45 CLPNTSC 51

RESULT 15
US-09-252-991A-22994
; Sequence 22994, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22994
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22994

Query Match 76.2%; Score 32; DB 4; Length 142;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
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Db 19 CCPTTSC 25

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Job time : 16.5342 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

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(without alignments)
66.262 Million cell updates/sec

Title: US-09-761-636A-12

Perfect score: 38
Sequence: 1 CVPLTC 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	817	2 T25674	hypothetical prote
2	37	97.4	293	2 T27621	hypothetical prote
3	35	92.1	1627	2 S65464	pregnancy-associat
4	34	89.5	367	2 T20914	hypothetical prote
5	33	86.8	332	2 I48933	adenosine recepto
6	33	86.8	415	2 A54126	endothelin recepto
7	33	86.8	467	2 AC2390	transposase all467
8	33	86.8	637	2 T08050	probable ethylene
9	33	86.8	650	2 A34498	glycoprotein antig
10	33	86.8	1236	1 A53970	i-phosphatidylinos
11	32	84.2	108	2 S12982	hypothetical 12.2K
12	32	84.2	137	2 T26433	hypothetical prote
13	32	84.2	156	2 C81364	probable periplasm
14	32	84.2	252	2 B82659	two-component syst
15	32	84.2	301	2 T40593	cytoplasmic dynein
16	32	84.2	314	2 B43652	ferredoxin [2Fe-2S
17	32	84.2	345	1 NB80	apolipoprotein H p
18	32	84.2	398	2 A35281	integumentary mucin
19	32	84.2	425	2 T40610	probable clathrin
20	32	84.2	518	2 AD1930	ammonium transport
21	32	84.2	972	2 A30363	glycoprotein GP330
22	32	84.2	1034	2 JC5598	mucin - rat
23	32	84.2	4660	2 T42737	Gp330 protein prec
24	31	81.6	40	2 E45495	beta-defensin-5 -
25	31	81.6	133	2 T29606	hypothetical prote
26	31	81.6	224	2 T27063	hypothetical prote
27	31	81.6	326	2 C69341	cobalt transport A
28	31	81.6	414	2 T50019	hypothetical prote
29	31	81.6	434	2 I50132	vasotocin receptor

30	31	81.6	471	2 AC3622	mannose-1-phosphat
31	31	81.6	588	2 T24121	hypothetical prote
32	31	81.6	718	2 JE0188	RES4-25 protein -
33	31	81.6	822	2 T01622	probable salt-indu
34	31	81.6	869	1 JC4858	VLDL receptor prec
35	31	81.6	1042	2 T26644	hypothetical prote
36	31	81.6	1313	2 T29027	hypothetical prote
37	31	81.6	1451	2 T30821	P-glycoprotein - S
38	31	81.6	2098	2 T13166	rough deal protein
39	31	81.6	2946	2 T00867	hypothetical prote
40	30	78.9	40	2 G45495	beta-defensin-7 -
41	30	78.9	40	2 I45495	beta-defensin-9 -
42	30	78.9	42	2 C45495	beta-defensin-3 -
43	30	78.9	42	2 F45495	beta-defensin-6 -
44	30	78.9	64	2 A47438	airway epithelial
45	30	78.9	64	2 A56128	lingual antimicrob

ALIGNMENTS

RESULT 1

T25674
hypothetical protein F08D12.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T25674
R:Le, T.; Waterston, R.
submitted to the EMBL Data Library, December 1996
A:Description: The sequence of C. elegans cosmid F08D12.
A:Reference number: Z20068
A:Accession: T25674
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-817 <LET>
A:Cross-references: EMBL:U08040; PIDN:AAB37929.1; GSPDB:GN00020; CESP:F08D12.6
A:Experimental source: strain Bristol N2; clone F08D12
C:Genetics:
A:Gene: CESP:F08D12.6
A:Map position: 2
A:Introns: 27/2; 329/3; 407/1; 477/3; 538/3; 622/2

Query Match 100.0%; Score 38; DB 2; Length 817;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6
|||
Db 479 CVPLTC 484

RESULT 2

T27621
hypothetical protein ZC504.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27621
R:Kershaw, J.
submitted to the EMBL Data Library, July 1995
A:Reference number: Z20394
A:Accession: T27621
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-293 <WIL>
A:Cross-references: UNIPROT:O18280; EMBL:Z50029; PIDN:CAA90343.1; GSPDB:GN00028; CESP:ZC504
A:Experimental source: clone ZC504
C:Genetics:
A:Gene: CESP:ZC504.5
A:Map position: X
A:Introns: 40/3; 140/3; 173/3; 255/3

Query Match 97.4%; Score 37; DB 2; Length 293;
Best Local Similarity 83.3%; Pred. No. 12;

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Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVPLTC 6
Db 123 CIPVTC 128

RESULT 3
S65464
pregnancy-associated plasma protein A precursor - human
N:Alternate names: PAPP-A
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C:Accession: S65464; S65463; A54220; I38097
R:Haaning, J.; Oxvig, C.; Overgaard, M.T.; Ebbesen, P.; Kristensen, T.; Sottrup-Jensen,
submitted to the EMBL Data Library, June 1995
A:Description: Complete cDNA sequence of the preproform of human pregnancy-associated pl
A:Reference number: S65464
A:Accession: S65464
A:Molecule type: mRNA
A:Residues: 1-1627 <HAA>
A:Cross-references: UNIPROT:Q13219; EMBL:U28727; NID:g1142969; PIDN:AA050543.1; PID:g114
R:Haaning, J.; Oxvig, C.; Overgaard, M.T.; Ebbesen, P.; Kristensen, T.; Sottrup-Jensen,
Eur. J. Biochem. 237, 159-163, 1996
A:Title: Complete cDNA sequence of the preproform of human pregnancy-associated plasma p
A:Reference number: S65463; MUID:96203921; PMID:8620868
A:Accession: S65463
A:Molecule type: mRNA
A:Residues: 1-102 <HAM>
A:Cross-references: EMBL:U28727
A:Note: the authors translated the codon CGA for residue 101 as Thr
R:Kristensen, T.; Oxvig, C.; Sand, O.; Moller, N.P.H.; Sottrup-Jensen, L.
Biochemistry 33, 1592-1598, 1994
A:Title: Amino acid sequence of human pregnancy-associated plasma protein-A derived from
A:Reference number: A54220; MUID:94146014; PMID:7508748
A:Accession: A54220
A:Molecule type: mRNA
A:Residues: 77-1627 <KRI>
A:Cross-references: GB:X68280; NID:g394649; PIDN:CAA48341.1; PID:g394650
R:Oxvig, C.; Sand, O.; Kristensen, T.; Gleich, G.J.; Sottrup-Jensen, L.
J. Biol. Chem. 268, 12243-12246, 1993
A:Title: Circulating human pregnancy-associated plasma protein-A is disulfide-bridged to
A:Reference number: I38097; MUID:93286045; PMID:7685339
A:Accession: I38097
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 77-1627 <RES>
A:Cross-references: EMBL:X68280; NID:g394649; PIDN:CAA48341.1; PID:g394650
C:Genetics:
A:Gene: GDB:PAPPA
A:Cross-references: GDB:134729; OMIM:176385
A:Map position: 9q33.1-9q33.1
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-80/Domain: propeptide #status predicted <PRO>
F:81-1627/Product: pregnancy-associated plasma protein A #status predicted <MAT>

Query Match 92.1%; Score 35; DB 2; Length 1627;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVPLTC 6
Db 1410 CIPVTC 1415

RESULT 4
T20914
hypothetical protein F14F8.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T20914
R:Lloyd, C.
submitted to the EMBL Data Library, March 1997
```

```
A:Reference number: Z19346
A:Accession: T20914
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-367 <WIL>
A:Cross-references: UNIPROT:Q9XU36; EMBL:Z92782; PIDN:CA807186.1; GSPDB:GN00023; CESP:F14
A:Experimental source: clone F14P8
C:Genetics:
A:Gene: CESP:F14P8.5
A:Map position: 5
A:Introns: 23/3; 97/2; 145/2; 301/2

Query Match 89.5%; Score 34; DB 2; Length 367;
Best Local Similarity 66.7%; Pred. No. 52;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVPLTC 6
Db 92 CIPVTC 97

RESULT 5
I48933
adenosine receptor subtype - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48933
R:Marquardt, D.L.; Walker, L.L.; Heinemann, S.
J. Immunol. 152, 4508-4515, 1994
A:Title: Cloning of two Adenosine Receptor Subtypes From Mouse Bone Marrow-Derived Mast (
A:Reference number: I48931; MUID:94209670; PMID:8157966
A:Accession: I48933
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-332 <RES>
A:Cross-references: UNIPROT:Q60614; EMBL:U05673; NID:g498337; PIDN:AAA19001.1; PID:g4983
C:Superfamily: adenosine receptor A1

Query Match 86.8%; Score 33; DB 2; Length 332;
Best Local Similarity 83.3%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CVPLTC 6
Db 166 CCPLTC 171

RESULT 6
A54126
endothelin receptor-AX - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C:Accession: A54126
R:Kumar, C.; Wangi, V.; Nuthulaganti, P.; Wu, H.L.; Pullen, M.; Brun, K.; Aliyar, H.; Mo
J. Biol. Chem. 269, 13414-13420, 1994
A:Title: Cloning and characterization of a novel endothelin receptor from Xenopus heart.
A:Reference number: A54126; MUID:94230448; PMID:8175772
A:Accession: A54126
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-415 <KUM>
A:Cross-references: UNIPROT:Q91548; GB:U06633; NID:g507893; PIDN:AAA19570.1; PID:g507894
A:Note: authors translated the codon ATG for residue 84 as His
C:Superfamily: endothelin receptor B

Query Match 86.8%; Score 33; DB 2; Length 415;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CVPLTC 6
Db 254 CVPLAC 259
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RESULT 7
AC2390
Transposase all4675 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AC2390
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AC2390
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-467 <KUR>
A:Cross-references: UNIPROT:O8YN93; GB:BA000019; PID:G17133812; GSPDB:G
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all4675

Query Match      86.8%; Score 33; DB 2; Length 467;
Best Local Similarity 83.3%; Pred. No. 98;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CVPLTC 6
      | ||||
Db      61 CCPLTC 66

RESULT 8
T08050
Probable ethylene receptor - muskmelon
C:Species: Cucumis melo (muskmelon)
C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C:Accession: T08050
R:Sato-Nara, K.; Yuhashi, K.; Higashi, K.; Hosoya, K.; Kubota, M.; Ezura, H.
submitted to the EMBL Data Library, December 1997
A:Description: Expression of an ERS homolog gene of melon (Cucumis melo L. reticulatus)
A:Reference number: Z16317
A:Accession: T08050
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-637 <SAT>
A:Cross-references: UNIPROT:O49077; EMBL:AF037368; NID:G2707333; PIDN:AAC99477.1; PID:G2

Query Match      86.8%; Score 33; DB 2; Length 637;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CVPLTC 6
      | ||||
Db      226 CVPYTC 231

RESULT 9
A34498
Glycoprotein antigen Bm86 precursor - southern cattle tick
C:Species: Boophilus microplus (southern cattle tick)
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C:Accession: A34498
R:Rand, K.N.; Moore, T.; Srikantha, A.; Spring, K.; Tellam, R.; Willadsen, P.; Cobon, G
Proc. Natl. Acad. Sci. U.S.A. 86, 9657-9661, 1989
A:Title: Cloning and expression of a protective antigen from the cattle tick Boophilus m
A:Reference number: A34498; MUID:90099323; PMID:2690068
A:Accession: A34498
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-650 <RAN>
A:Cross-references: UNIPROT:P20736; GB:M29321; NID:G161667; PID:G161668
C:Keywords: glycoprotein
F:209-246/Domain: EGF homology <EGF>

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Query Match      86.8%; Score 33; DB 2; Length 650;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CVPLTC 6
      | ||||
Db      147 CVPYTC 152

RESULT 10
AS3970
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) gamma-D - fruit f
C:Species: Drosophila melanogaster
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: AS3970
R:Emori, Y.; Sugaya, R.; Akimaru, H.; Higashijima, S.; Shishido, E.; Saigo, K.; Homma, Y.
J. Biol. Chem. 269, 19474-19479, 1994
A:Title: Drosophila phospholipase C-gamma expressed predominantly in blastoderm cells at
A:Reference number: AS3970; MUID:94308233; PMID:8034716
A:Accession: AS3970
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1236 <EMO>
A:Cross-references: UNIPROT:Q24284; GB:D29806
C:Genetics:
A:Gene: plc-gammad
A:Cross-references: FlyBase:FBgn0003416
C:Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase II; 1-phosphatic
hodiesterase domain Y homology; SH2 homology; SH3 homology
C:Keywords: phosphoric diester hydrolase
F:326-468/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom
F:589-688/Domain: SH2 homology <SH2B>
F:701-789/Domain: SH2 homology <SH2>
F:831-879/Domain: SH3 homology <SH3>
F:979-1095/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y hom

Query Match      86.8%; Score 33; DB 1; Length 1236;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CVPLTC 6
      | ||||
Db      1196 CVPLTC 1201

RESULT 11
SI2982
hypothetical 12.2K protein (68K signal recognition particle region) - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999
C:Accession: SI2982
R:Herz, J.; Flint, N.; Stanley, K.; Frank, R.; Dobberstein, B.
FEBS Lett. 276, 103-107, 1990
A:Title: The 68 kDa protein of signal recognition particle contains a glycine-rich region
A:Reference number: SI2981; MUID:91092392; PMID:1702390
A:Accession: SI2982
A:Molecule type: mRNA
A:Residues: 1-108 <HER>
A:Cross-references: GB:X53744; NID:G931; PIDN:CAA37774.1; PID:G933
C:Superfamily: dog hypothetical 12.2K protein (68K signal recognition particle region)

Query Match      84.2%; Score 32; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 CVPLTC 6
      | ||||
Db      20 CVPMS 25

RESULT 12
T26433

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Mon Apr 4 05:33:03 2005

hypothetical protein Y106G6H.16 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26433
R:McMurray, A.
submitted to the EMBL Data Library, October 1998
A:Reference number: Z20214
A:Accession: T26433
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-137 <WIL>
A:Cross-references: UNIPROT:Q9XWR9; EMBL:AL032631; PIDN:CAA21579.1; GSPDB:GN00019; CESP:
A:Experimental source: clone Y106G6H
C:Genetics:
A:Gene: CESP:Y106G6H.16
A:Map position: 1
A:Introns: 26/3; 61/3; 89/3

Query Match 84.2%; Score 32; DB 2; Length 137;
Best Local Similarity 83.3%; Pred. No. 55; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 0

Qy 1 CVPLTC 6
Db 45 CVPSTC 50

RESULT 13
C81364
probable periplasmic protein Cj0908 [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: C81364
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whithead, S.; Barrell
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: C81364
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-156 <PAR>
A:Cross-references: UNIPROT:Q9PP24; GB:AL1139076; GB:AL111168; NID:g6968128; PIDN:CAB7316
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cj0908

Query Match 84.2%; Score 32; DB 2; Length 156;
Best Local Similarity 83.3%; Pred. No. 61; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 0

Qy 1 CVPLTC 6
Db 36 CQPLTC 41

RESULT 14
B82659
two-component system, regulatory protein XFI626 [imported] - Xylella fastidiosa (strain
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2003
C:Accession: B82659
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: B82659
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-252 <SIM>
A:Cross-references: GB:AE003989; GB:AE003849; NID:g9106666; PIDN:AAF84435.1; GSPDB:GN001
A:Experimental source: strain 945c

Query Match 84.2%; Score 32; DB 2; Length 301;
Best Local Similarity 66.7%; Pred. No. 1e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 4; Conservative 1

Qy 1 CVPLTC 6
Db 101 CIPATC 106

Search completed: April 1, 2005, 09:33:28
Job time : 9.71233 secs

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
as-Neto, E.; Docena, C.; El-Dorry, H.; Faciniani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Praga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.D.; Marques, M.V.; Martins, E.
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XFI626
C:Superfamily: response regulator with LytR DNA-binding domain, Algr/VirR/ComE type; res

Query Match 84.2%; Score 32; DB 2; Length 252;
Best Local Similarity 83.3%; Pred. No. 90; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 0

Qy 1 CVPLTC 6
Db 234 CVPLLC 239

RESULT 15
T40593
cytoplasmic dynein intermediate chain - fission yeast (Schizosaccharomyces pombe) (fragme
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T40593
R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 1999
A:Reference number: Z21938
A:Accession: T40593
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-301 <SEE>
A:Cross-references: UNIPROT:O94518; EMBL:AL035216; PIDN:CAA22821.1; GSPDB:GN00067; SPDB:5
A:Experimental source: strain 972h-; cosmid c646
C:Genetics:
A:Gene: SPDB:SPBC646.17c
A:Map position: 2

Query Match 84.2%; Score 32; DB 2; Length 301;
Best Local Similarity 66.7%; Pred. No. 1e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 4; Conservative 1

Qy 1 CVPLTC 6
Db 101 CIPATC 106

Search completed: April 1, 2005, 09:33:28
Job time : 9.71233 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 03:33:32 ; Search time 36.7397 Seconds
(without alignments)
83.628 Million cell updates/sec

Title: US-09-761-636A-12
Perfect score: 38
Sequence: 1 CVPLTC 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	38	100.0	582	2	Q7QPM3	Q7qpm3 giardia lam
2	38	100.0	1451	2	Q7R2Y9	Q7r2y9 giardia lam
3	37	97.4	447	2	O18280	O18280 caenorhabdi
4	37	97.4	447	2	Q963E7	Q963e7 caenorhabdi
5	37	97.4	849	2	Q7SKG4	Q7skg4 human immun
6	36	94.7	551	2	Q769I2	Q769i2 ciona intes
7	36	94.7	3564	1	CSM1_MOUSE	Q923l3 mus musculu
8	36	94.7	3565	1	CSM1_HUMAN	Q96p27 homo sapien
9	35	92.1	148	2	Q676V2	Q676v2 human papil
10	35	92.1	257	2	Q7QYV8	Q7qyv8 giardia lam
11	35	92.1	318	2	Q6PTG3	Q6ptg3 strongyloce
12	35	92.1	322	2	Q6PTE0	Q6pte0 monoesiga br
13	35	92.1	426	2	Q9DGM2	Q9dgm2 brachydanio
14	35	92.1	468	2	Q9JUK57	Q9jks7 mus musculu
15	35	92.1	530	1	PDF2_RAT	O88484 rattus norv
16	35	92.1	530	1	Q6IN27	Q6in27 rattus norv
17	35	92.1	578	2	Q80VW3	Q80vw3 mus musculu
18	35	92.1	1367	2	Q9ES06	Q9es06 mus musculu
19	35	92.1	1345	2	Q8R4K8	Q8r4k8 mus musculu
20	35	92.1	1574	2	Q8R4K7	Q8r4k7 mus musculu
21	35	92.1	1627	1	PAPA_HUMAN	Q13219 homo sapien
22	35	92.1	1627	2	Q6G52	Q6g52 homo sapien
23	35	92.1	3487	1	CSM2_HUMAN	Q7z408 homo sapien
24	34	89.5	66	2	Q70JU9	Q70ju9 mytilus edu
25	34	89.5	66	2	Q70JUV0	Q70juv0 mytilus edu
26	34	89.5	116	2	Q6R647	Q6r647 capra hircu
27	34	89.5	152	2	Q8H347	Q8h347 oryza sativ
28	34	89.5	245	2	Q8LKU4	Q8lku4 sorghum bic
29	34	89.5	367	2	Q9XU36	Q9xu36 caenorhabdi
30	34	89.5	511	2	Q8S2A0	Q8s2a0 oryza sativ
31	34	89.5	570	2	Q8N9T9	Q8n9t9 homo sapien

32	34	89.5	574	2	Q7R5J3	Q7r5j3 giardia lam
33	34	89.5	592	2	Q7QT99	Q7qt99 giardia lam
34	33	86.8	66	2	Q9AIP4	Q9aip4 streptococc
35	33	86.8	66	2	Q9PTM2	Q9ptm2 coturnix co
36	33	86.8	68	2	Q9PTM3	Q9ptm3 gallus gall
37	33	86.8	93	2	Q78161	Q78161 human immun
38	33	86.8	118	2	Q7QWL2	Q7qw12 giardia lam
39	33	86.8	158	2	Q8F8J9	Q6f8j9 acinetobact
40	33	86.8	168	2	Q90YB8	Q90yb8 brachydanio
41	33	86.8	246	2	Q95YD9	Q95yd9 caenorhabdi
42	33	86.8	265	1	TPIS_SYNEL	Q8dkao synechococc
43	33	86.8	277	2	Q9PYV4	Q9pyv4 xestia c-ni
44	33	86.8	332	1	A42B_MOUSE	Q60614 mus musculu
45	33	86.8	395	2	Q9LID1	Q9lid1 arabidopsis

ALIGNMENTS

RESULT 1

Q7QPM3 PRELIMINARY; PRT; 582 AA.
AC Q7QPM3;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE GLP_54_18133_16385.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBSJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AACB01000166; EAA36970.1; -.
DR HSSP; P15555; 1EWV.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002049; Laminin_EGF.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00053; Laminin_EGF; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_5.
DR PROSITE; PS01186; EGF_2; 6.
DR PROSITE; PS0026; EGF_3; 1.
SQ SEQUENCE 582 AA; 61933 MW; 93A55F363A4CD838 CRC64;

Query Match 100.0%; Score 38; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 37; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

QY 1 CVPLTC 6
Db 392 CVPLTC 397

RESULT 2

Q7R2Y9 PRELIMINARY; PRT; 1451 AA.
AC Q7R2Y9;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE GLP_385_48908_44553.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardia.
OX NCBI_TaxID=184922;

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RN SEQUENCE FROM N.A.
RP STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Alley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB01000018; EAA41686.1; -.
DR HSSP; P35555; 1EMN.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002049; Laminin_EGF.
DR Pfam; PF00008; EGF; 1.
DR PROSITE; PS00022; EGF 1; 5.
DR PROSITE; PS01186; EGF_2; 6.
DR PROSITE; PS50026; EGF_3; 3.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN 1.
SQ SEQUENCE 1451 AA; 153516 MW; B355F8F33F62336C CRC64;

Query Match 100.0%; Score 38; DB 2; Length 1451;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6
DB 330 CVPLTC 335

RESULT 3
O18280 PRELIMINARY; PRT; 447 AA.
AC O18280;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein ZC504.5;
GN Name=gur-3; ORFNames=ZC504.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018 (1998).

[2]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RC Kershaw J.K.;
RA Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RL EMBL; Z50029; CAA90343.3; -.
DR PIR; T27621; T27621.
DR WormBase; WBGene00001804; gur-3.
DR WormPep; ZC504.5; CE30223.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005549; F:odorant binding; IEA.
DR GO; GO:0004984; F:olfactory receptor activity; IEA.
DR GO; GO:0007608; P:perception of smell; IEA.
KW Hypothetical protein.
SQ SEQUENCE 447 AA; 51227 MW; E916BEAA7C14C80C CRC64;

Query Match 97.4%; Score 37; DB 2; Length 447;
Best Local Similarity 83.3%; Pred. No. 2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6
DB 330 CVPLTC 335
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```
DB 302 CIPLTC 307
|:|||||
PRELIMINARY; PRT; 447 AA.
ID Q963E7
AC Q963E7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative chemoreceptor GUR-3.
GN Name=gur-3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Robertson H.M.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RE EMBL; AF387606; AAK70489.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005549; F:odorant binding; IEA.
DR GO; GO:0004984; F:olfactory receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007608; P:perception of smell; IEA.
KW Receptor.
SQ SEQUENCE 447 AA; 51176 MW; 3AB7B4216F048BEB CRC64;

Query Match 97.4%; Score 37; DB 2; Length 447;
Best Local Similarity 83.3%; Pred. No. 45;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6
DB 302 CIPLTC 307
|:|||||
PRELIMINARY; PRT; 849 AA.
ID Q7SKG4
AC Q7SKG4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22790439; PubMed=12908933; DOI=10.1089/088922203322230923;
RA Tovanabutra S., Watanaveeradej V., Viputtikul K., De Souza M.,
RA Razak M.H., Suriyanon V., Jittiwutikarn J., Sriplienchan S.,
RA Nitayaphan S., Benenson M.W., Sirisopana N., Renzullo P.O.,
RA Brown A.E., Robb M.L., Beyrer C., Celentano D.D., McNeil J.G.,
RA Birx D.L., Carr J.K., McCutchan F.E.;
RT "A new circulating recombinant form, CRF15_01B, reinforces the linkage
RT between IDU and heterosexual epidemics in Thailand.";
RL AIDS Res. Hum. Retroviruses 19:561-567 (2003).
DR EMBL; AF529572; AAQ95553.1; -.
DR HSSP; P04578; IDLB.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR007777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypeptide; Polyprotein;
```



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KW Transmembrane.
SQ SEQUENCE 849 AA; 96536 MW; D7AB6F8B670BAED3 CRC64;

Query Match
Best Local Similarity 97.4%; Score 37; DB 2; Length 849;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6
DB 125 CIPLTC 130

RESULT 6
Q76912 PRELIMINARY; PRT; 551 AA.
AC Q76912;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Von Willebrand Factor like 2 (Fragment).
GN Name=C1-WVFL2;
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Clonidae; Ciona.
OX NCBI_TaxID=7719;

[1]
SEQUENCE FROM N.A.
RA Sasaki A., Miyamoto Y., Satou Y., Satoh N., Ogaawara M.;
RT "Novel endostyle-specific genes in the ascidian Ciona intestinalis.";
RL Zool. Sci. 0:0-0(2003)
DR EMBL; AB112442; BAD05119.1; -.
DR InterPro; IPR006207; Cys_knot_C.
DR Pfam; PF00093; VWC; 1.
DR SMART; SM00041; CT; 1.
DR SMART; SM00214; VWC; 2.
DR PROSITE; PS01185; CTCK_1; UNKNOWN_1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS01208; VWFC_1; UNKNOWN_2.
DR PROSITE; PS0184; VWFC_2; 2.
FT NON_TER 1
SQ SEQUENCE 551 AA; 58926 MW; FFCAD37C1CDB19FD CRC64;

Query Match
Best Local Similarity 94.7%; Score 36; DB 2; Length 551;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6
DB 378 CVPITC 383

RESULT 7
CSM1_MOUSE STANDARD; PRT; 3564 AA.
AC Q923L3; Q8BUV1; QBHYQ3;
DT 29-MAR-2004 (Ref. 43, Created)
DT 29-MAR-2004 (Ref. 43, Last sequence update)
DT 05-JUL-2004 (Ref. 44, Last annotation update)
DE CUB and sushi multiple domains protein 1 precursor.
GN Name=Csm1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6;
RX MEDLINE=21365705; PubMed=11472063; DOI=10.1006/geno.2001.6587;
RA Sun P.C., Uppaluri R., Schmidt A.P., Pashia M.E., Quant E.C.,
RA Sunwoo J.B., Gollin S.M., Scholnick S.B.;
RT "transcript map of the 9p23 putative tumor suppressor region.";
RL Genomics 75:17-25(2001).

RN SEQUENCE FROM N.A. (ISOFORM 3), AND SEQUENCE OF 3250-3564 FROM N.A.
RP (ISOFORM 2).
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Hypothalamus;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,
RA Baldarelli R., Hill D.P., Bult C., Rume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Pavasvi N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wellie C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q923L3-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q923L3-2; Sequence=VSP_009037;
CC Note=No experimental confirmation available;
CC Name=3;
CC IsoId=Q923L3-3; Sequence=VSP_009036;
CC Note=No experimental confirmation available;
CC -!- SIMILARITY: Belongs to the CSMD family.
CC -!- SIMILARITY: Contains 14 CUB domains.
CC -!- SIMILARITY: Contains 28 Sushi (CCP/SCR) domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AY017475; AAG54083.1; -.
DR EMBL; AK038679; BAC30095.1; ALT_INIT.
DR EMBL; AK082377; BAC38482.1; -.
DR HSSP; Q9UCV4; INZI.
DR MGD; MGI:2137383; Csm1.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 14.
DR Pfam; PF00084; Sushi; 28.
DR PROSITE; PS01180; CUB; 14.
DR PROSITE; PS0923; SUSHI; 28.
KW Alternative splicing; Repeat; Signal; Sushi; Transmembrane.
FT SIGNAL 1 29
FT CHAIN 30 3564
FT DOMAIN 30 3487
FT TRANSMEM 3488 3508

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DOMAIN 3509 3564 Cytoplasmic (Potential).
FT DOMAIN CUB 1. 32 140
FT DOMAIN Sush1 1. 143 204
FT DOMAIN CUB 2. 208 312
FT DOMAIN Sush1 2. 347 408
FT DOMAIN CUB 3. 411 522
FT DOMAIN Sush1 3. 525 582
FT DOMAIN CUB 4. 584 692
FT DOMAIN Sush1 4. 695 756
FT DOMAIN CUB 5. 758 866
FT DOMAIN Sush1 5. 871 928
FT DOMAIN CUB 6. 930 1040
FT DOMAIN Sush1 6. 1043 1102
FT DOMAIN CUB 7. 1104 1212
FT DOMAIN Sush1 7. 1215 1275
FT DOMAIN CUB 8. 1277 1386
FT DOMAIN Sush1 8. 1389 1449
FT DOMAIN CUB 9. 1451 1559
FT DOMAIN Sush1 9. 1562 1623
FT DOMAIN CUB 10. 1625 1733
FT DOMAIN Sush1 10. 1739 1800
FT DOMAIN CUB 11. 1802 1910
FT DOMAIN Sush1 11. 1913 1972
FT DOMAIN CUB 12. 1974 2082
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FT DOMAIN CUB 13. 2146 2257
FT DOMAIN Sush1 13. 2256 2317
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FT DOMAIN Sush1 16. 2678 2735
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FT DOMAIN CUB 24. 3573 3632
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FT DOMAIN CUB 25. 3693 3752
FT DOMAIN Sush1 25. 3753 3812
FT DOMAIN CUB 26. 3813 3872
FT DOMAIN Sush1 26. 3873 3932
FT DOMAIN CUB 27. 3933 3992
FT DOMAIN Sush1 27. 3993 4052
FT DOMAIN CUB 28. 4053 4112
FT DOMAIN Sush1 28. 4113 4172
FT DOMAIN CUB 29. 4173 4232
FT DOMAIN Sush1 29. 4233 4292
FT DOMAIN CUB 30. 4293 4352
FT DOMAIN Sush1 30. 4353 4412
FT DOMAIN CUB 31. 4413 4472
FT DOMAIN Sush1 31. 4473 4532
FT DOMAIN CUB 32. 4533 4592
FT DOMAIN Sush1 32. 4593 4652
FT DOMAIN CUB 33. 4653 4712
FT DOMAIN Sush1 33. 4713 4772
FT DOMAIN CUB 34. 4773 4832
FT DOMAIN Sush1 34. 4833 4892
FT DOMAIN CUB 35. 4893 4952
FT DOMAIN Sush1 35. 4953 5012
FT DOMAIN CUB 36. 5013 5072
FT DOMAIN Sush1 36. 5073 5132
FT DOMAIN CUB 37. 5133 5192
FT DOMAIN Sush1 37. 5193 5252
FT DOMAIN CUB 38. 5253 5312
FT DOMAIN Sush1 38. 5313 5372
FT DOMAIN CUB 39. 5373 5432
FT DOMAIN Sush1 39. 5433 5492
FT DOMAIN CUB 40. 5493 5552
FT DOMAIN Sush1 40. 5553 5612
FT DOMAIN CUB 41. 5613 5672
FT DOMAIN Sush1 41. 5673 5732
FT DOMAIN CUB 42. 5733 5792
FT DOMAIN Sush1 42. 5793 5852
FT DOMAIN CUB 43. 5853 5912
FT DOMAIN Sush1 43. 5913 5972
FT DOMAIN CUB 44. 5973 6032
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FT DOMAIN Sush1 45. 6153 6212
FT DOMAIN CUB 46. 6213 6272
FT DOMAIN Sush1 46. 6273 6332
FT DOMAIN CUB 47. 6333 6392
FT DOMAIN Sush1 47. 6393 6452
FT DOMAIN CUB 48. 6453 6512
FT DOMAIN Sush1 48. 6513 6572
FT DOMAIN CUB 49. 6573 6632
FT DOMAIN Sush1 49. 6633 6692
FT DOMAIN CUB 50. 6693 6752
FT DOMAIN Sush1 50. 6753 6812
FT DOMAIN CUB 51. 6813 6872
FT DOMAIN Sush1 51. 6873 6932
FT DOMAIN CUB 52. 6933 6992
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RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizushima-Sugano J., Sato T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.; "Complete sequencing and characterization of 21,243 full-length human cDNAs.";

RT Nat. Genet. 36:40-45(2004).

RL [3]

RN [3]

RP SEQUENCE OF 825-3565 FROM N.A. (ISOFORM 4).

RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.;

RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";

RT Bioinformatics 19:2265-2270(2003).

RL Genome Res. 13:2265-2270(2003).

RN [4]

RP SEQUENCE OF 966-2013 FROM N.A. (ISOFORM 4), AND TISSUE SPECIFICITY.

RC TISSUE=Brain;

RX MEDLINE=21456161; PubMed=11572484;

RA Nagase T., Kikuno R., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. XXI. The complete sequences of 60 new cDNA clones from brain which code for large proteins.";

RT DNA Res. 8:179-187(2001).

RL [5]

RN [5]

RP DISEASE.

RX PubMed=12696061; DOI=10.1002/gcc.10191;

RA Toomes C., Jackson A., Maguire K., Wood J., Gollin S., Ishwad C., Paterson I., Prime S., Parkinson K., Bell S., Woods G., Markham A., Oliver R., Woodward R., Sloan P., Dixon M., Read A., Thakker N.;

RT "The presence of multiple regions of homozygous deletion at the CSMD1 locus in oral squamous cell carcinoma question the role of CSMD1 in head and neck carcinogenesis.";

RT Genes Chromosomes Cancer 37:132-140(2003).

RL [6]

RN [6]

RP DISEASE.

RX PubMed=14506705; DOI=10.1002/gcc.10279;

RA Scholnick S.B., Richter T.M.;

RT "The role of CSMD1 in head and neck carcinogenesis.";

RL Genes Chromosomes Cancer 38:281-283(2003).

CC -!- FUNCTION: Potential suppressor of squamous cell carcinomas.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=4;

CC Name=1;

CC IsoId=Q96P27-1; Sequence=Displayed;

CC Name=2; Synonyms=Short;

CC IsoId=Q96P27-2; Sequence=VSP_009034, VSP_009035;

CC Name=3;

CC IsoId=Q96P27-3; Sequence=VSP_009030, VSP_009031;

CC Note=No experimental confirmation available;

CC Name=4;

CC IsoId=Q96P27-4; Sequence=VSP_009032, VSP_009033;

CC -!- TISSUE SPECIFICITY: Weakly expressed in most tissues, except in brain. Expressed at intermediate level in brain, including cerebellum, substantia nigra, hippocampus and fetal brain.

CC -!- DISEASE: Defects in CSMD1 may be a cause of oral and oropharyngeal squamous cell carcinomas (OSCCs). Ref.5 and Ref.6 are however in disagreement: while Ref.6 considers CSMD1 as a strong candidate for OSCCs, Ref.5 thinks it is not.

CC -!- SIMILARITY: Belongs to the CSMD family.

CC -!- SIMILARITY: Contains 14 CUB domains.

CC -!- SIMILARITY: Contains 28 Sushi (CCP/SCR) domains.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

CC EMBL; AF333704; AAK73475.2; -.

DR EMBL; AY017307; AAG52948.1; -.

DR EMBL; AK126936; BAC86754.1; ALT_INIT.

DR EMBL; AY358174; AAO88541.1; ALT_INIT.

DR EMBL; AB067477; BAB67783.1; -.

DR Genew; HGNC:14026; CSMD1.

DR MIM; 608397; -.

DR InterPro; IPR000859; CUB.

DR InterPro; IPR00436; Sushi_SCR_CCP.

DR Pfam; PF00431; CUB; 6.

DR Pfam; PF00084; Sushi; 6.

DR PROSITE; PS01180; CUB; 14.

DR PROSITE; PS0923; SUSHI; 28.

KW Alternative splicing; Repeat; Signal; Sushi; Transmembrane.

FT SIGNAL 1 26 Potential.

FT CHAIN 27 3565 CUB and sushi multiple domains protein 1.

FT DOMAIN 27 3488 Extracellular (Potential).

FT TRANSMEM 3489 3509 Potential.

FT DOMAIN 3510 3565 Cytoplasmic (Potential).

FT DOMAIN 32 140 CUB 1.

FT DOMAIN 143 204 Sushi 1.

FT DOMAIN 208 312 CUB 2.

FT DOMAIN 347 409 Sushi 2.

FT DOMAIN 412 523 CUB 3.

FT DOMAIN 526 583 CUB 4.

FT DOMAIN 585 693 Sushi 4.

FT DOMAIN 696 757 Sushi 5.

FT DOMAIN 759 867 Sushi 6.

FT DOMAIN 872 929 Sushi 7.

FT DOMAIN 931 1041 Sushi 8.

FT DOMAIN 1044 1103 Sushi 9.

FT DOMAIN 1105 1213 CUB 10.

FT DOMAIN 1216 1276 Sushi 10.

FT DOMAIN 1278 1387 Sushi 11.

FT DOMAIN 1390 1450 Sushi 12.

FT DOMAIN 1452 1560 Sushi 13.

FT DOMAIN 1563 1624 Sushi 14.

FT DOMAIN 1626 1734 Sushi 15.

FT DOMAIN 1740 1801 Sushi 16.

FT DOMAIN 1803 1911 CUB 11.

FT DOMAIN 1914 1973 Sushi 11.

FT DOMAIN 1975 2083 CUB 12.

FT DOMAIN 2147 2258 CUB 13.

FT DOMAIN 2257 2318 Sushi 13.

FT DOMAIN 2320 2431 CUB 14.

FT DOMAIN 2431 2493 Sushi 14.

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FT DOMAIN 2679 2736 Sushi 18.

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FT DOMAIN 2858 2915 Sushi 21.

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FT DOMAIN 3154 3211 Sushi 26.

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FT DOMAIN 3274 3333 Sushi 28.

FT CARBOHYD 40 40 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 57 57 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 588 588 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 687 687 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 956 956 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 1016 1016 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1035 1035 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1185 1185 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1198 1198 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1400 1400 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1455 1455 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1573 1573 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1645 1645 N-linked (GlcNAc...) (Potential).

Query Match 94.7%; Score 36; DB 1; Length 3565;
Best Local Similarity 83.3%; Pred. No. 5.3e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 1 CVPLTC 6
|:|:|
Db 2734 CVPITC 2739

RESULT 9
Q676V2
ID Q676V2 PRELIMINARY; PRT; 148 AA.
AC Q676V2
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative transforming protein E6.
OS Human papillomavirus type 62.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=37117;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15346342;
RA Fu L., Terai M., Matsukura T., Herrero R., Burk R.D.;
RT "Detection of a Mixed Population of candHPV62 Containing Wild-Type
RT and Disrupted E1 Open-Reading Frame in a 45-Year-Old Woman with Normal
RT Cytology";
RL J. Infect. Dis. 190:1303-1309(2004).
DR EMBL; AY395706; AAR32246.1; -;
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 148 AA; 17061 MW; C0EF71566CD02689 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 148;
Best Local Similarity 83.3%; Pred. No. 39;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6
|:|:|
Db 106 CMPLTC 111

RESULT 10
Q7QY8
ID Q7QY8 PRELIMINARY; PRT; 257 AA.
AC Q7QY8
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP 164_18200_17427.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

DR EMBL; AACB01000047; EAA40245.1; -;
DR HSP; P35555; IEMN.
DR InterPro; IPR002919; Cysrich TIL.
DR InterPro; IPR006149; EB region.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01683; EB; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
SQ SEQUENCE 257 AA; 28090 MW; 00D199E390BD0752 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 257;
Best Local Similarity 66.7%; Pred. No. 66;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6
|:|:|
Db 64 CIPITC 69

RESULT 11
O6PTG3
ID O6PTG3 PRELIMINARY; PRT; 318 AA.
AC O6PTG3
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Methionine adenosyltransferase (Fragment).
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15084738; DOI=10.1073/pnas.0401670101;
RA Peterson K.J., Lyons J.B., Nowak K.S., Takacs C.M., Wargo M.J.,
RA McPeck M.A.;
RT "Estimating metazoan divergence times with a molecular clock";
RL Proc. Natl. Acad. Sci. U.S.A. 101:6536-6541(2004).
CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC methionine and ATP (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and
CC 1 potassium ion per subunit (By similarity).
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.
DR EMBL; AY580282; AAT06211.1; -;
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004478; F:methionine adenosyltransferase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.
DR InterPro; IPR002133; S-AdoMet synt.
DR Pfam; PF02773; S-AdoMet synt_C; 1.
DR Pfam; PF02772; S-AdoMet synt_M; 1.
DR Pfam; PF00438; S-AdoMet synt_N; 1.
DR PIRSF; PIRSF00497; MAT; 1.
DR TIGRfams; TIGR01034; metK; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
KW ATP-binding; Magnesium; Metal-binding; One-carbon metabolism;
KW Potassium; Transferase.
FT NON_TER 1
FT NON_TER 318
SQ SEQUENCE 318 AA; 34519 MW; F4BD7C686403E35A CRC64;

Query Match 92.1%; Score 35; DB 2; Length 318;
Best Local Similarity 83.3%; Pred. No. 81;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6
|:|:|

Db 117 CMPLTC 122

RESULT 12

Q6PTE0 PRELIMINARY; PRT; 322 AA.

AC Q6PTE0;

DT 05-JUL-2004 (TREMELrel. 27, Created)

DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)

DE Methionine adenosyltransferase (Fragment).

OS Monosiga brevicollis.

OC Eukaryota; Chonoflagellida; Codonosigidae; Monosiga.

OX NCBI_TaxID=81824;

RN [1]

SEQUENCE FROM N.A.

RP PubMed=15084738; DOI=10.1073/pnas.0401670101;

RA Peterson K.J., Lyons J.B., Nowak K.S., Takacs C.M., Wargo M.J.,

RA McPeak M.A.;

RT "Estimating metazoan divergence times with a molecular clock.";

RL Proc. Natl. Acad. Sci. U.S.A. 101:6536-6541(2004).

CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from methionine and ATP (By similarity).

CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate + diphosphate + S-adenosyl-L-methionine.

CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and 1 potassium ion per subunit (By similarity).

CC -!- PATHWAY: Activated methyl cycle.

CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.

DR EMBL; AY580305; RAT06214.1; -.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0000287; F:magnesium ion binding; IEA.

DR GO; GO:0004478; F:methionine adenosyltransferase activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.

DR InterPro: IPR002133; S-AdoMet synt.

DR Pfam; PF02773; S-AdoMet synt_C; 1.

DR Pfam; PF02772; S-AdoMet synt_M; 1.

DR Pfam; PF00438; S-AdoMet synt_N; 1.

DR PIRSF; PIRSF000497; NAT; 1.

DR TIGRFAMs; TIGR01034; metK; 1.

DR PROSITE; PS00376; ADOMET SYNTHETASE 1; 1.

DR PROSITE; PS00377; ADOMET SYNTHETASE 2; 1.

KW ATP-binding; Magnesium; Metal-binding; One-carbon metabolism;

KW Potassium; Transferase.

FT NON_TER 1 1.

FT NON_TER 322 322

SQ SEQUENCE 322 AA; 34973 MW; 320B31E1784E7392 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 322;

Best Local Similarity 83.3%; Pred. NO. 82;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6

Db 120 CMPLTC 125

RESULT 13

Q9DGM2 PRELIMINARY; PRT; 426 AA.

AC Q9DGM2;

DT 01-MAR-2001 (TREMELrel. 16, Created)

DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)

DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)

DE Endothelin receptor B1 (SI:4Z2N24.3) (Endothelin receptor B).

GN Name=ednrb1;

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RA Parichy D.M., Kelish R.N., Mellgren E., Lopes S., Rawls J.,

RA Johnson S.L.;

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Corby N.;

RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF275636; AAG00977.1; -.

DR EMBL; AL606722; CAE17596.1; -.

DR ZFIN; ZDB-GENE-980526-16; ednrb1.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004962; F:endothelin receptor activity; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.

DR InterPro: IPR00499; Endthln receptor.

DR InterPro: IPR001112; ETB receptor.

DR InterPro: IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7cm_1; 1.

DR PRINTS; PR00571; ENDOTHELINR.

DR PRINTS; PR00366; ENDOTHELINR.

DR PRINTS; PR00237; GPCR_RHODOPSIN.

DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; UNKNOWN 1.

DR PROSITE; PS00262; G PROTEIN RECEPTOR FL 2; 1.

SQ SEQUENCE 426 AA; 48770 MW; F92C0B0B3046E4A3 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 426;

Best Local Similarity 83.3%; Pred. NO. 1.1e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6

Db 265 CMPLTC 270

RESULT 14

Q9JK57 PRELIMINARY; PRT; 468 AA.

AC Q9JK57;

DT 01-OCT-2000 (TREMELrel. 15, Created)

DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE Pregnancy-associated plasma protein A (fragment).

GN Name=Pappa;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Whole embryo;

RA Olesen C., Hansen C., Hayashizaki Y., Bykov A., Tommerup N.;

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF260433; AAF70319.1; -.

DR HSSP; P08174; 1H03.

DR MEROPS; M43.004; -.

DR MGD; MGI:97479; Pappa.

DR GO; GO:0004175; F:endorpeptidase activity; IEA.

DR InterPro: IPR000800; Notch_region.

DR InterPro: IPR000436; Sushi_SCR_CCP.

DR Pfam; PF00084; Sushi; 5.

DR SMART; SM00032; CCP; 4.

DR SMART; SM00004; NL; 1.

DR PROSITE; PS50923; SUSHI; 2.

FT NON_TER 1 1

SQ SEQUENCE 468 AA; 51133 MW; 85768E10D7D34FDA CRC64;

Query Match 92.1%; Score 35; DB 2; Length 468;

Best Local Similarity 83.3%; Pred. NO. 1.2e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Job time : 38.7397 secs

QY 1 CVPLTC 6
Db 251 CVPVTC 256

RESULT 15
PDP2_RAT STANDARD; PRT; 530 AA.
AC O88484;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE [Pyruvate dehydrogenase [lipoamide]]-phosphatase 2, mitochondrial
DE precursor (EC 3.1.3.43) (PDP 2) (Pyruvate dehydrogenase phosphatase,
DE catalytic subunit 2) (PDP2 2).
GN Name=Pdp2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98316337; PubMed=9651365; DOI=10.1074/jbc.273.28.17680;
RA Huang B., Gudi R., Wu P., Harris R.A., Hamilton J., Popov K.M.;
RT "Isoenzymes of pyruvate dehydrogenase phosphatase. DNA-derived amino
RT acid sequences, expression, and regulation.";
RL J. Biol. Chem. 273:17680-17688(1998).
CC -!- FUNCTION: Catalyzes the dephosphorylation and concomitant
CC reactivation of the alpha subunit of the E1 component of the
CC pyruvate dehydrogenase complex.
CC -!- CATALYTIC ACTIVITY: [Pyruvate dehydrogenase (lipoamide)] phosphate
CC + H(2)O = [pyruvate dehydrogenase (lipoamide)] + phosphate.
CC -!- COFACTOR: Magnesium.
CC -!- SUBUNIT: Heterodimer of a catalytic subunit and a FAD protein of
CC unknown function (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- TISSUE SPECIFICITY: Highly expressed in liver.
CC -!- SIMILARITY: Belongs to the PP2C family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF062741; AAC40168.1; -.
DR RGD; 628812; Pdp2.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C_2
DR SMART; SM00331; PP2C_SIG; 1.
DR SMART; SM00332; PP2CC; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydroxylase; Magnesium; Mitochondrion; Protein phosphatase;
KW Transit peptide.
FT TRANSIT 1 67 Mitochondrion (Potential).
FT CHAIN 68 530 [Pyruvate dehydrogenase [lipoamide]]-
FT phosphate 2.
SQ SEQUENCE 530 AA; 59654 MW; 5AB688FAC78AD9CD CRC64;
Query Match 92.1%; Score 35; DB 1; Length 530;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6
Db 303 CLPLTC 308

Search completed: April 1, 2005, 09:26:05

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 03:27:37 ; Search time 45.2877 Seconds
(without alignments)
51.240 Million cell updates/sec

Title: US-09-761-636A-12

Perfect score: 38

Sequence: 1 CVPLTC 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	6	4	AU04531 VEGF base
2	36	94.7	144	5	Abb53096 Human ORF
3	36	94.7	613	4	AU00816 Human Imm
4	36	94.7	713	8	Adh71152 Human pro
5	36	94.7	776	8	Adh71148 Human pro
6	36	94.7	776	8	Adh71150 Human pro
7	36	94.7	882	4	AAB83372
8	36	94.7	882	8	Adh71164 Human pro
9	36	94.7	883	4	AAB83371
10	36	94.7	884	8	Adh71162 Human pro
11	36	94.7	3069	5	AAE20787
12	36	94.7	3069	5	AAE20900
13	36	94.7	3095	5	AAE20788
14	36	94.7	3100	5	AAE20789
15	36	94.7	3100	5	AAE20901
16	36	94.7	3104	5	ABG79168
17	36	94.7	3104	8	Adh71168 Human pro
18	36	94.7	3104	8	Adh71166 Human pro
19	36	94.7	3104	8	Adh71138 Human pro
20	36	94.7	3389	7	ADJ70480 Human hea
21	36	94.7	3483	8	Adh71144 Human pro
22	36	94.7	3546	8	Adh71136 Human pro
23	35	92.1	95	4	AU48199
24	35	92.1	95	4	ABM44718
25	35	92.1	310	6	ADA55489

26	35	92.1	368	7	ADD27716	Human adi
27	35	92.1	530	7	ADD46650	Rat Prote
28	35	92.1	530	7	ADE55158	Rat Prote
29	35	92.1	1232	8	ADQ39741	Human myo
30	35	92.1	1420	8	ADQ39740	Human myo
31	35	92.1	1420	8	ADQ39742	Human myo
32	35	92.1	1603	4	AAU32498	Novel hum
33	35	92.1	1627	7	ADN39345	Cancer/an
34	35	92.1	1627	8	ADQ39743	Human myo
35	35	92.1	1752	4	ABG11138	Novel hum
36	35	92.1	2612	8	ADH71142	Human pro
37	35	92.1	3130	8	ADH71146	Human pro
38	34	89.5	570	7	ADB56588	Human pro
39	34	89.5	701	8	ADP04659	Sea squir
40	33	86.8	10	3	AAB23798	Phage dis
41	33	86.8	60	4	AAU40081	Propionib
42	33	86.8	60	4	AAU66225	Propionib
43	33	86.8	60	6	ABM36600	Propionib
44	33	86.8	60	6	ABM62744	Propionib
45	33	86.8	66	5	ABP29076	Streptoco

ALIGNMENTS

RESULT 1
AAU04531
ID AAU04531 standard; peptide; 6 AA.
XX
AC AAU04531;
XX
DT 26-SEP-2001 (first entry)
XX
DE VEGF based monocyclic peptide 9.
XX
KW Human; VEGF: vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..6
FT /note= "This bond cyclises the peptide"
XX
PN WO200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX
(LUDW-) LUDWIG INST CANCER RES.
XX
PI Achen MG, Hughes RA, Stackner S, Cendron A;
XX
XX WPI; 2001-442248/47.
XX
PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.
XX
PS Claim 49; Page 32; 102pp; English.
XX
CC The sequence represents a monomeric monocyclic peptide of the invention,
CC whose 3-dimensional structure is modelled on the expose loop of human
CC VEGF (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 38; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVPLTC 6
 Db 1 CVPLTC 6

RESULT 2
 ID ABB53096 standard; protein; 144 AA.

AC ABB53096;
 DT 12-FEB-2002 (first entry)
 DE Human ORF2 protein.

XX ORF2; human; pharmacogenomics; cancer; hyperproliferative disorder;
 KW dysproliferative disorder; neurodegenerative disorder; organ transplant;
 KW cardiovascular disease; cytokine; cell proliferation; immunomodulatory;
 KW cell differentiation; haematopoiesis; tissue growth; thrombolytic;
 KW neutropenic; neuroprotective; antiarthritic; antimicrobial; vulnery;
 KW cytostatic; antidiabetic; virucide; antifertility; anticonvulsant;
 KW vasotropic; antiparkinsonian; dermatological; antirheumatic; antitumor;
 KW antiulcer; osteopathic; tranquiliser; cerebroprotective; hepatotropic;
 KW antiinflammatory; tumour inhibition.

XX Homo sapiens.

OS WO200177155-A2.

XX 18-OCT-2001.

PD 06-APR-2001; 2001WO-US040469.

FF 06-APR-2000; 2000US-0195576P.

XX 05-APR-2001; 2001US-00826734.

XX (CURA-) CURAGEN CORP.

XX Fernandes E, Vernet CAM, Mishnu VS, Leach MD, Shinkets RA;
 PI Zerhusen BD, Kekuda R;

XX WPI: 2002-049131/06.

DR N-PSDB; ABA90195.

XX

PT New polypeptides and polynucleotides, useful for treating diseases such
 PT as cancer, Alzheimer's disease, atherosclerosis, diseases associated with
 PT liver, comprises polypeptides and polynucleotides of open reading frame
 PT proteins.

XX Claim 11; Page 82; 11pp; English.

XX The present invention provides the protein and coding sequences of human
 CC ORFX, where X is any number between 1 and 132. These sequences can be
 CC used to diagnose and treat ORFX related disorders, including cancer,
 CC hyperproliferative and dysproliferative disorders, neurodegenerative
 CC disorders, disorders related to organ transplantation or cardiovascular
 CC diseases, and may have cell proliferation or differentiation, cytokine,
 CC immunomodulatory, haematopoiesis regulating, tissue growth, inhibit or
 CC activin, chemotactic or chemokinetic, haemostatic or thrombolytic and/or
 CC antiinflammatory activities. The present sequence is one of the ORFX
 CC proteins of the invention

XX Sequence 144 AA;

Query Match 94.7%; Score 36; DB 5; Length 144;
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVPLTC 6
 Db 117 CVPITC 122

RESULT 3
 ID AAU00816 standard; protein; 613 AA.

XX AAU00816;

XX 01-JUN-2001 (first entry)

XX Human Immunoglobulin superfamily, IgsF, protein #2.

XX Human; Immunoglobulin superfamily protein; IgsF; Immune response;
 KW inflammatory response; cell-cell interaction; cell-surface recognition;
 KW neural disorder; immune system disorder; muscular disorder;
 KW reproductive disorder; gastrointestinal disorder; proliferative disorder; cancer;
 KW cardiovascular disorder; renal disorder; proliferative disorder; cancer;
 KW acquired immunodeficiency syndrome; anaemia; rheumatoid arthritis;
 KW Alzheimer's disease; Crohn's disease; liver cancer; leukaemia;
 KW Hodgkin's lymphoma; Parkinson's disease; Huntington's disease; dementia;
 KW atherosclerosis; stroke; diabetes mellitus; Addison's disease;
 XX urticaria; severe combined immunodeficiency; antibody.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Domain 4..52 /label= Immunoglobulin_like_domain

FT Region 6..11 /label= Immunogenic_epitope

FT Region 73..79 /label= Immunogenic_epitope

FT Region 121..127 /label= Immunogenic_epitope

FT Region 141..146 /label= Immunogenic_epitope

FT Region 223..230 /label= Immunogenic_epitope

FT Region 253..260 /label= Immunogenic_epitope

FT Region 328..336 /label= Immunogenic_epitope

FT Region 374..383 /label= Immunogenic_epitope

FT Region 392..404 /label= Immunogenic_epitope

FT Region /label= Immunogenic_epitope
FT 484..500
FT /label= Immunogenic_epitope
FT 511..517
FT /label= Immunogenic_epitope
FT 577..583
FT /label= Immunogenic_epitope
FT 605..610
FT /label= Immunogenic_epitope

XX WO200118176-A1.

XX 15-MAR-2001.

XX 29-AUG-2000; 2000WO-US023662.

XX 03-SEP-1999; 99US-0152248P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (NIJ/) NI J.

XX Young PE, Ruben SM, Shi Y;

XX WPI: 2001-203084/20.

XX N-PSDB; AAS00146.

XX Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.

XX Claim 11; Page 238-239; 247pp; English.

XX The sequence is a Human Immunoglobulin superfamily, IgSF, protein, a diverse family of proteins involved in cell-cell interactions, cell-surface recognition, intercellular communication and immune and inflammatory responses. Polypeptides and antibodies directed to polypeptides of the present invention are useful to provide immunological probes for differential identification of tissues. Antibodies can be used to assay levels of polypeptides encoded by polynucleotides of the present invention. Polypeptides of the present invention can be used to treat or prevent diseases or conditions such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders, renal disorders, proliferative disorders, and/or cancerous diseases and conditions. Polynucleotides of the invention are also useful in treating the above disorders. Examples of the disorders include common variable adhesion deficiency syndrome, acquired immunodeficiency syndrome (AIDS), anaemia, rheumatoid arthritis, Alzheimer's disease, Crohn's disease, liver cancer, leukaemia, Hodgkin's lymphoma, Parkinson's disease, Huntington's disease, dementia, arteriosclerosis, stroke, diabetes mellitus, Addison's disease, urticaria, severe combined immunodeficiency (SCID). Many more examples of diseases and disorders are given in the specification

XX Sequence 613 AA;

Query Match 94.7%; Score 36; DB 4; Length 613;

Best Local Similarity 83.3%; Pred. NO. 8.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPITC 6

DB 264 CVPITC 269

RESULT 4

ADH71152

ID ADH71152 standard; protein; 713 AA.

XX ADH71152;

XX 25-MAR-2004 (first entry)

XX Human protein of the invention NOV4i SEQ ID NO:48.

XX human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX Homo sapiens.
OS WO2003102155-A2.
XX 11-DEC-2003.
XX 03-JUN-2003; 2003WO-US017430.
XX 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-038796P.
PR 07-JUN-2002; 2002US-038818P.
PR 07-JUN-2002; 2002US-0388931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387698P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402258P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 15-AUG-2002; 2002US-0406317P.
PR 26-AUG-2002; 2002US-0406182P.

PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Alsebrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JK, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VV, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigar M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX
DR WPI; 2004-081935/08.
DR N-PSDB; ADH71151.
XX
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
PS Example 4; SEQ ID NO 48; 1880pp; English.
XX
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nontropic, anorectic, antidiabetic, antimicrobial, and
CC antilipemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridization probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC represents a NOVX polypeptide of the invention.
XX
SQ Sequence 713 AA;

Query Match 94.7%; Score 36; DB 8; Length 713;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVP LTC 6
Db 587 CVP LTC 592

RESULT 5
ADH71148
ID ADH71148 standard; protein; 776 AA.
XX
AC ADH71148;
XX

DT 25-MAR-2004 (first entry)
XX Human protein of the invention NOV4g SEQ ID NO:44.
DE
XX human, cytostatic; immunomodulator; neuroprotective; nontropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX Homo sapiens.
OS
XX WO2003102155-A2.
FN
XX 11-DEC-2003.
PD
XX 03-JUN-2003; 2003WO-US017430.
PF
XX 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-038796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389146P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390066P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 21-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.

PR 13-AUG-2002; 2002US-0403531P.
 PR 13-AUG-2002; 2002US-0403532P.
 PR 13-AUG-2002; 2002US-0403563P.
 PR 13-AUG-2002; 2002US-0406317P.
 PR 15-AUG-2002; 2002US-0403617P.
 PR 26-AUG-2002; 2002US-0406182P.
 PR 26-AUG-2002; 2002US-0406355P.
 PR 27-AUG-2002; 2002US-0406240P.
 PR 12-SEP-2002; 2002US-0410084P.
 PR 20-SEP-2002; 2002US-0412528P.
 PR 23-SEP-2002; 2002US-0412731P.
 PR 30-SEP-2002; 2002US-0414801P.
 PR 30-SEP-2002; 2002US-0414803P.
 PR 30-SEP-2002; 2002US-0414840P.
 PR 30-SEP-2002; 2002US-0414954P.
 PR 09-OCT-2002; 2002US-0417186P.
 PR 09-OCT-2002; 2002US-0417408P.
 PR 23-OCT-2002; 2002US-0420639P.
 PR 28-OCT-2002; 2002US-0421156P.
 PR 31-OCT-2002; 2002US-0422690P.
 PR 01-NOV-2002; 2002US-0423130P.
 PR 05-NOV-2002; 2002US-00423798.
 PR 05-NOV-2002; 2002US-0423798P.
 PR 12-NOV-2002; 2002US-0423453P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
 PI Catterton E, Chavarez A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
 PI Ettenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
 PI Gusev V, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
 PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
 PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
 PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
 PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
 PI Zhong H;
 XX
 XX WPI; 2004-081935/08.
 DR N-PSDB; ADH71149.
 DR
 XX
 XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
 PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
 XX
 XX Example 4; SEQ ID NO 46; 1880pp; English.
 PS
 XX The invention relates to a novel isolated polypeptide (NOVX). A
 CC polypeptide of the invention has cytostatic, immunomodulatory, and
 CC neuroprotective, norepinephrine, anorectic, antidiabetic, antimicrobial, and
 CC antiparasitic activity, and may have a use in gene therapy, and as a
 CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
 CC any of the 303 fully defined nucleotide sequences given in the
 CC specification. The polypeptide is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease. The
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,
 CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
 CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
 CC further used as hybridisation probes, in chromosome mapping, tissue
 CC typing, preventive medicine, and pharmacogenomics. The present sequence
 CC represents a NOVX polypeptide of the invention.
 XX
 SQ Sequence 776 AA;
 Query Match 94.7%; Score 36; DB 8; Length 776;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CVPITC 6
 Db 650 CVPITC 655

RESULT 7
 AAB83372
 ID AAB83372 standard; protein; 882 AA.
 XX
 AC AAB83372;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 XX NOV16 protein sequence.
 XX
 KW NOV, Cytostatic; contraceptive; antiinflammatory; immunomodulatory;
 KW cardiovascular; casein kinase II phosphorylation site; contraception;
 KW serine/threonine kinase; Feutz-Jeghers syndrome; cellular proliferation;
 KW dermal growth factor; cell development; apoptosis; cell adhesion;
 KW growth migration; cell structure; motility; cancer; immune disorder;
 KW inflammatory disorder; cellular adhesion disorder; long-QT syndrome;
 KW cardiovascular disease; hypertrophic cardiomyopathy; marfan syndrome;
 KW therapy; NOV1; NOV2; NOV3; NOV4; NOV5; NOV6; NOV7; NOV8; NOV9; NOV10;
 KW NOV11; NOV12; NOV13; NOV14; NOV15; NOV16.
 XX
 OS Unidentified.
 XX
 PN WO200136638-A2.
 XX
 XX 25-MAY-2001.
 PD
 XX
 PF 17-NOV-2000; 2000WO-US031543.
 XX
 PR 19-NOV-1999; 99US-0166336P.
 PR 29-NOV-1999; 99US-0167785P.
 PR 08-MAR-2000; 2000US-0187844P.
 PR 16-NOV-2000; 2000US-00715417.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shinkets RA, Lichenstein H, Vernet C, Fernandes E;
 XX
 XX WPI; 2001-648134/74.
 DR N-PSDB; AAF87127.
 DR
 XX
 PT Novel human polypeptides and the nucleic acids that encode them useful
 PT for preventing, diagnosing and treating e.g. cancer, inflammation and
 PT immune disorders.
 XX
 PS Claim 1; Page 50-52; 141pp; English.
 XX
 CC This sequence is the NOV16 protein. The invention relates to the NOV1-
 CC NOV16 proteins, and their coding sequences. The proteins have cytostatic;
 CC contraceptive; antiinflammatory; immunomodulatory; and cardiovascular
 CC activities. The sequences may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate NOVX expression. They
 CC may be used to treat disorders associated with decreased expression by
 CC rectifying mutations or deletions in a patient's genome that affect the
 CC activity of protein by expressing inactive proteins or to supplement the
 CC patients own production of protein. They are used to produce NOVX
 CC proteins, by inserting the nucleic acid into a cell and culturing it to
 CC express the protein. The DNA may be used as DNA probes in assays to
 CC detect and quantitate the presence of similar DNAs in samples, and which
 CC patients may need restorative therapy. The NOVX protein may also be used
 CC as antigens in the production of antibodies (Abs) against NOVX and in
 CC assays to identify modulators of NOVX expression and activity. The anti-
 CC NOVX Abs and antagonist are used to down regulate expression and
 CC activity. The anti-NOVX Abs are used for detecting the presence of NOVX
 CC in samples. Disorders that may be prevented, diagnosed and/or treated
 CC vary depending on the NOVX protein. NOV1, NOV3, NOV5, NOV7, NOV9-11 and
 CC NOV13-16 have casein kinase II phosphorylation sites characteristic of
 CC serine/threonine kinases, and are used to treat kinase-related disorders
 CC (e.g. Feutz-Jeghers syndrome, cellular proliferation and contraception).
 CC NOV2-3, NOV6 and NOV8 are homologous to the dermal growth factor (EGF)
 CC -like super family and are involved in, e.g. regulation of cell
 CC development, apoptosis, cell adhesion, growth migration, cell structure
 CC and motility and protein management, and are used to treat cancers,
 CC inflammatory disorders, immune disorders and cellular adhesion disorders.

CC NOV6-10 are homologous to EGF-like fibrillin proteins and are used to
 CC treat cardiovascular disease e.g. hypertrophic cardiomyopathy, long-QT
 CC syndrome and marfan syndrome
 XX
 SQ Sequence 882 AA;
 Query Match 94.7%; Score 36; DB 4; Length 882;
 Best Local Similarity 83.3%; Pred.No. 1.2e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CVP LTC 6
 Db 264 CVP LTC 269
 RESULT 8
 ADH71164
 ID ADH71164 standard; protein; 882 AA.
 AC ADH71164;
 XX
 XX 25-MAR-2004 (first entry)
 DT Human protein of the invention NOV40 SEQ ID NO:60.
 DE
 DE human; cytostatic; immunomodulator; neuroprotective; nootropic;
 XX anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
 KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
 KW obesity; diabetes; infectious disease; metabolic syndrome X;
 KW dyslipidaemia.
 XX
 OS Homo sapiens.
 XX
 XX WO2003102155-A2.
 XX
 PD 11-DEC-2003.
 XX
 PF 03-JUN-2003; 2003WO-US017430.
 XX
 XX 03-JUN-2002; 2002US-0385120P.
 PR 04-JUN-2002; 2002US-0385784P.
 PR 05-JUN-2002; 2002US-0386041P.
 PR 05-JUN-2002; 2002US-0386047P.
 PR 06-JUN-2002; 2002US-0386376P.
 PR 06-JUN-2002; 2002US-0386453P.
 PR 06-JUN-2002; 2002US-0386864P.
 PR 06-JUN-2002; 2002US-0387016P.
 PR 07-JUN-2002; 2002US-0386796P.
 PR 07-JUN-2002; 2002US-0386816P.
 PR 07-JUN-2002; 2002US-0386931P.
 PR 07-JUN-2002; 2002US-0386942P.
 PR 07-JUN-2002; 2002US-0386971P.
 PR 07-JUN-2002; 2002US-0387262P.
 PR 08-JUN-2002; 2002US-0296960P.
 PR 10-JUN-2002; 2002US-0387400P.
 PR 10-JUN-2002; 2002US-0387535P.
 PR 11-JUN-2002; 2002US-0387610P.
 PR 11-JUN-2002; 2002US-0387625P.
 PR 11-JUN-2002; 2002US-0387634P.
 PR 11-JUN-2002; 2002US-0387668P.
 PR 11-JUN-2002; 2002US-0387696P.
 PR 11-JUN-2002; 2002US-0387702P.
 PR 11-JUN-2002; 2002US-0387836P.
 PR 11-JUN-2002; 2002US-0387859P.
 PR 12-JUN-2002; 2002US-0387933P.
 PR 12-JUN-2002; 2002US-0387934P.
 PR 12-JUN-2002; 2002US-0387960P.
 PR 12-JUN-2002; 2002US-0388022P.
 PR 12-JUN-2002; 2002US-0388096P.
 PR 13-JUN-2002; 2002US-0388123P.
 PR 14-JUN-2002; 2002US-0389118P.
 PR 14-JUN-2002; 2002US-0389120P.
 PR 14-JUN-2002; 2002US-0389144P.

PR 14-JUN-2002; 2002US-0389146P.
 PR 17-JUN-2002; 2002US-0389729P.
 PR 17-JUN-2002; 2002US-0389742P.
 PR 18-JUN-2002; 2002US-0389884P.
 PR 19-JUN-2002; 2002US-0390006P.
 PR 19-JUN-2002; 2002US-0390209P.
 PR 21-JUN-2002; 2002US-0390763P.
 PR 17-JUL-2002; 2002US-0396706P.
 PR 06-AUG-2002; 2002US-0401628P.
 PR 09-AUG-2002; 2002US-0402156P.
 PR 09-AUG-2002; 2002US-0402256P.
 PR 09-AUG-2002; 2002US-0402389P.
 PR 12-AUG-2002; 2002US-0402786P.
 PR 12-AUG-2002; 2002US-0402816P.
 PR 12-AUG-2002; 2002US-0402821P.
 PR 12-AUG-2002; 2002US-0402832P.
 PR 13-AUG-2002; 2002US-0403448P.
 PR 13-AUG-2002; 2002US-0403459P.
 PR 13-AUG-2002; 2002US-0403531P.
 PR 13-AUG-2002; 2002US-0403532P.
 PR 13-AUG-2002; 2002US-0403563P.
 PR 15-AUG-2002; 2002US-0403617P.
 PR 26-AUG-2002; 2002US-0406182P.
 PR 26-AUG-2002; 2002US-0406355P.
 PR 27-AUG-2002; 2002US-0406240P.
 PR 12-SEP-2002; 2002US-0410084P.
 PR 20-SEP-2002; 2002US-0412528P.
 PR 23-SEP-2002; 2002US-0412731P.
 PR 30-SEP-2002; 2002US-0414801P.
 PR 30-SEP-2002; 2002US-0414839P.
 PR 30-SEP-2002; 2002US-0414840P.
 PR 30-SEP-2002; 2002US-0414954P.
 PR 09-OCT-2002; 2002US-0417186P.
 PR 09-OCT-2002; 2002US-0417406P.
 PR 23-OCT-2002; 2002US-0420639P.
 PR 28-OCT-2002; 2002US-0421156P.
 PR 31-OCT-2002; 2002US-0422690P.
 PR 01-NOV-2002; 2002US-0423130P.
 PR 05-NOV-2002; 2002US-00423798.
 PR 12-NOV-2002; 2002US-0425453P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
 PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
 PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
 PI Gusev VI, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
 PI Maciachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
 PI Padigar M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;
 PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
 PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
 PI Zhong H;
 XX
 XX WPI; 2004-081935/08.
 DR N-PSDB; ADH71163.
 XX
 XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
 PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
 XX
 PS Example 4; SEQ ID NO 60; 1880pp; English.
 XX
 CC The invention relates to a novel isolated polypeptide (NOVX). A
 CC polypeptide of the invention has cytostatic, immunomodulator,
 CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
 CC antilipemic activity, and may have a use in gene therapy, and as a
 CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
 CC any of the 303 fully defined nucleotide sequences given in the
 CC specification. The polypeptide is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease. The
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,

CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
 CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
 CC further used as hybridisation probes, in chromosome mapping, tissue
 CC typing, preventive medicine, and pharmacogenomics. The present sequence
 CC represents a NOVX polypeptide of the invention.
 XX
 SQ Sequence 882 AA;
 Query Match 94.7%; Score 36; DB 8; Length 882;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CVPLTC 6
 Db 264 CVPITC 269
 RESULT 9
 AAB83371
 ID AAB83371 standard; protein; 883 AA.
 XX
 AC AAB83371;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE NOV15 protein sequence.
 XX
 KW NOV. Cytostatic; contraceptive; antiinflammatory; immunomodulatory;
 KW cardiovascular; casein kinase II phosphorylation site; contraception;
 KW serine/threonine kinase; Peutz-Jeghers syndrome; cellular proliferation;
 KW epidermal growth factor; cell development; apoptosis; cell adhesion;
 KW growth migration; cell structure; motility; cancer; immune disorder;
 KW inflammatory disorder; cellular adhesion disorder; long-QT syndrome;
 KW cardiovascular disease; hypertrophic cardiomyopathy; marfan syndrome;
 KW therapy; NOV1; NOV2; NOV3; NOV4; NOV5; NOV6; NOV7; NOV8; NOV9; NOV10;
 KW NOV11; NOV12; NOV13; NOV14; NOV15; NOV16.
 XX
 OS Unidentified.
 XX
 PN WO200136639-A2.
 XX
 XX 25-MAY-2001.
 XX
 PF 17-NOV-2000; 2000WO-US031543.
 XX
 PR 19-NOV-1999; 99US-0166336P.
 PR 29-NOV-1999; 99US-0167785P.
 PR 08-MAR-2000; 2000US-0187844P.
 PR 16-NOV-2000; 2000US-00715417.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shinkets RA, Lichenstein H, Vernet C, Fernandes E;
 XX
 DR WPI; 2001-648134/74.
 DR N-PSDB; AAP87126.
 XX
 PT Novel human polypeptides and the nucleic acids that encode them useful
 PT for preventing, diagnosing and treating e.g. cancer, inflammation and
 PT immune disorders.
 XX
 PS Claim 1; Page 46-48; 141pp; English.
 XX
 CC This sequence is the NOV15 protein. The invention relates to the NOV1-
 CC NOV16 proteins, and their coding sequences. The proteins have Cytostatic;
 CC contraceptive; antiinflammatory; immunomodulatory; and cardiovascular
 CC activities. The sequences may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate NOVX expression. They
 CC may be used to treat disorders associated with decreased expression by
 CC rectifying mutations or deletions in a patient's genome that affect the
 CC activity of protein by expressing inactive proteins or to supplement the
 CC patients own production of protein. They are used to produce NOVX

CC proteins, by inserting the nucleic acid into a cell and culturing it to
 CC express the protein. The DNA may be used as DNA probes in assays to
 CC detect and quantitate the presence of similar DNAs in samples, and which
 CC patients may need restorative therapy. The NOVX protein may also be used
 CC as antigens in the production of antibodies (Abs) against NOVX and in
 CC assays to identify modulators of NOVX expression and activity. The anti-
 CC NOVX Abs and antagonist are used to down regulate expression and
 CC activity. The anti-NOVX Abs are used for detecting the presence of NOVX
 CC in samples. Disorders that may be prevented, diagnosed and/or treated
 CC vary depending on the NOVX protein. NOV1, NOV3, NOV5, NOV7, NOV9-11 and
 CC NOV13-16 have casein kinase II phosphorylation sites characteristic of
 CC serine/threonine kinases, and are used to treat kinase-related disorders
 CC (e.g. Peutz-Jeghers syndrome, cellular proliferation and contraception).
 CC NOV2-3, NOV6 and NOV8 are homologous to the epidermal growth factor (EGF)
 CC -like super family and are involved in, e.g. regulation of cell
 CC development, apoptosis, cell adhesion, growth migration, cell structure
 CC and motility and protein management, and are used to treat cancers,
 CC inflammatory disorders, immune disorders and cellular adhesion disorders.
 CC NOV6-10 are homologous to EGF-like fibrillin proteins and are used to
 CC treat cardiovascular disease e.g. hypertrophic cardiomyopathy, long-QT
 CC syndrome and marfan syndrome
 XX
 SQ Sequence 883 AA;
 Query Match 94.7%; Score 36; DB 4; Length 883;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CVPLTC 6
 Db 264 CVPITC 269
 RESULT 10
 ADH71162
 ID ADH71162 standard; protein; 884 AA.
 XX
 AC ADH71162;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Human protein of the invention NOV4n SEQ ID NO:58.
 XX
 KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
 KW anorectic; antidiabetic; antimicrobial; antilepatic; gene therapy;
 KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
 KW obesity; diabetes; infectious disease; metabolic syndrome X;
 KW dyslipidaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO2003102155-A2.
 XX
 PD 11-DEC-2003.
 XX
 PF 03-JUN-2003; 2003WO-US017430.
 XX
 PR 03-JUN-2002; 2002US-0385120P.
 PR 04-JUN-2002; 2002US-0385784P.
 PR 05-JUN-2002; 2002US-0386041P.
 PR 06-JUN-2002; 2002US-0386047P.
 PR 06-JUN-2002; 2002US-0386376P.
 PR 06-JUN-2002; 2002US-0386453P.
 PR 06-JUN-2002; 2002US-0386864P.
 PR 07-JUN-2002; 2002US-0387016P.
 PR 07-JUN-2002; 2002US-0386798P.
 PR 07-JUN-2002; 2002US-0386816P.
 PR 07-JUN-2002; 2002US-0386931P.
 PR 07-JUN-2002; 2002US-0386942P.
 PR 07-JUN-2002; 2002US-0386971P.
 PR 07-JUN-2002; 2002US-0387262P.
 PR 08-JUN-2002; 2002US-0296960P.
 PR 10-JUN-2002; 2002US-0387400P.

10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 21-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0406317P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
XX
XX (CURA-) CURAGEN CORP.
PR Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VI, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Scire P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX

DR WPI: 2004-081935/08.
XX N-PSDB; ADH71161.
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX Example 4; SEQ ID NO 58; 1890pp; English.
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC represents a NOVX polypeptide of the invention.
XX Sequence 884 AA;
SQ

Query Match 94.7%; Score 36; DB 8; Length 884;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CVP LTC 6
Db 264 CVP LTC 269

RESULT 11
AAE20787
ID AAE20787 standard; protein; 3069 AA.
XX
AC AAE20787;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human C3b/C4b complement receptor like protein #1.
XX
KW Human; C3b/C4b complement receptor-like molecule; immune system disorder;
KW gene therapy; rheumatoid arthritis; psoriatic arthritis; osteoarthritis;
KW inflammatory arthritis; inflammatory joint disease; Alzheimer's disease;
KW multiple sclerosis; inflammatory bowel disease; nervous system disorder;
KW transplant rejection; autoimmune disease; ischaemic condition; nootropic;
KW metabolic disorder; immunomodulatory; neuroprotective; diabetes; lupus;
KW infertility; vasodilator; obesity; cardiac.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 387 /label= Unknown
FT FT Misc-difference 461 /label= Unknown
FT FT Misc-difference 586 /label= Unknown
FT FT Misc-difference 1272 /label= Unknown
FT FT
XX WO200210199-A2.
XX
XX 07-FEB-2002.
XX
XX 24-JUL-2001; 2001WO-US023232.
XX
XX 02-AUG-2000; 2000US-0222504P.
PR

```

PR 28-NOV-2000; 2000US-00728787.
XX (AMGE-) AMGEN INC.
XX
XX Welcher AA, Elliott GS;
XX
XX WPI; 2002-303934/34.
DR N-PSDB; AAD33318.
XX
XX Nucleic acid encoding a novel C3b/C4b Complement Receptor-like nucleic
PT acid molecule, useful for treating, preventing and diagnosing rheumatoid
PT arthritis, psoriatic arthritis, inflammatory arthritis, and multiple
PT sclerosis.
XX
XX Claim 13; Fig 1; 251pp; English.
PS
XX The invention relates to a nucleic acid encoding a novel C3b/C4b
CC complement receptor (CR)-like nucleic acid molecule. The C3b/C4b CR-like
CC polypeptide and nucleic acid molecules may be used to treat, prevent,
CC ameliorate, diagnose and/or detect diseases such as immune system
CC disorders such as rheumatoid arthritis, psoriatic arthritis, inflammatory
CC arthritis, osteoarthritis, inflammatory joint disease, autoimmune
CC disease, multiple sclerosis, lupus, inflammatory bowel disease,
CC transplant rejection, nervous system disorders (e.g. Alzheimer's
CC disease), ischaemic conditions, metabolic disorders (e.g. obesity and
CC diabetes) and infertility. The invention is useful in gene therapy. The
CC present sequence is human C3b/C4b complement receptor like protein. Note:
CC The present sequence is stated to be the same as that referred to as SEQ
CC ID NO:2 (AAE20900) shown in page 176-189 of the specification. However
CC the sequences differ at position 695
XX
XX Sequence 3069 AA;
XX
XX Query Match 94.7%; Score 36; DB 5; Length 3069;
XX Best Local Similarity 83.3%; Pred. No. 3.6e+03;
XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CVPLTC 6
XX |||:|
XX 2238 CVPITC 2243
XX
XX RESULT 12
XX AAE20900
XX ID AAE20900 standard; protein; 3069 AA.
XX
XX AC AAE20900;
XX
XX DT 01-JUL-2002 (first entry)
XX
XX DE Human C3b/C4b complement receptor like protein #1, alternative version.
XX
XX KW Human; C3b/C4b complement receptor-like molecule; immune system disorder;
XX gene therapy; rheumatoid arthritis; psoriatic arthritis; osteoarthritis;
XX inflammatory arthritis; inflammatory joint disease; Alzheimer's disease;
XX multiple sclerosis; inflammatory bowel disease; nervous system disorder;
XX transplant rejection; autoimmune disease; ischaemic condition; neutropenic;
XX metabolic disorder; immunomodulatory; neuroprotective; diabetes; lupus;
XX infertility; vasodilator; obesity; cardiant.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 387
XX FT Misc-difference 461
XX FT Misc-difference 461
XX FT Misc-difference 586
XX FT Misc-difference 586
XX FT Misc-difference 695
XX FT Misc-difference 695
XX FT Misc-difference 695
XX FT Misc-difference 695
XX FT Misc-difference 1272
XX FT Misc-difference 1272

```

```

FT XX /label= Unknown
PN XX WO200210199-A2.
XX
XX PD 07-FEB-2002.
XX
XX XX 24-JUL-2001; 2001WO-US023232.
XX
XX PF 02-AUG-2000; 2000US-0222504P.
XX
XX PR 28-NOV-2000; 2000US-00728787.
XX
XX XX (AMGE-) AMGEN INC.
XX
XX PI Welcher AA, Elliott GS;
XX
XX DR WPI; 2002-303934/34.
XX
XX DR N-PSDB; AAD33318.
XX
XX Nucleic acid encoding a novel C3b/C4b Complement Receptor-like nucleic
PT acid molecule, useful for treating, preventing and diagnosing rheumatoid
PT arthritis, psoriatic arthritis, inflammatory arthritis, and multiple
PT sclerosis.
XX
XX Claim 13; Page 176-189; 251pp; English.
PS
XX The invention relates to a nucleic acid encoding a novel C3b/C4b
CC complement receptor (CR)-like nucleic acid molecule. The C3b/C4b CR-like
CC polypeptide and nucleic acid molecules may be used to treat, prevent,
CC ameliorate, diagnose and/or detect diseases such as immune system
CC disorders such as rheumatoid arthritis, psoriatic arthritis, inflammatory
CC arthritis, osteoarthritis, inflammatory joint disease, autoimmune
CC disease, multiple sclerosis, lupus, inflammatory bowel disease,
CC transplant rejection, nervous system disorders (e.g. Alzheimer's
CC disease), ischaemic conditions, metabolic disorders (e.g. obesity and
CC diabetes) and infertility. The invention is useful in gene therapy. The
CC present sequence is human C3b/C4b complement receptor like protein. The
CC alternative version. Note: The present sequence is stated to be the same
CC as that referred to as SEQ ID NO:2 (AAE20787) shown in figure 1 of the
CC specification. However the sequences differ at position 695
XX
XX Sequence 3069 AA;
XX
XX Query Match 94.7%; Score 36; DB 5; Length 3069;
XX Best Local Similarity 83.3%; Pred. No. 3.6e+03;
XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CVPLTC 6
XX |||:|
XX 2238 CVPITC 2243
XX
XX DB
XX
XX RESULT 13
XX AAE20788
XX ID AAE20788 standard; protein; 3095 AA.
XX
XX AC AAE20788;
XX
XX DT 01-JUL-2002 (first entry)
XX
XX DE Rat C3b/C4b complement receptor like protein.
XX
XX KW Rat; C3b/C4b complement receptor-like molecule; immune system disorder;
XX gene therapy; rheumatoid arthritis; psoriatic arthritis; osteoarthritis;
XX inflammatory arthritis; inflammatory joint disease; Alzheimer's disease;
XX multiple sclerosis; inflammatory bowel disease; nervous system disorder;
XX transplant rejection; autoimmune disease; ischaemic condition; neutropenic;
XX metabolic disorder; immunomodulatory; neuroprotective; diabetes; lupus;
XX infertility; vasodilator; obesity; cardiant.
XX
XX OS Rattus rattus.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 196

```


FT /label= Unknown
 FT Misc-difference 847
 FT /note= "xaa can be any amino acid"
 FT /label= Unknown
 FT /note= "xaa can be any amino acid"
 XX
 PN WO200210199-A2.
 XX
 XX 07-FEB-2002.
 PD
 XX
 XX 24-JUL-2001; 2001WO-US023232.
 XX
 XX 02-AUG-2000; 2000US-0222504P.
 PR 28-NOV-2000; 2000US-00728787.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX Welcher AA, Elliott GS;
 XX
 XX WPI; 2002-303934/34.
 DR N-PSDB; AAD33319.
 DR

Nucleic acid encoding a novel C3b/C4b Complement Receptor-like nucleic acid molecule, useful for treating, preventing and diagnosing rheumatoid arthritis, psoriatic arthritis, inflammatory arthritis, and multiple sclerosis.

Claim 13; Fig 3; 251pp; English.

The invention relates to a nucleic acid encoding a novel C3b/C4b complement receptor (CR)-like nucleic acid molecule. The C3b/C4b CR-like polypeptide and nucleic acid molecules may be used to treat, prevent, ameliorate, diagnose and/or detect diseases such as immune system disorders such as rheumatoid arthritis, psoriatic arthritis, inflammatory arthritis, osteoarthritis, inflammatory joint disease, autoimmune disease, multiple sclerosis, lupus, inflammatory bowel disease, transplant rejection, nervous system disorders (e.g. Alzheimer's disease), ischaemic conditions, metabolic disorders (e.g. obesity and diabetes) and infertility. The invention is useful in gene therapy. The present sequence is rat C3b/C4b complement receptor like protein

Sequence 3095 AA;

Query Match 94.7%; Score 36; DB 5; Length 3095;
 Best Local Similarity 83.3%; Pred. No. 3.7e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6
 |||:|

DB 2264 CVPITC 2269

RESULT 14

AAE20789

ID AAE20789 standard; protein; 3100 AA.

XX AC AAE20789;

XX 01-JUL-2002 (first entry)

DE Human C3b/C4b complement receptor like protein #2.

XX Human; C3b/C4b complement receptor-like molecule; immune system disorder; gene therapy; rheumatoid arthritis; psoriatic arthritis; osteoarthritis; inflammatory arthritis; inflammatory joint disease; Alzheimer's disease; multiple sclerosis; inflammatory bowel disease; nervous system disorder; transplant rejection; autoimmune disease; ischaemic condition; nontropic; metabolic disorder; immunomodulatory; neuroprotective; diabetes; lupus; infertility; vasodilator; obesity; Cardiant.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FH

FT Misc-difference 418
 FT /label= Unknown
 FT Misc-difference 492
 FT /label= Unknown
 FT Misc-difference 617
 FT /label= Unknown
 FT Misc-difference 1303
 FT /label= Unknown
 XX

PN WO200210199-A2.

XX 07-FEB-2002.

XX 24-JUL-2001; 2001WO-US023232.

XX 02-AUG-2000; 2000US-0222504P.

PR 28-NOV-2000; 2000US-00728787.

XX (AMGE-) AMGEN INC.

XX Welcher AA, Elliott GS;

XX WPI; 2002-303934/34.

DR N-PSDB; AAD33320.

XX Nucleic acid encoding a novel C3b/C4b Complement Receptor-like nucleic acid molecule, useful for treating, preventing and diagnosing rheumatoid arthritis, psoriatic arthritis, inflammatory arthritis, and multiple sclerosis.

Claim 13; Fig 2; 251pp; English.

The invention relates to a nucleic acid encoding a novel C3b/C4b complement receptor (CR)-like nucleic acid molecule. The C3b/C4b CR-like polypeptide and nucleic acid molecules may be used to treat, prevent, ameliorate, diagnose and/or detect diseases such as immune system disorders such as rheumatoid arthritis, psoriatic arthritis, inflammatory arthritis, osteoarthritis, inflammatory joint disease, autoimmune disease, multiple sclerosis, lupus, inflammatory bowel disease, transplant rejection, nervous system disorders (e.g. Alzheimer's disease), ischaemic conditions, metabolic disorders (e.g. obesity and diabetes) and infertility. The invention is useful in gene therapy. The present sequence is human C3b/C4b complement receptor like protein. Note: The present sequence is stated to be the same as that referred to as SEQ ID NO:7 (AAE20901) shown in page 239-251 of the specification. However the sequences differ at position 726

Sequence 3100 AA;

Query Match 94.7%; Score 36; DB 5; Length 3100;

Best Local Similarity 83.3%; Pred. No. 3.7e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTC 6
 |||:|

DB 2269 CVPITC 2274

RESULT 15

AAE20901

ID AAE20901 standard; protein; 3100 AA.

XX AC AAE20901;

XX 01-JUL-2002 (first entry)

DE Human C3b/C4b complement receptor like protein #2, alternative version.

XX Human; C3b/C4b complement receptor-like molecule; immune system disorder; gene therapy; rheumatoid arthritis; psoriatic arthritis; osteoarthritis; inflammatory arthritis; inflammatory joint disease; Alzheimer's disease; multiple sclerosis; inflammatory bowel disease; nervous system disorder; transplant rejection; autoimmune disease; ischaemic condition; nontropic; gene therapy; rheumatoid arthritis; psoriatic arthritis; osteoarthritis; inflammatory arthritis; inflammatory joint disease; Alzheimer's disease; multiple sclerosis; inflammatory bowel disease; nervous system disorder; transplant rejection; autoimmune disease; ischaemic condition; nontropic;

KW metabolic disorder; immunomodulatory; neuroprotective; diabetes; lupus;
XX infertility; vasodilator; obesity; cardiac.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 418 /label= Unknown

FT Misc-difference 492 /label= Unknown

FT Misc-difference 617 /label= Unknown

FT Misc-difference 726 /label= Unknown

FT Misc-difference 726 /label= Unknown

FT /note= "Encoded by CTR"

XX

PN WO200210199-A2.

XX

PD 07-FEB-2002.

XX

XX 24-JUL-2001; 2001WO-US023232.

XX

PR 02-AUG-2000; 2000US-0222504P.

PR 28-NOV-2000; 2000US-00728787.

XX

PA (AMGE-) AMGEN INC.

XX

PI Welcher AA, Elliott GS;

XX

DR WPI; 2002-303934/34.

DR N-PSDB; AAD33320.

XX

XX Nucleic acid encoding a novel C3b/C4b Complement Receptor-like nucleic
PT acid molecule, useful for treating, preventing and diagnosing rheumatoid
PT arthritis, psoriatic arthritis, inflammatory arthritis, and multiple
PT sclerosis.

PS Claim 13; Page 239-251; 251pp; English.

XX

XX The invention relates to a nucleic acid encoding a novel C3b/C4b
CC complement receptor (CR)-like nucleic acid molecule. The C3b/C4b CR-like
CC polypeptide and nucleic acid molecules may be used to treat, prevent,
CC ameliorate, diagnose and/or detect diseases such as immune system
CC disorders such as rheumatoid arthritis, psoriatic arthritis, inflammatory
CC arthritis, osteoarthritis, inflammatory joint disease, autoimmune
CC disease, multiple sclerosis, lupus, inflammatory bowel disease,
CC transplant rejection, nervous system disorders (e.g. Alzheimer's
CC disease), ischaemic conditions, metabolic disorders (e.g. obesity and
CC diabetes) and infertility. The invention is useful in gene therapy. The
CC present sequence is human C3b/C4b complement receptor like protein,
CC alternative version. Note: The present sequence is stated to be the same
CC as that referred to as SEQ ID NO:7 (AAE20789) shown in figure 2 of the
CC specification. However the sequences differ at position 726

XX Sequence 3100 AA;

Query Match 94.7%; Score 36; DB 5; Length 3100;
Best Local Similarity 83.3%; Pred. No. 3.7e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CVPLTC 6

Db 2269 CVPLTC 2274

Search completed: April 1, 2005, 09:18:22
Job time : 47.2877 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 06:17:29 ; Search time 10.1644 Seconds
(without alignments)
66.262 Million cell updates/sec

Title: US-09-761-636A-11

Perfect score: 42

Sequence: 1 CVPLTSC 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	92.9	2543	T31687	surface antigen - p
2	38	90.5	380	D44490	retrovirus-related
3	36	85.7	980	T00045	celldextrin phosph
4	36	85.7	2533	T28675	alpha-SiD immobili
5	36	85.7	2533	T28674	alpha-SiD-immobili
6	34	81.0	1506	T30886	integumentary muc
7	34	81.0	1513	A54895	mucin 2, intestina
8	34	81.0	2476	T34022	zonadhesin - pig
9	33	78.6	55	S66336	protein kinase AK2
10	33	78.6	191	I46412	keratin KAP5.4 - s
11	33	78.6	207	A64655	hypothetical prote
12	33	78.6	207	B71943	hypothetical prote
13	33	78.6	223	B38346	ultra-high-sulfur
14	33	78.6	230	A38346	ultra-high-sulfur
15	33	78.6	303	WZBEM6	gene 20 protein -
16	33	78.6	303	C33374	hypothetical prote
17	33	78.6	515	T23089	hypothetical prote
18	33	78.6	647	T23814	hypothetical prote
19	33	78.6	670	F88297	protein M28.1 [imp
20	33	78.6	891	H86306	F20D23.20 protein
21	33	78.6	1227	T43963	hypothetical prote
22	33	78.6	3020	A43932	mucin 2 precursor,
23	33	78.6	3133	S52093	hemocytin - silkw
24	32	76.2	77	JC4790	proteinase inhibit
25	32	76.2	270	T47421	hypothetical prote
26	32	76.2	303	T42933	hypothetical prote
27	32	76.2	305	B53782	peroxisome assembl
28	32	76.2	452	F84712	hypothetical prote
29	32	76.2	491	A49179	melanoma antigen h

30 32 76.2 662 2 I38400 melanoma-associate
31 32 76.2 668 2 A41234 melanocyte-specifi
32 32 76.2 1319 2 S55598 tegument protein 0
33 32 76.2 2044 2 T13704 still life protein
34 32 76.2 2180 2 T29764 hypothetical prote
35 32 76.2 2395 1 S50820 surface protein ty
36 32 76.2 5376 2 T42215 zonadhesin - mouse
37 31 73.8 63 2 S08572 chymotrypsin/elasc
38 31 73.8 110 2 S16496 hypothetical prote
39 31 73.8 120 2 A33787 vascular endotheli
40 31 73.8 128 2 I51295 vascular endotheli
41 31 73.8 146 2 S57956 ovine vascular end
42 31 73.8 161 2 T27849 hypothetical prote
43 31 73.8 169 1 A38946 ultra high-sulfur
44 31 73.8 182 2 A36686 glioma-derived vas
45 31 73.8 190 2 A35987

ALIGNMENTS

RESULT 1

T31687
surface antigen - Paramesium primaurelia
C:Species: Paramesium primaurelia
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: T31687
R:Bourgain-Guglielmetti, P.; Caron, F.
Journal of Eukaryot. Microbiol. 43, 303-314, 1996
A:Title: Molecular characterization of the D surface protein gene subfamily in Paramesium
A:Reference number: Z21061; MUID:96313351; PMID:8768434
A:Accession: T31687
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2543 <BOU>
A:Cross-references: UNIPROT:P90649; EMBL:X96616; NID:G1235576; PIDN:CAA65436.1
C:Genetics:
A:Genetic code: SGC5
C:Superfamily: G surface protein

Query Match 92.9%; Score 39; DB 2; Length 2543;
Best Local Similarity 71.4%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
Db 2158 CIPITSC 2164
I:|||||

RESULT 2

D44490
retrovirus-related reverse transcriptase homolog (clone NVC) - pteromalid wasp (Nasonia
C:Species: Nasonia vitripennis
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: D44490; F40442
R:Burke, W.D.; Eickbush, D.G.; Xiong, Y.; Jakubczak, J.; Eickbush, T.H.
Mol. Biol. Evol. 10, 163-185, 1993
A:Title: Sequence relationship of retrotransposable elements R1 and R2 within and between
A:Reference number: A4490; MUID:93196484; PMID:8383793
A:Contents: retrotransposable element R1
A:Accession: D44490
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-380 <BUR>
A:Cross-references: UNIPROT:Q03271
A>Note: sequence extracted from NCBI backbone (NCBIP:127237)
R:Jakubczak, J.L.; Burke, W.D.; Eickbush, T.H.
Proc. Natl. Acad. Sci. U.S.A. 88, 3295-3299, 1991
A:Title: Retrotransposable elements R1 and R2 interrupt the rRNA genes of most insects.
A:Reference number: A40442; MUID:91195337; PMID:1849649
A:Accession: F40442
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar
A:Molecule type: DNA

A;Residues: 304-320 <JAK>
C;Superfamily: silkworm pol protein

Query Match 90.5%; Score 38; DB 2; Length 380;
Best Local Similarity 85.7%; Pred. No. 8.2;
Matches 6; Conservative 1; Mismatches 0; Indels

Qy 1 CVPLTSC 7
|||:|
Db 356 CVPLSSC 362

RESULT 3

T00045
celldextrin phosphorylase - Clostridium thermocellum
C:Species: Clostridium thermocellum
C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C:Accession: T00045
R:Kawaguchi, T.; Ikeuchi, Y.; Tsutsumi, N.; Kan, A.; Sumitani, J.; Arai, M.
J. Ferment. Bioeng. 85, 144-149, 1998
A:Title: Cloning, nucleotide sequence, and expression of the Clostridium thermocellum celA
A:Reference number: Z14077
A:Accession: T00045
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-980 <KAW>
A:Cross-references: UNIPROT:O24780; EMBL:AB006822; NID:d1117395; PID:d1117395; PID:BAA22081.1; PID:d1117395
A:Experimental source: ATCC 27405
C:Genetics:
A:Gene: cdp

Query Match 85.7%; Score 36; DB 2; Length 980;
Best Local Similarity 57.1%; Pred. No. 44;
Matches 4; Conservative 3; Mismatches 0; Indels

Qy 1 CVPLTSC 7
Db 550 CIPMTAC 556

RESULT 4

T28675
alpha-51D immobilization antigen - Paramesium tetraurelia
C;Species: Paramesium tetraurelia
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28675
R;Schwegmann, K.J.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z20506
A;Accession: T28675
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2533 <SCH>
A;cross-references: UNIPROT:P90589; EMBL:X96400; PIDN:CAAG5264.1
C;Genetics:
A;Gene: alpha-51D
A;Genetic code: SGC5
A;Introns: 280/3; 538/2
C;Superfamily: G surface protein

Query Match 85.7%; Score 36; DB 2; Length 2533;
Best Local Similarity 57.1%; Pred. No. 98;
Matches 4; Conservative 3; Mismatches 0; Indels

QY	1	CVPLTSC 7
		: : :
Db	2149	CIPITNC 2155

RESULT 5

T28674
alpha-51D-immobilization antigen - *Paramecium tetraurelia*
C; Species: *Paramecium tetraurelia*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28674
R;Schmidt, H.J.
submitted to the EMBL Data Library, March 1995
A;Reference number: Z20505
A;Accession: T28674
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2533 <SCH>
A;Cross-references: UNIPROT:Q27183; EMBL:X85135; NID:g728634; PID:g728635;
C;Genetics:
A;Genetic code: SGCS
A;Note: alpha-51D
C;Superfamily: G surface protein

Query Match 85.7%; Score 36; DB 2; Length 2533;
Best Local Similarity 57.1%; Pred. No. 98;
Matches 4; Conservative 3; Mismatches 0; Gaps 0;

Qy 1 CVPLTSC 7
|:|:|:|
Dp 2149 CIPITNC 2155

RESIST. 6

T30886
integumentary mucin B.1 - African clawed frog (fragment)
C/Species: Xenopus laevis (African clawed frog)
C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C/Accession: T30886
R/Joba, W.; Hoffmann, W.
J. Biol. Chem. 272, 1805-1810, 1997
A/Title: Similarities of integumentary mucin B.1 (FIM-B.1) from Xenopus laevis and B.1 from Rana lessonae
A/Reference number: Z20920; MUID:97153143; PMID:8999864
A/Accession: T30886
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1506 <JOB>
A/Cross-references: UNIPROT:P79827; EMBL:Y08296; NID:gl839051; PIDN:CAA6960
C/Genetics:
A/Note: FIM-B.1
C/Superfamily: pig submaxillary mucin

Query Match	81.0%;	Score 34;	DB 2;	Length 1506;
Best Local Similarity	71.4%;	Pred. No. 1.5e+02;		
Matches 5;	Conservative	1;	Mismatches 1;	Indels 0;
Gaps	0;			

QY	1	CVPLTSC	7
		:	
Db	1292	CVPLSKC	1

RESUIT. 7

A54895
mucin 2, intestinal/tracheal - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C:Accession: A54895
R:Omori, H.; Dohrman, A.P.; Gallup, M.; Tsuda, T.; Kai, H.; Gum Jr., J.R.;
J. Biol. Chem. 269, 17833-17840, 1994
A:Title: Molecular cloning of the amino-terminal region of a rat MUC 2 mucin
A:Reference number: A54895; PMID:8027037
A:Accession: A54895
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1513 <OHM>
A:Cross-references: UNIPROT:Q62635; GB:U07615
C:Superfamily: von Willebrand factor; von Willebrand factor type A repeat h
C:Keywords: intestine

Query Match	81.0%;	Score 34;	DB 2;	Length 1513;
Best Local Similarity	71.4%;	Pred. No. 1.5e+02;		
Matches	5;	Conservative	1;	Mismatches 1;
				Indels 0;
				Gaps 0;

QY 1 CVPLTSC 7
||||:|
Db 709 CVPLSKC 715

RESULT 8
T34022
zonadhesin - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C:Accession: T34022
R:Hardy, D.M.; Garbers, D.L.
J. Biol. Chem. 270, 26025-26028, 1995
A:Title: A sperm membrane protein that binds in a species-specific manner to the egg ext
A:Reference number: Z21464; MUID:96064658; PMID:7592795
A:Accession: T34022
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-2476 <HAR>
A:Cross-references: UNIPROT:Q28983; EMBL:U40024; NID:g1066465; PID:g1066466; PIDN:AAC484
A:Experimental source: strain Meishan; testis
C:Genetics:
A:Gene: Zan
C:Function:
A:Description: may be involved in sperm adhesion to the zona pellucida

Query Match 81.0%; Score 34; DB 2; Length 2476;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
||||:|
Db 1505 CVPLSQC 1511

RESULT 9
S66336
protein kinase AK23 (EC 2.7.1.-) - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 16-Aug-2004
C:Accession: S66336; S58262
R:Thuemmler, F.; Kirchner, M.; Teuber, R.; Ditttrich, P.
Plant Mol. Biol. 29, 551-565, 1995
A:Title: Differential accumulation of the transcripts of 22 novel protein kinase genes i
A:Reference number: S66314; MUID:96123233; PMID:8534852
A:Accession: S66336
A:Molecule type: DNA
A:Residues: 1-55 <THU>
A:Cross-references: UNIPROT:Q38989; EMBL:X86968; NID:g928913; PIDN:CAA60531.1; PID:g9289
C:Genetics:
A:Gene: AK23
C:Superfamily: protein kinase homology
C:Keywords: ATP; phosphotransferase; protein kinase
F:1-55/Domain: protein kinase homology (fragment) <KIN>

Query Match 78.6%; Score 33; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTS 6
|||||
Db 27 CVPLTS 32

RESULT 10
146412
keratin KAP5.4 - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: 146412; S34215
R:Jenkins, B.J.; Powell, B.C.
J. Invest. Dermatol. 103, 310-317, 1994

A:Title: Differential expression of genes encoding a cysteine-rich keratin family in the
A:Reference number: 146412; MUID:94358466; PMID:7521375
A:Accession: 146412
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-191 <JEN>
A:Cross-references: UNIPROT:Q28583; EMBL:X73434; NID:g313719; PIDN:CAA51829.1; PID:g31371
C:Genetics:
A:Gene: KRTAP5.4
C:Superfamily: ultra-high-sulfur keratin

Query Match 78.6%; Score 33; DB 2; Length 191;
Best Local Similarity 71.4%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
||||:|
Db 91 CVPVCSC 97

RESULT 11
A64655
hypothetical protein HP1081 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: A64655
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney,
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: A64655
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-207 <TOM>
A:Cross-references: UNIPROT:Q25713; GB:AE000615; GB:AE000511; NID:g2314230; PIDN:AAD0813

Query Match 78.6%; Score 33; DB 2; Length 207;
Best Local Similarity 71.4%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
||||:|
Db 134 CVPQTTC 140

RESULT 12
B71943
hypothetical protein jhp0344 - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: B71943
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; J
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: B71943
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-207 <ARN>
A:Cross-references: UNIPROT:Q9ZM78; GB:AE001470; GB:AE001439; NID:g4154869; PIDN:AAD05923
A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp0344

Query Match 78.6%; Score 33; DB 2; Length 207;
Best Local Similarity 71.4%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 03:33:32 ; Search time 42.863 Seconds
(without alignments)

83.628 Million cell updates/sec

Title: US-09-761-636A-11

Perfect score: 42

Sequence: 1 CVPLTSC 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Query Length	DB ID	Description
1	39	92.9	575	2 Q8IRB8	Q8IRB8 drosophila
2	39	92.9	2543	2 P90649	P90649 paramacium
3	38	90.5	127	2 Q9GMW9	Q9GMW9 macaca fasc
4	38	90.5	383	1 P013 NASVI	P013 NASVI
5	37	88.1	594	2 Q833X0	Q833X0 enterococcu
6	36	85.7	271	1 K105 HUMAN	P60370 homo sapien
7	36	85.7	337	2 O18464	O18464 herdmania m
8	36	85.7	556	2 Q6XQ8	Q6XQ8 fugu rubrip
9	36	85.7	980	2 Q24780	Q24780 clostridium
10	36	85.7	2533	2 Q90589	Q90589 paramacium
11	36	85.7	2533	2 Q27183	Q27183 paramacium
12	36	85.7	4998	2 Q8CG65	Q8CG65 mus musculus
13	36	85.7	5141	2 Q700K0	Q700K0 rattus norv
14	35	83.3	265	2 Q726V5	Q726V5 desulfovibr
15	35	83.3	292	1 K109 HUMAN	P60411 homo sapien
16	35	83.3	298	1 K10B HUMAN	P60412 homo sapien
17	35	83.3	379	2 Q823I4	Q823I4 chlamydomophi
18	35	83.3	389	2 Q97887	Q97887 bos taurus
19	35	83.3	401	2 Q709J0	Q709J0 anopheles g
20	35	83.3	565	2 Q8TF36	Q8TF36 homo sapien
21	35	83.3	685	1 BMR_HUMAN	Q8n8u9 homo sapien
22	35	83.3	685	1 BMR_MOUSE	Q8c169 mus musculus
23	35	83.3	727	1 KP1_BOVIN	Q28161 bos taurus
24	35	83.3	745	2 Q81YA6	Q81YA6 homo sapien
25	35	83.3	1569	2 Q6W4X9	Q6W4X9 homo sapien
26	35	83.3	1637	2 Q9XSU8	Q9XSU8 bos taurus
27	35	83.3	5146	2 Q8SPM4	Q8SPM4 bos taurus
28	35	83.3	23015	2 Q81Q18	Q81Q18 drosophila
29	34	81.0	201	2 Q6IKI6	Q6IKI6 drosophila
30	34	81.0	221	1 K103 HUMAN	Q6369 homo sapien
31	34	81.0	496	2 Q7S723	Q7S723 neurospora

32	34	81.0	912	1 ANDR_CROCR	Q8mik0 crocuta cro
33	34	81.0	1193	2 Q6JLA0	Q6JLA0 lymphocysti
34	34	81.0	1246	2 Q6LA40	Q6LA40 homo sapien
35	34	81.0	1374	2 Q6LA41	Q6LA41 homo sapien
36	34	81.0	1506	2 P79927	P79927 xenopus lae
37	34	81.0	1513	1 MUC2_RAT	Q62635 rattus norv
38	34	81.0	2476	1 ZAN_FIG	Q28983 sus scrofa
39	34	81.0	2551	1 SBN2_HUMAN	Q8wwq8 h stabilin
40	34	81.0	2843	2 Q9Y6R7	Q9Y6R7 homo sapien
41	33	78.6	55	2 Q38989	Q38989 arabidopsis
42	33	78.6	101	2 Q91F35	Q91F35 cydia pomon
43	33	78.6	120	2 Q86BW2	Q86BW2 ascidia syd
44	33	78.6	143	2 Q9ACU2	Q9ACU2 streptomyce
45	33	78.6	191	2 Q28583	Q28583 ovis aries

ALIGNMENTS

RESULT 1					
Q8IRB8					
ID	Q8IRB8	PRELIMINARY;	PRT;	575 AA.	
AC	Q8IRB8;				
DT	01-MAR-2003 (TREMELrel. 23, Created)				
DT	01-MAR-2003 (TREMELrel. 23, Last sequence update)				
DT	01-MAR-2004 (TREMELrel. 26, Last annotation update)				
DE	CG32260-PA.				
GN	ORFNames=CG32260;				
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;				
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OC	Ephydroidea; Drosophilidae; Drosophila.				
OX	NCBI_TaxID=7227;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=10731132; PubMed=10731132; DOI=10.1126/science.287.5461.2185;				
RA	Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,				
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,				
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,				
RA	Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,				
RA	Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,				
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,				
RA	Abriel J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,				
RA	Baltes R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,				
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,				
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,				
RA	Burtis K.C., Buesam D.A., Butler H., Cadieu E., Center A., Chandra I.,				
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,				
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,				
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,				
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,				
RA	Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,				
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,				
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,				
RA	Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,				
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,				
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,				
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,				
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,				
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,				
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,				
RA	Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,				
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,				
RA	Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,				
RA	Shue B.C., Sidman-Kimos I., Simpson M., Skupski M.P., Smith T.,				
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,				
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,				
RA	Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,				
RA	Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,				
RA	Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,				
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,				
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;				
RT	"The genome sequence of Drosophila melanogaster.";				

Science 287:2185-2195(2000).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Konniller B., Carlson J.W., Halpern A.,
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
Paclet J.M., Park S., Pfeiffer B.D., Richards S., Sodergrén E.J.,
Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
RN SEQUENCE FROM N.A.
RP MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bargman C.M., Konniller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
[4]
RN SEQUENCE FROM N.A.
RP MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
[5]
RN SEQUENCE FROM N.A.
RP FlyBase;
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
[6]
RN SEQUENCE FROM N.A.
RP FlyBase;
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AE003480; AAN11589.1; -.
DR HSP; P00760; 3BTK.
DR FlyBase; FBgn0052260; CG32260.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1a.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 575 AA; 62063 MW; 9D2D66174BB99921 CRC64;

Query Match 92.9%; Score 39; DB 2; Length 575;
Best Local Similarity 85.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
Db 204 CLPLTSC 210

RESULT 2
P90649

P90649 PRELIMINARY; PRT; 2543 AA.
AC P90649;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 156D surface antigen.
OS Paramesitium primaurelia.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC Paramesitium.
OX NCBI_TaxID=5886;
RN [1]_TaxID=5886;
RP SEQUENCE FROM N.A.
RC STRAIN=156;
RX MEDLINE=96313351; PubMed=8768434;
RA Bourgain-Guiliemetti F., Caron;
RT "Molecular characterization of the D surface protein gene subfamily in
Paramesitium primaurelia.";
RL J. Eukaryot. Microbiol. 43:303-313(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=156;
RA Caron F.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X96616; CAA65436.1; -.
DR PIR; T31687; T31687.
DR InterPro; IPR002895; Paramesitium_SA.
DR Pfam; PF01508; Paramesitium_SA; 20.
DR SMART; SM00639; PSA; 25.
SQ SEQUENCE 2543 AA; 267040 MW; 82BFF797CB012902 CRC64;

Query Match 92.9%; Score 39; DB 2; Length 2543;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
Db 2158 CIPITSC 2164

RESULT 3
Q9GMW9 PRELIMINARY; PRT; 127 AA.
AC Q9GMW9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]_TaxID=9541;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain parietal lobe;
RX MEDLINE=21458551; PubMed=11574149; DOI=10.1016/S0378-1119(01)00665-5;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirata M., Suto Y.,
Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;
RT "Assignment of 118 novel cDNAs of cynomolgus monkey brain to human
chromosomes.";
RL Gene 275:31-37(2001).
DR EMBL; AB047606; BAB12130.1; -.
KW Hypothetical protein.
SQ SEQUENCE 127 AA; 12961 MW; EE168525256992C0 CRC64;

Query Match 90.5%; Score 38; DB 2; Length 127;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
Db 107 CVPLSSC 113


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RESULT 4
POL3 NASVI
ID POL3 NASVI STANDARD; PRT; 383 AA.
AC Q03271;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Retrovirus-related Pol polyprotein from type I retrotransposable
DE element R1 [Contains: Reverse transcriptase (EC 2.7.7.49);
DE Endonuclease] (Fragment).
OS Nasonia vitripennis (parasitic wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Chalcidoidea;
OC Pteromalidae; Pteromalinae; Nasonia.
OX NCBI_TaxID=7425;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=93196484; PubMed=8383793;
RA Burke W.D., Eickbush D.G., Xiong Y., Jakubczak J.L., Eickbush T.H.;
RT "Sequence relationship of retrotransposable elements R1 and R2 within
RT and between divergent insect species.";
RL Mol. Biol. Evol. 10:163-185(1993).
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + [DNA](N).
CC -!- SIMILARITY: Contains 1 reverse transcriptase domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L00942; AA303339.1; -
DR PIR; D44490; D44490.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF00078; RVT; 1.
DR PROSITE; PS50878; RT_POL; 1.
DR Endonuclease; Hydrolase; Nuclease; RNA-directed DNA polymerase;
KW Transferase; Transposable element.
FT NON_TER 1
FT DOMAIN <1 88 Reverse transcriptase.
FT DOMAIN 229 383 Nucleic acid-binding endonuclease.
FT SEQUENCE 383 AA; 43411 MW; DE296B380925251B CRC64;

Query Match 90.5%; Score 38; DB 1; Length 383;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CVPLTSC 7
DB 359 CVPLSSC 365

RESULT 5
Q833X0
ID Q833X0 PRELIMINARY; PRT; 594 AA.
AC Q833X0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glycosyl hydrolase, family 35.
OS OrderedLocustNase-EF1805;
OX Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RN SEQUENCE FROM N.A.
RX STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,

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RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.P.,
RA Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
RA Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
RA Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis.";
RL Science 299:2071-2074 (2003).
CC -!- SIMILARITY: Belongs to family 35 of glycosyl hydrolases.
DR EMBL; AE016952; AA081573.1; -
DR TIGR; EF1805; -
DR GO; GO:0009341; C:beta-galactosidase complex; IEA.
DR GO; GO:0004565; F:beta-galactosidase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001944; Glyco_hydro_35.
DR Pfam; PF01301; Glyco_hydro_35; 1-
DR PRINTS; PR00742; GLHYDRLASE35.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 594 AA; 68456 MW; 4940914DE5174E0D CRC64;

Query Match 88.1%; Score 37; DB 2; Length 594;
Best Local Similarity 71.4%; Pred. No. 78;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CVPLTSC 7
DB 485 CLPMTSC 491

RESULT 6
K105 HUMAN
ID K105 HUMAN STANDARD; PRT; 271 AA.
AC P60370; Q70LJ3;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Keratin associated protein 10-5 (Keratin associated protein 10.5)
DE (High sulfur keratin associated protein 10.5) (Keratin associated
DE protein 18-5) (Keratin associated protein 18.5).
GN Name=KRTAP10-5;
GN Synonyms=KAP10-5, KAP18-5, KRTAP10.5, KRTAP18-5, KRTAP18.5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A., AND VARIANTS ASN-20; LEU-235 AND ARG-268.
RP TISSUE=Root hairs;
RX PubMed=15028290; DOI=10.1016/j.ygeno.2003.09.024;
RA Shibuya K., Obayashi I., Asakawa S., Minoshima S., Kudoh J.,
RA Shimizu N.;
RT "A cluster of 21 keratin-associated protein genes within introns of
RT another gene on human chromosome 21q22.3.";
RL Genomics 83:679-693(2004).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=20289799; PubMed=10830953; DOI=10.1038/35012518;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
RA Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyma S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordiek G., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,
RA Ramser J., Beck A., Klages S., Hennig S., Rieselmann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehrach H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21.";
RL Nature 405:311-319(2000).

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RN SEQUENCE OF 261-271 FROM N.A.
RP TISSUE=Scalp;
RX PubMed:14962103;
RA Rogers M.A., Langbein L., Winter H., Beckmann I., Praetzel S.,
Schweizer J.;
RT "Hair keratin associated proteins: characterization of a second high
sulfur KAP gene domain on human chromosome 21.";
RL J. Invest. Dermatol. 122:147-158(2004).
CC -!- FUNCTION: In the hair cortex, hair keratin intermediate filaments
are embedded in an interfibrillar matrix, consisting of hair
keratin-associated protein (KRTAP), which are essential for the
formation of a rigid and resistant hair shaft through their
extensive disulfide bond cross-linking with abundant cysteine
residues of hair keratins. The matrix proteins include the high-
sulfur and high-glycine-tyrosine keratins.
CC -!- SUBUNIT: Interacts with hair keratins.
CC -!- TISSUE SPECIFICITY: Restricted to hair root, not detected in any
others tissues.
CC -!- SIMILARITY: Belongs to the KRTAP type 10 family.
CC
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CC
CC EMBL; AB076352; BAD01539.1; -;
CC EMBL; AL773602; -; NOT ANNOTATED_CDS.
CC EMBL; AJ566384; CAD97464.1; -;
CC Genbank; HGNC:22969; KRTAP10-5.
CC InterPro; IPR002494; Keratin B2.
KW Keratin; Multigene family; Polymorphism; Repeat.
FT DOMAIN 26 255 22 X 5 AA repeats of C-C-X(3).
FT REPEAT 26 30 1.
FT REPEAT 51 55 2.
FT REPEAT 73 77 3.
FT REPEAT 78 82 4.
FT REPEAT 88 92 5.
FT REPEAT 93 97 6.
FT REPEAT 98 102 7.
FT REPEAT 110 114 8.
FT REPEAT 120 124 9.
FT REPEAT 130 134 10.
FT REPEAT 135 139 11.
FT REPEAT 140 144 12.
FT REPEAT 152 156 13.
FT REPEAT 162 166 14.
FT REPEAT 177 181 15.
FT REPEAT 187 191 16.
FT REPEAT 199 203 17.
FT REPEAT 209 213 18.
FT REPEAT 214 218 19.
FT REPEAT 233 237 20.
FT REPEAT 240 244 21.
FT REPEAT 251 255 22.
FT VARIANT 20 20 D -> N.
FT VARIANT 235 235 /FTID=VAR_017696.
FT VARIANT 268 268 V -> L.
FT VARIANT 268 268 /FTID=VAR_017697.
FT CONFLICT 268 268 P -> R.
FT CONFLICT 268 268 /FTID=VAR_017698.
FT CONFLICT 268 268 P -> R (in Ref. 3).
SQ SEQUENCE 271 AA; 27567 MW; 20B32DB262D523ED CRC64;

Query Match 85.7%; Score 36; DB 1; Length 271;
Best Local Similarity 71.4%; Pred. No. 56;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
||||:|

Db 234 CVPISSC 240

RESULT 7
Q18464
ID O18464 PRELIMINARY; PRT; 337 AA.
AC O18464;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein HMEGFL-1 precursor.
GN Name=HMEGFL-1;
OS Herdmania momus (Brown sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyrosida; Herdmania.
OX NCBI_TaxID=7733;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=curvata;
RX MEDLINE=98049320; PubMed=9389452;
RA DOI=10.1002/(SICI)1097-0177(199711)210:3<264::AID-AJA7>3.3.CO;2-D;
RA Arnold J.M., Eri R., Dagnan B.M., Lavin M.F.;
RT "Novel gene containing multiple epidermal growth factor-like motifs
RT transiently expressed in the papillae of the ascidian tadpole
RT larvae.";
RL Dev. Dyn. 210:264-273(1997).
DR EMBL; U82540; AAB67704.1; -;
DR HSSP; Q90248; LHX2.
DR InterPro; IPR002919; Cysrich_TIL.
DR InterPro; IPR006210; IEGF.
DR SMART; PF01826; TIL; 4.
DR SMART; SM00181; EGF; 4.
KW Hypothetical protein; Signal.
FT SIGNAL 1 18 Potential.
FT CHAIN 19 337 unknown protein.
SQ SEQUENCE 337 AA; 35617 MW; 5CCA0924118DFC6 CRC64;

Query Match 85.7%; Score 36; DB 2; Length 337;
Best Local Similarity 71.4%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
||||:|
Db 199 CVPISSC 205

RESULT 8
Q6XQM8
ID Q6XQM8 PRELIMINARY; PRT; 556 AA.
AC Q6XQM8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Nicotinate phosphoribosyltransferase-like protein.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorphs; Tetraodontiformes;
OC Tetraontoidea; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang C.-H., Peng J., Chen Y.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY214333; AAB69611.1; -;
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR InterPro; IPR007229; NAPTase.
DR Pfam; PF04095; NAPTase; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 556 AA; 60962 MW; 7CB26180DB6B37F6A CRC64;

Query Match 85.7%; Score 36; DB 2; Length 556;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
|:|:|
Db 403 CIPVSC 409

RESULT 9

ID O24780 PRELIMINARY; PRT; 980 AA.
AC O24780;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Cellodextrin phosphorylase.
GN Name=cdp;
OS Clostridium thermocellum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1515;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC27405;
RA Kawaguchi T., Ikeuchi Y., Teutsomi N., Kan A., Sumitani J., Arai M.;
RT "Cloning, nucleotide sequence, and expression of the Clostridium
RT thermocellum cellodextrin phosphorylase gene and its application to
RT synthesis of cellulase inhibitors.";
RL J. Ferment. Bioeng. 85:144-149 (1998).
DR EMBL; AB006822; BAA22081.1; -.
DR PIR; T00045; T00045.
DR InterPro; IPR010383; Glyco_transf_36.
DR Pfam; PF06165; Glyco_transf_36; 1_
DR SMART; SM00639; PSA; 27.
SQ SEQUENCE 980 AA; 111183 MW; 8A8C8EE3F5370831 CRC64;

Query Match 85.7%; Score 36; DB 2; Length 980;

Best Local Similarity 57.1%; Pred. No. 2e+02; Indels 0; Gaps 0;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
|:|:|
Db 550 CIPMTAC 556

RESULT 10

ID P90589 PRELIMINARY; PRT; 2533 AA.
AC P90589;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Alpha-51D immobilization antigen.
GN Name=alpha-51D;
OS Paramacium tetraurelia.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC Paramacium.
OX NCBI_TaxID=5888;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=51;
RA Schwegmann K., Klein H., Schmidt H.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=51;
RA Schwegmann K.J.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X36400; CAA5264.1; -.
DR PIR; T28675; T28675.
DR InterPro; IPR002895; Paramacium SA.
DR Pfam; PF01508; Paramacium SA; 21.
DR SMART; SM00639; PSA; 27.
SQ SEQUENCE 2533 AA; 264141 MW; EAED7F21E408C371 CRC64;

Query Match 85.7%; Score 36; DB 2; Length 2533;

Best Local Similarity 57.1%; Pred. No. 5.2e+02; Indels 0; Gaps 0;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
|:|:|
Db 2149 CIPITNC 2155

RESULT 11

ID Q27183 PRELIMINARY; PRT; 2533 AA.
AC Q27183;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Alpha-51D-immobilization antigen.
GN Name=alpha-51D-gene;
OS Paramacium tetraurelia.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC Paramacium.
OX NCBI_TaxID=5888;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=51;
RA Schmidt H.J.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; X85135; CAA59447.1; -.
DR PIR; T28674; T28674.
DR InterPro; IPR002895; Paramacium SA.
DR Pfam; PF01508; Paramacium SA; 22.
DR SMART; SM00639; PSA; 27.
SQ SEQUENCE 2533 AA; 263995 MW; 261BD09806BC344D CRC64;

Query Match 85.7%; Score 36; DB 2; Length 2533;

Best Local Similarity 57.1%; Pred. No. 5.2e+02; Indels 0; Gaps 0;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
|:|:|
Db 2149 CIPITNC 2155

RESULT 12

ID Q8CG65 PRELIMINARY; PRT; 4998 AA.
AC Q8CG65;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE SCO-spondin.
GN Name=Scospondin; Synonyms=sco-spondin;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Brain;
RA Goncalves N., Simon-Charottes D., Creveaux I., Meinzel A.,
RA Guenet J.-L., Meinzel R.;
RT "Mouse SCO-spondin, a gene of the thrombospondin type 1 repeat (TSR)
RT superfamily expressed in the brain.";
RL Gene 312:263-270 (2003).
CC -!- SIMILARITY: Contains 1 F5/8 type C domain.
DR EMBL; AJ491857; CAD42654.1; -.
DR HSSP; P01130; 1AJJ.
DR MGD; MGI:2674311; Scospondin.
DR GO; GO:0005737; C:cytoplasm; IC.
DR InterPro; IPR000923; BlueCu 1.
DR InterPro; IPR002919; Cysrich_TIL.
DR InterPro; IPR006207; Cys_knot_C.
DR InterPro; IPR006209; EGF_like.


```

OY 1 CVPLTSC 7
DB 7 CVPVTD 13

RESULT 15
K109_HUMAN
ID K109_HUMAN STANDARD; PRT; 292 AA.
AC P60411; Q70LJ1;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Keratin associated protein 10-9 (Keratin associated protein 10.9)
DE (High sulfur keratin associated protein 10.9) (Keratin associated
DE protein 18-9) (Keratin associated protein 18.9).
GN Name=KRTAP10-9;
GN Synonyms=KAP10.9, KAP18-9, KRTAP10.9, KRTAP18-9, KRTAP18.9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT TYR-182.
RC TISSUE=Root hairs;
RX PubMed=15028290; DOI=10.1016/j.ygeno.2003.09.024;
RA Shibuya K., Obayashi I., Asakawa S., Minoshima S., Kudoh J.,
RA Shimizu N.;
RT "A cluster of 21 keratin-associated protein genes within introns of
RT another gene on human chromosome 21q22.3.";
RL Genomics 83:679-693(2004).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20289799; PubMed=10830953; DOI=10.1038/35012518;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
RA Onki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Folley A.,
RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordieck G., Hornischer K., Brandt P.,
RA Scharfe W., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,
RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA Wehmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehrach H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21.";
RL Nature 405:311-319(2000).
RN [3]
RP SEQUENCE OF 244-292 FROM N.A.
RC TISSUE=Scalp;
RX PubMed=14962103;
RA Rogers M.A., Langbein L., Winter H., Beckmann I., Praetzel S.,
RA Schweizer J.;
RT "Hair keratin associated proteins: characterization of a second high
RT sulfur KAP gene domain on human chromosome 21.";
RL J. Invest. Dermatol. 122:147-158(2004).
CC -!- FUNCTION: In the hair cortex, hair keratin intermediate filaments
CC are embedded in an interfilamentous matrix, consisting of hair
CC keratin-associated protein (KRTAP), which are essential for the
CC formation of a rigid and resistant hair shaft through their
CC extensive disulfide bond cross-linking with abundant cysteine
CC residues of hair keratins. The matrix proteins include the high-
CC sulfur and high-glycine-tyrosine keratins.
CC -!- SUBUNIT: Interacts with hair keratins.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms are produced;
CC Name=1;
CC IsoId=P60411-1; Sequence=Displayed;
CC -!- TISSUE SPECIFICITY: Restricted to hair root, not detected in any
CC others tissues.
CC -!- SIMILARITY: Belongs to the KRTAP type 10 family.

```

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EMBL; AB076356; BAD01543.1; -
EMBL; AL773602; -; NOT ANNOTATED_CDS.
EMBL; AJ566386; CAD97456.1; -
Genew; HGNC:22971; KRTAP10-9.
InterPro; IPR002494; Keratin_B2.
Alternative splicing; Keratin; Multigene family; Polymorphism; Repeat.
FT DOMAIN 26 254 25 X 5 AA repeats of C-C-X(3).
FT REPEAT 1.
FT REPEAT 2.
FT REPEAT 3.
FT REPEAT 4.
FT REPEAT 5.
FT REPEAT 6.
FT REPEAT 7.
FT REPEAT 8.
FT REPEAT 9.
FT REPEAT 10.
FT REPEAT 11.
FT REPEAT 12.
FT REPEAT 13.
FT REPEAT 14.
FT REPEAT 15.
FT REPEAT 16.
FT REPEAT 17.
FT REPEAT 18.
FT REPEAT 19.
FT REPEAT 20.
FT REPEAT 21.
FT REPEAT 22.
FT REPEAT 23.
FT REPEAT 24.
FT REPEAT 25.
FT VARIANT 182
FT CONFLICT 257 R -> C (in Ref. 3).
SQ SEQUENCE 292 AA; 29976 MW; 5BAB527FB59C46B9 CRC64;
Query Match 83.3%; Score 35; DB 1; Length 292;
Best Local Similarity 71.4%; Pred. No. 96;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 CVPLTSC 7
DB 244 CVPVSSC 250

Search completed: April 1, 2005, 09:26:03
Job time : 44.863 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 03:27:37 ; Search time 52.8356 Seconds
(without alignments)
51.240 Million cell updates/sec

Title: US-09-761-636A-11

Perfect score: 42

Sequence: 1 CVPLTSC 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	7	AAU04530	Aau04530 VEGF base
2	38	90.5	50	AAU62562	Aau62562 Propionib
3	38	90.5	50	ABM59081	Abm59081 Propionib
4	38	90.5	74	ABG13170	Abg13170 Novel hum
5	37	88.1	64	ABBI6042	Abbi6042 Human ner
6	37	88.1	273	ADT49843	Adt49843 Murine TA
7	37	88.1	371	ADT49844	Adt49844 Murine TA
8	37	88.1	378	ADT49883	Adt49883 Murine TA
9	37	88.1	616	ADH88495	Adh88495 Enterococ
10	36	85.7	91	AAU64239	Aau64239 Propionib
11	36	85.7	91	ABM60758	Abm60758 Propionib
12	36	85.7	4561	ABG30203	Abg30203 Novel hum
13	36	85.7	9222	ABG21064	Abg21064 Novel hum
14	35	83.3	61	AAU96565	Aau96565 Human rep
15	35	83.3	61	ABB96569	Abb96569 Human tes
16	35	83.3	65	AAU18859	Aau18859 Novel pro
17	35	83.3	65	AAU94953	Aau94953 Human rep
18	35	83.3	80	AAU49012	Aau49012 Propionib
19	35	83.3	80	ABM45531	Abm45531 Propionib
20	35	83.3	196	ABW02001	Abw02001 Human cro
21	35	83.3	270	AAU99932	Aau99932 Human pol
22	35	83.3	270	ABG65083	Abg65083 Human alb
23	35	83.3	270	ADL78350	Adl78350 Albumin f
24	35	83.3	281	ADW07963	Adw07963 Novel pro
25	35	83.3	292	ADU92159	Adu92159 Human hai

26	35	83.3	298	7	ADJ92163	Adj92163 Human hai
27	35	83.3	445	4	AAE07062	Aae07062 Human gen
28	35	83.3	445	5	ABG65086	Abg65086 Human alb
29	35	83.3	445	8	ADL78353	Adl78353 Albumin f
30	35	83.3	464	4	AAE07119	Aae07119 Human gen
31	35	83.3	575	8	ADO41983	Ado41983 Human cel
32	35	83.3	627	5	AAU99293	Aau99293 Human cho
33	35	83.3	627	8	ADS18361	Ads18361 Human NHP
34	35	83.3	646	7	ABW02006	Abw02006 Human cro
35	35	83.3	685	5	AAU99292	Aau99292 Human cho
36	35	83.3	685	6	ABU11857	Abu11857 Human sec
37	35	83.3	685	7	ADE07923	Ade07923 Novel pro
38	35	83.3	685	7	ABW02004	Abw02004 Human cro
39	35	83.3	685	7	ADM04861	Adm04861 Human pro
40	35	83.3	685	8	ADO00978	Ado00978 Human hom
41	35	83.3	685	8	ADS18359	Ads18359 Human NHP
42	35	83.3	745	6	AAO29572	Aao29572 Human Pg4
43	35	83.3	745	7	ADC56921	Adc56921 Cytoskele
44	35	83.3	867	8	ADM87331	Adm87331 Human pro
45	35	83.3	1569	8	ADR18921	Adr18921 Human muc

ALIGNMENTS

RESULT 1
AAU04530
ID AAU04530 standard; peptide; 7 AA.
XX
AC AAU04530;
XX
DT 26-SEP-2001 (first entry)
XX
DE VEGF based monocyclic peptide 8.
XX
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..7 /note= "This bond cyclises the peptide"
XX
PN WO200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Achen MG, Hughes RA, Stackner S, Cendron A;
XX
DR WPI; 2001-442248/47.
XX
PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.
XX
PS Claim 49; Page 32; 102pp; English.
XX
CC The sequence represents a monomeric monocyclic peptide of the invention,
CC whose 3-dimensional structure is modelled on the expose loop of human
CC VEGFD (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and
CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
CC peptides) and a cyclic peptide with at least one amino acid deleted prior
CC to cyclisation are used to interfere with angiogenesis.
CC neovascularisation or lymphangiogenesis in a mammal with a condition
CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
CC The condition is diabetic retinopathy, psoriasis, arthropathy,
CC hemangioma, vascularised malignant or benign tumour, post-recovery
CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
CC trauma, substance-induced neovascularisation of the liver, excessive
CC hormone-related angiogenic dysfunction, diabetes induced neovascular
CC sequelae, hypertension induced neovascular sequelae, or chronic liver
CC infection. The peptides are also used to modulate vascular permeability
CC in a mammal (the mammal has a condition characterised by fluid
CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
CC or brain. The peptides are used to image blood vessels and lymphatic
CC vasculature. The monomeric and bicyclic peptides are used to interfere
CC with at least one biological activity induced by VEGF, VEGF-C or -D and
CC are also used in combination with an anti-inflammatory agent, to treat a
CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
CC diabetic retinopathy
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 42; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. NO. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
DB 1 CVPLTSC 7

RESULT 2
AAU62562
ID AAU62562 standard; protein; 50 AA.
AC AAU62562;
XX
XX 27-FEB-2002 (first entry)
DE Propionibacterium acnes immunogenic protein #23458.
XX
XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
OS
XX Propionibacterium acnes.
XX
XX WO200181581-A2.
XX
XX 01-NOV-2001.
XX
XX 20-APR-2001; 2001WO-US012865.
XX
XX 21-APR-2000; 2000US-0199047P.
XX
XX 02-JUN-2000; 2000US-0208841P.
XX
XX 07-JUL-2000; 2000US-0216747P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
XX WPI: 2001-616774/71.
XX
XX N-PSDB; AAS59627.
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
XX vaccinating against and diagnosing infections, especially useful for
XX treating acne vulgaris.
XX

PS
XX Example 1; SEQ ID NO 23757; 1069pp; English.
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 50 AA;

Query Match 90.5%; Score 38; DB 4; Length 50;
Best Local Similarity 85.7%; Pred. NO. 49;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
DB 22 CAPLTSC 28

RESULT 3
ABM59081
ID ABM59081 standard; protein; 50 AA.
XX
XX AC ABM59081;
XX
XX 20-OCT-2003 (first entry)
XX
XX Propionibacterium acnes predicted ORF-encoded polypeptide #23757.
DE
XX Acne vulgaris; antiseborrheic; dermatological; antibacterial;
KW immunostimulant; immune response; vaccine.
XX
XX OS Propionibacterium acnes.
XX
XX PN WO2003033515-A1.
XX
XX 24-APR-2003.
XX
XX 11-OCT-2002; 2002WO-US032727.
XX
XX 15-OCT-2001; 2001US-00978825.
XX
XX (CORI-) CORIXA CORP.
XX
XX Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
PI Barth B, Vallie-Douglas J;
XX
XX WPI: 2003-381789/36.
XX
XX N-PSDB; ACF64556.
XX
XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
XX polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
XX or for stimulating an immune response specific for a P. acnes protein.
PS Example 1; SEQ ID NO 23757; 1481pp; English.
XX
XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
XX

CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridization. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 50 AA;

Query Match 90.5%; Score 38; DB 6; Length 50;
 Best Local Similarity 85.7%; Pred. No. 49;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
 |||||
 Db 22 CAPLTSC 28

RESULT 4
 ABG13170
 ID ABG13170 standard; protein; 74 AA.

XX AC ABG13170;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #13161.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX XX WPI; 2001-639362/73.

XX DR N-PSDB; AAS77357.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX PS Claim 20; SEQ ID NO 43529; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activities. The
 CC polypeptide and polynucleotide sequences have application in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 74 AA;

Query Match 90.5%; Score 38; DB 4; Length 74;
 Best Local Similarity 85.7%; Pred. No. 70;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
 |||||
 Db 29 CVPLSSC 35

RESULT 5
 ABB16042

ID ABB16042 standard; protein; 64 AA.

XX AC ABB16042;

XX DT 23-JAN-2002 (first entry)

XX DE Human nervous system related polypeptide SEQ ID NO 4699.

XX KW Human; nontropic; neuroprotective; cytostatic; dermatological; virucide;
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
 KW antiparkinsonian; antiscikling; antianaemic; antiarthritis; cancer;
 KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
 KW antiallergic; antidiabetic; antilucer; anticonvulsant; antifungal;
 KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine.

XX OS Homo sapiens.

XX PN WO200159063-A2.

XX PD 16-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US001334.

XX PR 31-JAN-2000; 2000US-0179065P.

XX PR 04-FEB-2000; 2000US-0180628P.

XX PR 24-FEB-2000; 2000US-0184664P.

XX PR 02-MAR-2000; 2000US-0186350P.

XX PR 16-MAR-2000; 2000US-0189874P.

XX PR 17-MAR-2000; 2000US-0190076P.

XX PR 18-APR-2000; 2000US-0198123P.

XX PR 19-MAY-2000; 2000US-0205151P.

XX PR 07-JUN-2000; 2000US-0209467P.

XX PR 28-JUN-2000; 2000US-0214886P.

XX PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225477P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 23-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0233297P.
PR 14-SEP-2000; 2000US-0233398P.
PR 14-SEP-2000; 2000US-0233399P.
PR 14-SEP-2000; 2000US-0233400P.
PR 14-SEP-2000; 2000US-0233401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 20-OCT-2000; 2000US-0242221P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251160P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-541565/60.
XX N-PSDB; ABA12368.
XX
PT Nucleic acids encoding 324 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system cancers
XX
PS Claim 11; SEQ ID NO 4699; 1701pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABA11004-ABA21534) and proteins
CC (AB14678-AB18001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,

CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 64 AA;
 Query Match 88.1%; Score 37; DB 4; Length 64;
 Best Local Similarity 85.7%; Pred. No. 89;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CVPLTSC 7
 Db 28 CXPLTSC 34
 RESULT 6
 ADT49843
 ID ADT49843 standard; protein; 273 AA.
 AC ADT49843;
 DT 16-DEC-2004 (first entry)
 DE Murine TAKEDA002 partial sequence/betacellulin antibody SEQ ID NO:50.
 XX
 KW TAKEDA002; BTC; betacellulin; antidiabetic; antilipemic;
 KW antiarteriosclerotic; nephrotropic; ophthalmological; cardiovascular;
 KW cytostatic; antiinflammatory; immunosuppressive; osteopathic;
 KW antiarthritic; neuroprotective; nontropic; gene therapy;
 KW diabetes mellitus; hyperlipemia; arteriosclerosis; nephropathy;
 KW retinopathy; cardiovascular disease; cancer; fibrosis;
 KW autoimmune disease; inflammatory disease; osteoarthritis; osteoporosis;
 KW Alzheimer's disease; neurodegenerative disorder;
 KW cell proliferative disorder.
 XX
 OS Mus musculus.
 XX WO2004083241-A2.
 XX 30-SEP-2004.
 XX 18-MAR-2004; 2004WO-JP003699.
 XX 19-MAR-2003; 2003US-0456007P.
 XX 02-APR-2003; 2003US-0459944P.
 XX (TAKE) TAKEDA CHEM IND LTD.
 XX Sakamoto T, Takeda S;
 XX WPI; 2004-691021/67.
 XX New protein complexes comprising BTC and a second protein (e.g.
 PT mLOC243548, mDLK1 or mPACE4) useful for diagnosing, preventing or
 PT treating disorders such as diabetes mellitus, nephropathy, cardiovascular
 PT disease or cancer.
 XX Disclosure; SEQ ID NO 50; 493pp; English.
 XX The invention relates to an isolated protein complex having a first
 CC protein which is betacellulin (BTC) or its homologue, derivative or
 CC fragment, interacting with a second protein selected from mLOC243548,
 CC mDLK1, mPACE4, mBC032073(1598), mTHBS2, mFBLN5, mAKO09011, mHRMTL2,
 CC mMATN3, mNID1, mTASP(459), mINPP5B, mTAKEDA008, UBB, mTREX1, mSGT and
 CC CAMLG, or homologue, derivative or fragment. A complex of the invention
 CC has antidiabetic, antilipemic, antiarteriosclerotic, nephrotropic,

CC ophthalmological, cardiovascular-gen., cytostatic, antiinflammatory,
 CC immunosuppressive, osteopathic, antiarthritic, neuroprotective, and
 CC nontropic activity, and may have a use in gene therapy. The composition
 CC and methods are useful for treating physiological disorders associated
 CC with diabetes mellitus, hyperlipemia, arteriosclerosis, nephropathy,
 CC retinopathy, cardiovascular disease, cancer, fibrosis, autoimmune
 CC disease, inflammatory disease, osteoarthritis, osteoporosis, Alzheimer's
 CC disease, neurodegenerative disorder or cell proliferative disorder. These
 CC may also be used for diagnosing or preventing the disorders cited above,
 CC or for screening for agents that may be used to prevent or treat those
 CC disorders. The present sequence is used in the exemplification of the
 CC invention.
 XX
 SQ Sequence 273 AA;
 Query Match 88.1%; Score 37; DB 8; Length 273;
 Best Local Similarity 85.7%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CVPLTSC 7
 Db 57 CVPLASC 63
 RESULT 7
 ADT49844
 ID ADT49844 standard; protein; 371 AA.
 AC ADT49844;
 DT 16-DEC-2004 (first entry)
 DE Murine TAKEDA002 partial sequence/betacellulin antibody SEQ ID NO:51.
 XX
 KW TAKEDA002; BTC; betacellulin; antidiabetic; antilipemic;
 KW antiarteriosclerotic; nephrotropic; ophthalmological; cardiovascular;
 KW cytostatic; antiinflammatory; immunosuppressive; osteopathic;
 KW antiarthritic; neuroprotective; nontropic; gene therapy;
 KW diabetes mellitus; hyperlipemia; arteriosclerosis; nephropathy;
 KW retinopathy; cardiovascular disease; cancer; fibrosis;
 KW autoimmune disease; inflammatory disease; osteoarthritis; osteoporosis;
 KW Alzheimer's disease; neurodegenerative disorder;
 KW cell proliferative disorder.
 XX
 OS Mus musculus.
 XX WO2004083241-A2.
 XX 30-SEP-2004.
 XX 18-MAR-2004; 2004WO-JP003699.
 XX 19-MAR-2003; 2003US-0456007P.
 XX 02-APR-2003; 2003US-0459944P.
 XX (TAKE) TAKEDA CHEM IND LTD.
 XX Sakamoto T, Takeda S;
 XX WPI; 2004-691021/67.
 XX New protein complexes comprising BTC and a second protein (e.g.
 PT mLOC243548, mDLK1 or mPACE4) useful for diagnosing, preventing or
 PT treating disorders such as diabetes mellitus, nephropathy, cardiovascular
 PT disease or cancer.
 XX Disclosure; SEQ ID NO 51; 493pp; English.
 XX The invention relates to an isolated protein complex having a first
 CC protein which is betacellulin (BTC) or its homologue, derivative or
 CC fragment, interacting with a second protein selected from mLOC243548,
 CC mDLK1, mPACE4, mBC032073(1598), mTHBS2, mFBLN5, mAKO09011, mHRMTL2,
 CC mMATN3, mNID1, mTASP(459), mINPP5B, mTAKEDA008, UBB, mTREX1, mSGT and
 CC CAMLG, or homologue, derivative or fragment. A complex of the invention
 CC has antidiabetic, antilipemic, antiarteriosclerotic, nephrotropic,

CC CAMLG, or homologue, derivative or fragment. A complex of the invention
 CC has antidiabetic, antilipemic, antiarteriosclerotic, nephrotropic,
 CC ophthalmological, cardiovascular-gen., cytostatic, antiinflammatory,
 CC immunosuppressive, osteopathic, antiarthritic, neuroprotective, and
 CC neurotropic activity, and may have a use in gene therapy. The composition
 CC and methods are useful for treating physiological disorders associated
 CC with diabetes mellitus, hyperlipemia, arteriosclerosis, nephropathy,
 CC retinopathy, cardiovascular disease, cancer, fibrosis, autoimmune
 CC disease, inflammatory disease, osteoarthritis, osteoporosis, Alzheimer's
 CC disease, neurodegenerative disorder or cell proliferative disorder. These
 CC may also be used for diagnosing or preventing the disorders cited above,
 CC or for screening for agents that may be used to prevent or treat those
 CC disorders. The present sequence is used in the exemplification of the
 CC invention.
 XX
 SQ Sequence 371 AA;

Query Match 88.1%; Score 37; DB 8; Length 371;
 Best Local Similarity 85.7%; Pred. No. 4.2e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
 Db 50 CVPLASC 56
 |||||

RESULT 8
 ADT49883
 ID ADT49883 standard; protein; 378 AA.

AC ADT49883;

DT 16-DEC-2004 (first entry)

DE Murine TAKEDA002 partial sequence SEQ ID NO:90.

XX TAKEDA002; BTC; betacellulin; antidiabetic; antilipemic;
 KW antiarteriosclerotic; nephrotropic; ophthalmological; cardiovascular;
 KW cytostatic; antiinflammatory; immunosuppressive; osteopathic;
 KW antiarthritic; neuroprotective; nontropic; gene therapy;
 KW diabetes mellitus; hyperlipemia; arteriosclerosis; nephropathy;
 KW retinopathy; cardiovascular disease; cancer; fibrosis;
 KW autoimmune disease; inflammatory disease; osteoarthritis; osteoporosis;
 KW Alzheimer's disease; neurodegenerative disorder;
 KW cell proliferative disorder.

OS Mus musculus.

PN WO2004083241-A2.

PD 30-SEP-2004.

PF 18-MAR-2004; 2004WO-JP003699.

PR 19-MAR-2003; 2003US-0456007P.

PR 02-APR-2003; 2003US-0459944P.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Sakamoto T, Takeda S;

XX WPI; 2004-691021/67.

DR N-PSDB; ADT49908.

PT New protein complexes comprising BTC and a second protein (e.g.

PT mLOC243548; mDLK1 or mPACE4) useful for diagnosing, preventing or
 PT treating disorders such as diabetes mellitus, nephropathy, cardiovascular
 PT disease or cancer.

XX Disclosure; SEQ ID NO 90; 493pp; English.

XX The invention relates to an isolated protein complex having a first
 CC protein which is betacellulin (BTC) or its homologue, derivative or

CC fragment, interacting with a second protein selected from mLOC243548,
 CC mDLK1, mPACE4, mBC032073(1598), mTHB32, mFBLN5, mAKO09011, mHRMT1L2,
 CC mMATN3, mNID1, mTASP(459), mINPP5B, mTAKEDA008, UBB, mTREX1, mSGT and
 CC CAMLG, or homologue, derivative or fragment. A complex of the invention
 CC has antidiabetic, antilipemic, antiarteriosclerotic, nephrotropic,
 CC ophthalmological, cardiovascular-gen., cytostatic, antiinflammatory,
 CC immunosuppressive, osteopathic, antiarthritic, neuroprotective, and
 CC neurotropic activity, and may have a use in gene therapy. The composition
 CC and methods are useful for treating physiological disorders associated
 CC with diabetes mellitus, hyperlipemia, arteriosclerosis, nephropathy,
 CC retinopathy, cardiovascular disease, cancer, fibrosis, autoimmune
 CC disease, inflammatory disease, osteoarthritis, osteoporosis, Alzheimer's
 CC disease, neurodegenerative disorder or cell proliferative disorder. These
 CC may also be used for diagnosing or preventing the disorders cited above,
 CC or for screening for agents that may be used to prevent or treat those
 CC disorders. The present sequence is used in the exemplification of the
 CC invention.
 XX
 SQ Sequence 378 AA;

Query Match 88.1%; Score 37; DB 8; Length 378;

Best Local Similarity 85.7%; Pred. No. 4.3e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
 Db 57 CVPLASC 63
 |||||

RESULT 9

ADH88495

ID ADH88495 standard; protein; 616 AA.

AC ADH88495;

DT 22-APR-2004 (first entry)

XX Enterococcus faecalis polypeptide #2975.

DE Enterococcus faecalis infection; transcription regulatory element;
 KW antibacterial.

XX Enterococcus faecalis.

OS Enterococcus faecalis.

PN US6617156-B1.

XX 09-SEP-2003.

PF 13-AUG-1998; 98US-00134000.

PR 15-AUG-1997; 97US-0055778P.

XX (DOUC/) DOUCETTE-STAMM L A.

PA (BUSH/) BUSH D.

PI Doucette-Stamm LA, Bush D;

DR WPI; 2003-895394/82.

DR N-PSDB; ADH85090.

XX New nucleic acid comprising a sequence encoding an Enterococcus faecalis
 PT polypeptide, useful for preparing a composition for diagnosing or
 PT treating E. faecalis infection.

XX Disclosure; SEQ ID NO 6380; 193pp; English.

XX The invention relates to Enterococcus faecalis polynucleotides and
 CC polypeptides. The invention also relates to a recombinant expression
 CC vector comprising a polynucleotide operably linked to a transcription
 CC regulatory element, a cell comprising a recombinant vector, a method for
 CC producing an E. faecalis polypeptide, an isolated nucleic acid comprising
 CC a sequence not given in the specification, a recombinant vector
 CC comprising the nucleic acid and a cell comprising the recombinant vector.

CC The polynucleotides can be used to detect the presence of *E. faecalis* in
 CC a sample. The sequences are useful for preparing a composition for
 CC diagnosing or treating *Enterococcus faecalis* infection. This sequence
 CC represents an *E. faecalis* polypeptide of the invention.
 XX
 XX
 SQ Sequence 616 AA;

Query Match 88.1%; Score 37; DB 7; Length 616;
 Best Local Similarity 71.4%; Pred. No. 6.7e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CVPLTSC 7
 |.:|:|:|
 Db 507 CLPWTSC 513

RESULT 10

AAU64239
 ID AAU64239 standard; protein; 91 AA.

XX
 AC AAU64239;

XX
 DT 27-FEB-2002 (first entry)

XX
 DE Propionibacterium acnes immunogenic protein #25135.

XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.

XX
 OS Propionibacterium acnes.

XX
 PN WO200181581-A2.

XX
 PD 01-NOV-2001.

XX
 PF 20-APR-2001; 2001WO-US012865.

XX
 PR 21-APR-2000; 2000US-0199047P.

PR
 02-JUN-2000; 2000US-0208841P.

PR
 07-JUL-2000; 2000US-0216747P.

XX
 PA (CORI-) CORIXA CORP.

XX
 PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

XX
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX
 PT WPI; 2001-616774/71.
 PT N-PSDB; AAS59641.
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.

XX
 PS Example 1; SEQ ID NO 25434; 1069pp; English.

XX
 CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by

CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX
 SQ Sequence 91 AA;

Query Match 85.7%; Score 36; DB 4; Length 91;
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CVPLTSC 7
 |.:|:|:|
 Db 75 CVPLTSC 81

RESULT 11

ABM60758
 ID ABM60758 standard; protein; 91 AA.

XX
 AC ABM60758;

XX
 DT 20-OCT-2003 (first entry)

DE Propionibacterium acnes predicted ORF-encoded polypeptide #25434.

XX
 KW Acne vulgaris; antisborrheic; dermatological; antibacterial;
 KW immunostimulant; immune response; vaccine.

XX
 OS Propionibacterium acnes.

XX
 PN WO2003033515-A1.

XX
 PD 24-APR-2003.

XX
 PF 11-OCT-2002; 2002WO-US032727.

XX
 PR 15-OCT-2001; 2001US-00978825.

XX
 PR (CORI-) CORIXA CORP.

XX
 PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;

PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;

PI Barth B, Vallieve-Douglass J;

XX
 DR WPI; 2003-381789/36.

XX
 DR N-PSDB; ACF64570.

XX
 PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.

XX
 PS Example 1; SEQ ID NO 25434; 1481pp; English.

XX
 CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for

CC nucleic acid hybridisation. The vaccine composition is useful for the
CC stimulation of an immune response against P. acnes, or for treating acne,
CC and the kit is useful for performing a diagnostic assay. The present
CC sequence represents a polypeptide predicted to be encoded by an ORF (open
CC reading frame) contained within the P. acnes polynucleotides of the
CC invention. Note: the sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 91 AA;

Query Match 85.7%; Score 36; DB 6; Length 91;
Best Local Similarity 85.7%; Pred. NO. 1.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
Db 75 CVPTSC 81

RESULT 12
ABG30203
ID ABG30203 standard; protein; 4561 AA.

XX AC ABG30203;
XX DT 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #30194.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.

XX WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX DR N-PSDB; AAS94390.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX Claim 20; SEQ ID NO 60562; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG30010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 4561 AA;

Query Match 85.7%; Score 36; DB 4; Length 4561;
Best Local Similarity 71.4%; Pred. NO. 5.7e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
Db 2931 CVPISSC 2937

RESULT 13
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ID ABG21064 standard; protein; 9222 AA.

XX AC ABG21064;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #21055.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX DR N-PSDB; AAS85251.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX Claim 20; SEQ ID NO 51423; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic

CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 9222 AA;

Query Match 85.7%; Score 36; DB 4; Length 9222;
Best Local Similarity 71.4%; Pred. No. 1.1e+04;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CVPLTSC 7

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Db 3655 CVPISSC 3661

RESULT 14

AA096565

ID AA096565 standard; protein; 61 AA.

XX AC AA096565;

XX DT 21-NOV-2001 (first entry)

XX DE Human reproductive system related antigen SEQ ID NO: 5223.

KW Human; reproductive system related antigen; reproductive system disorder;
cancer; gene therapy.

XX OS Homo sapiens.

XX PN WO200155320-A2.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US001339.

XX PR 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216847P.

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PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

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PR 14-AUG-2000; 2000US-0225759P.

PR 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

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PR 22-AUG-2000; 2000US-0227182P.

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PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.
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PR 01-DEC-2000; 2000US-0250391P.
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PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

XX
PA
XX
PI

XX WPI; 2001-483232/52.
XX Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer.
XX Claim 11; SEQ ID NO 1953; 766pp; English.
XX The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, CC reproductive system, immune, respiratory, neurological and CC gastrointestinal disorders, infections, and particularly cancer, CC especially testicular cancers. The present sequence is a protein of the CC invention
XX Sequence 61 AA;

Query Match 83.3%; Score 35; DB 4; Length 61;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 40 CVPLGSC 46

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GenCore version 5.1.6
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Title: US-09-761-636A-11

Perfect score: 42

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	37	88.1	253	15	Sequence 248060,
4	36	85.7	75	16	US-10-424-599-248060
5	35	83.3	61	10	Sequence 193668,
6	35	83.3	65	10	Sequence 118478,
7	35	83.3	196	14	US-09-764-891-5223
8	35	83.3	270	11	Sequence 3611, Ap
9	35	83.3	270	11	US-10-120-018-5
10	35	83.3	270	14	Sequence 5, Appl
11	35	83.3	270	15	US-09-833-245-1832
12	35	83.3	445	11	Sequence 48, Appl
13	35	83.3	462	15	Sequence 48, Appl
14	35	83.3	462	15	US-10-191-254-48
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17	35	83.3	462	15	US-10-120-018-16
18	35	83.3	462	15	Sequence 58, Appl

14	35	83.3	464	14	US-10-120-018-17	Sequence 17, Appl
15	35	83.3	627	16	US-10-451-417-4	Sequence 4, Appl
16	35	83.3	646	14	US-10-120-018-12	Sequence 12, Appl
17	35	83.3	685	14	US-10-120-018-9	Sequence 9, Appl
18	35	83.3	685	15	US-10-108-260A-3546	Sequence 3546, Ap
19	35	83.3	685	15	US-10-263-929-116	Sequence 116, App
20	35	83.3	685	16	US-10-451-417-2	Sequence 2, Appl
21	35	83.3	685	16	US-10-475-446-12	Sequence 12, Appl
22	35	83.3	867	15	US-10-112-944-424	Sequence 424, App
23	34	81.0	89	11	US-09-833-245-1243	Sequence 1243, Ap
24	34	81.0	109	14	US-10-029-386-29056	Sequence 29056, A
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26	34	81.0	351	15	US-10-112-944-906	Sequence 906, App
27	34	81.0	1653	14	US-10-133-172-20	Sequence 20, Appl
28	34	81.0	2420	15	US-10-028-248A-4	Sequence 4, Appl
29	34	81.0	2420	15	US-10-107-782-4	Sequence 2, Appl
30	34	81.0	2675	15	US-10-028-248A-2	Sequence 2, Appl
31	34	81.0	2675	15	US-10-107-782-2	Sequence 2, Appl
32	34	81.0	5405	9	US-09-922-217-1116	Sequence 1116, Ap
33	34	81.0	5405	13	US-10-025-380-1116	Sequence 1116, Ap
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35	33	78.6	55	15	US-10-296-115-748	Sequence 748, App
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37	33	78.6	125	16	US-10-437-963-149232	Sequence 149232,
38	33	78.6	130	15	US-10-424-599-215673	Sequence 215673,
39	33	78.6	159	15	US-10-425-114-41558	Sequence 41558, A
40	33	78.6	207	9	US-09-881-752A-46	Sequence 46, Appl
41	33	78.6	207	15	US-10-335-977-8827	Sequence 8827, Ap
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43	33	78.6	370	16	US-10-437-963-104490	Sequence 104490,
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ALIGNMENTS

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; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-11

Query Match 100.0%; Score 42; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
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QY 1 CVPLTSC 7

DB 1 CVPLTSC 7

RESULT 2

US-10-424-599-248060

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; Sequence 248060, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 248060
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_66028C.1.pep
US-10-424-599-248060

Query Match          90.5%; Score 38; DB 15; Length 118;
Best Local Similarity 85.7%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CVPLTSC 7
Db      29 CTELTSC 35

RESULT 3
US-10-424-599-199668
; Sequence 199668, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 199668
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_22324C.1.pep
US-10-424-599-199668

Query Match          88.1%; Score 37; DB 15; Length 253;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CVPLTSC 7
Db     109 CVPLASC 115

RESULT 4
US-10-437-963-118478
; Sequence 118478, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
```

```
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 118478
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_21786C.1.pep
US-10-437-963-118478

Query Match          85.7%; Score 36; DB 16; Length 75;
Best Local Similarity 71.4%; Pred. No. 64;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 CVPLTSC 7
Db      53 CIPLTHC 59

RESULT 5
US-09-764-891-5223
; Sequence 5223, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5223
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (58)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (60)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-891-5223

Query Match          83.3%; Score 35; DB 10; Length 61;
Best Local Similarity 85.7%; Pred. No. 79;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CVPLTSC 7
Db      40 CVPLGSC 46

RESULT 6
US-09-764-891-3611
; Sequence 3611, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 1611
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-891-3611

Query Match      83.3%; Score 35; DB 10; Length 65;
Best Local Similarity 71.4%; Pred. No. 83;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1  CVPLTSC 7
Db      41  CLPLSSC 47

RESULT 7
US-10-120-018-5
; Sequence 5, Application US/10120018
; Publication No. US20030194708A1
; GENERAL INFORMATION:
; APPLICANT: Binnerts et al
; TITLE OF INVENTION: Human Homolog of Crossveinless Materials and Methods
; FILE REFERENCE: 28110/37995
; CURRENT APPLICATION NUMBER: US/10/120,018
; CURRENT FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-120-018-5

Query Match      83.3%; Score 35; DB 14; Length 196;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1  CVPLTSC 7
Db      50  CIPSSC 56

RESULT 8
US-09-833-245-1832
; Sequence 1832, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PFS46PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1832
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (113)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (118)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (157)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (268)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-1832

Query Match      83.3%; Score 35; DB 11; Length 270;
Best Local Similarity 57.1%; Pred. No. 3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1  CVPLTSC 7
Db      161  CIPSSC 167

RESULT 9
US-10-091-458-48
; Sequence 48, Application US/10091458
; Publication No. US20030068627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ06C1
; CURRENT APPLICATION NUMBER: US/10/091,458
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 09/764,900
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
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Best Local Similarity 57.1%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 3

QY 1 CVPLTSC 7
Db 161 CIPISSC 167

RESULT 10
US-10-191-254-48
; Sequence 48, Application US/10191254
; Publication No. US20040005650A1
; GENERAL INFORMATION:
; APPLICANT: Rozen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ06C2
; CURRENT APPLICATION NUMBER: US/10/191,254
; CURRENT FILING DATE: 2002-08-27
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 10/091,458
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,900
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (113)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (118)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (157)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (268)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-191-254-48

Query Match 83.3%; Score 35; DB 15; Length 270;
Best Local Similarity 57.1%; Pred. No. 3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
Db 161 CIPISSC 167

RESULT 11

US-09-833-245-1835
; Sequence 1835, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1835
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (147)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (288)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (293)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (332)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (443)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-1835

Query Match 83.3%; Score 35; DB 11; Length 445;
Best Local Similarity 57.1%; Pred. No. 4.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
Db 336 CIPISSC 342

RESULT 12
US-10-120-018-16
; Sequence 16, Application US/10120018
; Publication No. US20030194708A1
; GENERAL INFORMATION:
; APPLICANT: Binnerts et al
; TITLE OF INVENTION: Human Homolog of Crossveinless Materials and Methods
; FILE REFERENCE: 28110/37995
; CURRENT APPLICATION NUMBER: US/10/120,018
; CURRENT FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-120-018-16

Query Match 83.3%; Score 35; DB 14; Length 462;
Best Local Similarity 71.4%; Pred. No. 4.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVPLTSC 7
Db 113 CIPVSSC 119

```
RESULT 13
US-10-016-248-58
; Sequence 58, Application US/10016248
; Publication No. US20040033491A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-218
; CURRENT APPLICATION NUMBER: US/10/016,248
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315,639
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-016-248-58
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Query Match      83.3%; Score 35; DB 15; Length 462;
Best Local Similarity 71.4%; Pred. No. 4.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY      1  CVPLTSC 7
Db      113  CVPVSSC 119
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RESULT 14
US-10-120-018-17
; Sequence 17, Application US/10120018
; Publication No. US20030194708A1
; GENERAL INFORMATION:
; APPLICANT: Binnerts et al
; TITLE OF INVENTION: Human Homolog of Crossveinless Materials and Methods
; FILE REFERENCE: 28110/37995
; CURRENT APPLICATION NUMBER: US/10/120,018
; CURRENT FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (166)..(166)
; OTHER INFORMATION: wherein "X" is unknown or other
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (307)..(307)
; OTHER INFORMATION: wherein "X" is unknown or other
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (312)..(312)
; OTHER INFORMATION: wherein "X" is unknown or other
; FEATURE:
; NAME/KEY: MISC FEATURE
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; LOCATION: (351)..(351)
; OTHER INFORMATION: wherein "X" is unknown or other
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (462)..(462)
; OTHER INFORMATION: wherein "X" is unknown or other
US-10-120-018-17
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Query Match      83.3%; Score 35; DB 14; Length 464;
Best Local Similarity 57.1%; Pred. No. 4.9e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY      1  CVPLTSC 7
Db      355  CIPISSC 361
```

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RESULT 15
US-10-451-417-4
; Sequence 4, Application US/10451417
; Publication No. US20040110921A1
; GENERAL INFORMATION:
; APPLICANT: ORITA, Satoshi et al
; TITLE OF INVENTION: A NOVEL POLYPEPTIDE AND ITS DNA
; FILE REFERENCE: 0032-0276P
; CURRENT APPLICATION NUMBER: US/10/451,417
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: JP 401584/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-451-417-4
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Query Match      83.3%; Score 35; DB 16; Length 627;
Best Local Similarity 57.1%; Pred. No. 6.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY      1  CVPLTSC 7
Db      336  CIPISSC 342
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Job time : 172.027 secs
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OM protein - protein search, using sw model

Run on: April 1, 2005, 07:04:23 ; Search time 19.9726 Seconds
(without alignments)
33.638 Million cell updates/sec

Title: US-09-761-636A-10

Perfect score: 50

Sequence: 1 CSVPLTVC 9

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	86.0	1487	3	US-08-840-062-7
2	41	82.0	422	4	US-09-489-039A-10842
3	37	74.0	259	4	US-09-270-767-38568
4	37	74.0	259	4	US-09-270-767-53785
5	36	72.0	168	4	US-09-252-991A-20364
6	36	72.0	201	2	US-08-688-342-1
7	36	72.0	201	2	US-09-113-788-1
8	35	70.0	186	4	US-09-270-767-35046
9	35	70.0	186	4	US-09-270-767-50263
10	35	70.0	359	3	US-08-586-165-4
11	34	68.0	49	4	US-09-270-767-61436
12	34	68.0	134	4	US-09-621-976-4725
13	34	68.0	240	4	US-09-270-767-45901
14	34	68.0	242	4	US-09-270-767-43981
15	34	68.0	386	1	US-08-134-012-3
16	34	68.0	386	1	US-08-520-519-3
17	34	68.0	386	3	US-09-039-798-3
18	34	68.0	400	4	US-09-673-395A-479
19	34	68.0	586	4	US-09-652-603-2
20	34	68.0	659	4	US-09-538-092-1206
21	34	68.0	664	4	US-09-949-016-10347
22	34	68.0	747	2	US-08-816-693A-51
23	34	68.0	747	3	US-08-885-291-51
24	34	68.0	747	3	US-09-496-672-51
25	33	66.0	126	4	US-09-402-016A-4
26	33	66.0	254	4	US-09-543-681A-4919
27	33	66.0	403	4	US-09-543-681A-6083

28	33	66.0	1326	4	US-09-949-016-6806	Sequence 6806, Ap
29	33	66.0	1339	4	US-09-949-016-10448	Sequence 10448, A
30	33	66.0	1478	4	US-09-949-016-8315	Sequence 8315, Ap
31	33	66.0	1753	4	US-09-248-796A-19154	Sequence 19154, A
32	32	64.0	109	3	US-09-469-186-1	Sequence 1, Appli
33	32	64.0	109	4	US-09-469-185-1	Sequence 1, Appli
34	32	64.0	109	4	US-10-100-037-1	Sequence 1, Appli
35	32	64.0	110	4	US-09-847-524-6	Sequence 6, Appli
36	32	64.0	134	3	US-08-543-246B-20	Sequence 20, Appli
37	32	64.0	171	4	US-09-252-991A-26927	Sequence 26927, A
38	32	64.0	191	4	US-09-949-016-8069	Sequence 8069, Ap
39	32	64.0	197	4	US-09-431-888-8	Sequence 8, Appli
40	32	64.0	216	3	US-08-543-246B-9	Sequence 9, Appli
41	32	64.0	216	3	US-08-543-246B-24	Sequence 24, Appli
42	32	64.0	228	4	US-09-489-039A-13837	Sequence 13837, A
43	32	64.0	276	4	US-09-252-991A-18128	Sequence 18128, A
44	32	64.0	294	4	US-09-252-991A-30882	Sequence 30882, A
45	32	64.0	321	3	US-08-915-795-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-08-840-062-7
; Sequence 7, Application US/08840062
; Patent No. 6117977
; GENERAL INFORMATION:
; APPLICANT: LASKY, LAURENCE A.
; APPLICANT: WU, KAI
; TITLE OF INVENTION: TYPE C LECTINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/840,062
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregler, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1019r1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1487 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-840-062-7

Query Match 86.0%; Score 43; DB 3; Length 1487;
Best Local Similarity 77.8%; Pred. No. 43;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CSVPLTVC 9

Db 929 CSVPLPSC 937

RESULT 2

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US-09-489-039A-10842
; Sequence 10842, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10842
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10842

Query Match      82.0%; Score 41; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 SVPLTSVC 9
      |||||
Db      387 SVPLTSVC 394

RESULT 3
US-09-761-767-38568
; Sequence 38568, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38568
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-38568

Query Match      74.0%; Score 37; DB 4; Length 259;
Best Local Similarity 55.6%; Pred. No. 76;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 CSVPPLTSVC 9
      |||||
Db      107 CSIPPLVELC 115

RESULT 4
US-09-270-767-53785
; Sequence 53785, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53785
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-53785

; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-53785

Query Match      74.0%; Score 37; DB 4; Length 259;
Best Local Similarity 55.6%; Pred. No. 76;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 CSVPPLTSVC 9
      |||||
Db      107 CSIPPLVELC 115

RESULT 5
US-09-252-991A-20364
; Sequence 20364, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20364
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20364

Query Match      72.0%; Score 36; DB 4; Length 168;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CSVPPLTSVC 9
      |||||
Db      104 CSVPATCTC 112

RESULT 6
US-08-688-342-1
; Sequence 1, Application US/08688342
; Patent No. 5871964
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/688,342
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
```

; REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 201 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: MMLR1DT01
; CLONE: 515847
US-08-688-342-1

Query Match 72.0%; Score 36; DB 2; Length 201;
Best Local Similarity 66.7%; Pred. No. 86;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
Db 187 CSVPSYSIC 195

RESULT 7

US-09-113-788-1
; Sequence 1, Application US/09113788
; Patent No. 5969104
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,788
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/688,342
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 201 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: MMLR1DT01
; CLONE: 515847
US-09-113-788-1

Query Match 72.0%; Score 36; DB 2; Length 201;
Best Local Similarity 66.7%; Pred. No. 86;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
Db 187 CSVPSYSIC 195

RESULT 8

US-09-270-767-35046
; Sequence 35046, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 35046
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-35046

Query Match 70.0%; Score 35; DB 4; Length 186;
Best Local Similarity 44.4%; Pred. No. 1.2e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
Db 100 CNIPLSQLC 108

RESULT 9

US-09-270-767-50263
; Sequence 50263, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 50263
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-50263

Query Match 70.0%; Score 35; DB 4; Length 186;
Best Local Similarity 44.4%; Pred. No. 1.2e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
Db 100 CNIPLSQLC 108

RESULT 10

US-08-586-165-4
; Sequence 4, Application US/08586165
; Patent No. 6054298
; GENERAL INFORMATION:
; APPLICANT: Laufer, Edward M.

APPLICANT: Orozco, Olivia E.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Fringe Proteins and Pattern Formation
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/586,165
FILING DATE: 16-JAN-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: HU95-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1118
US-08-586-165-4

Query Match 70.0%; Score 35; DB 3; Length 359;
Best Local Similarity 44.4%; Pred. No. 2.3e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPPLTSVC 9
Db 293 CSIPWKC 301

RESULT 11
US-09-270-767-61436
Sequence 61436, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 61436
LENGTH: 49
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-61436

Query Match 68.0%; Score 34; DB 4; Length 49;
Best Local Similarity 55.6%; Pred. No. 45;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPPLTSVC 9

Db 40 CSVPILWIC 48
||||:|

RESULT 12
US-09-621-976-4725
Sequence 4725, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 4725
LENGTH: 134
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: 52
OTHER INFORMATION: Xaa = *, Tyr
NAME/KEY: UNSURE
LOCATION: 49, 51
OTHER INFORMATION: Xaa = Ala, Gly
NAME/KEY: UNSURE
LOCATION: 44
OTHER INFORMATION: Xaa = Cys, Trp
NAME/KEY: UNSURE
LOCATION: 47
OTHER INFORMATION: Xaa = Gly, Arg
NAME/KEY: UNSURE
LOCATION: 53
OTHER INFORMATION: Xaa = Lys, Arg
NAME/KEY: UNSURE
LOCATION: 45
OTHER INFORMATION: Xaa = Phe, Leu
US-09-621-976-4725

Query Match 68.0%; Score 34; DB 4; Length 134;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSVPPLTSVC 9
Db 21 CDVPLYDIC 29

RESULT 13
US-09-270-767-45901
Sequence 45901, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 45901
LENGTH: 240
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45901

Query Match 68.0%; Score 34; DB 4; Length 240;

Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 CSVPLTSVC 9
Db 231 CSVPLWIC 239

RESULT 14
US-09-270-767-43981
; Sequence 43981, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43981
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43981

Query Match 68.0%; Score 34; DB 4; Length 242;
Best Local Similarity 75.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SVPLTSVC 9
Db 129 SIPRTSVC 136

RESULT 15
US-08-134-012-3
; Sequence 3, Application US/08134012
; Patent No. 5516652
; GENERAL INFORMATION:
; APPLICANT: Abramovitz, Mark
; APPLICANT: Boie, Yves
; APPLICANT: Grygorczyk, Richard
; APPLICANT: Metters, Kathleen
; APPLICANT: Rushmore, Thomas H.
; APPLICANT: Slipetz, Deborah M.
; TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR IP
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Wallen
; STREET: 126 E. Lincoln Avenue.
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/134,012
; FILING DATE: 06-OCT-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Wallen, John W
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: 19098
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 386 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-134-012-3

Query Match 68.0%; Score 34; DB 1; Length 386;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
Db 251 CSLPLTIRC 259

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Job time: 19.9726 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 07:04:23 ; Search time 24.411 seconds

(without alignments)
33.638 Million cell updates/sec

Title: US-09-761-636A-7

Perfect score: 61

Sequence: 1 CISVPLTSVPC 11

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	70.5	109	3	US-09-469-186-1
2	43	70.5	109	4	US-09-469-185-1
3	43	70.5	109	4	US-10-100-037-1
4	43	70.5	110	4	US-09-847-524-6
5	43	70.5	197	4	US-09-431-888-8
6	43	70.5	321	3	US-08-915-795-9
7	43	70.5	321	4	US-09-847-524-4
8	43	70.5	321	4	US-09-296-275-9
9	43	70.5	325	3	US-08-915-795-3
10	43	70.5	325	4	US-09-296-275-3
11	43	70.5	354	3	US-08-915-795-5
12	43	70.5	354	4	US-09-296-275-5
13	43	70.5	354	4	US-09-375-248-6
14	43	70.5	354	4	US-09-468-647A-109
15	43	70.5	354	4	US-09-169-079-22
16	43	70.5	354	4	US-09-214-982-1
17	43	70.5	358	3	US-08-915-795-8
18	43	70.5	358	4	US-09-847-524-2
19	43	70.5	358	4	US-09-296-275-8
20	43	70.5	358	4	US-09-438-046-15
21	43	70.5	362	4	US-09-949-016-11286
22	41	67.2	121	4	US-09-513-999C-8157
23	40	65.6	79	4	US-09-134-000C-4906
24	38	62.3	663	3	US-08-959-004-5
25	38	62.3	676	4	US-09-949-016-9494
26	37	60.7	53	4	US-09-270-767-58153
27	37	60.7	140	4	US-09-270-767-48740

28	37	60.7	151	4	US-09-270-767-42833	Sequence 42833, A
29	37	60.7	300	4	US-09-949-016-10727	Sequence 10727, A
30	37	60.7	600	4	US-09-328-352-7636	Sequence 7636, Ap
31	37	60.7	1248	4	US-10-042-810-2	Sequence 2, Appl1
32	37	60.7	1278	4	US-10-042-810-4	Sequence 4, Appl1
33	37	60.7	1338	4	US-09-631-603-2	Sequence 2, Appl1
34	36	59.0	337	4	US-09-693-242-2	Sequence 2, Appl1
35	36	59.0	337	4	US-09-786-442B-2	Sequence 2, Appl1
36	36	59.0	344	4	US-09-270-767-58767	Sequence 58767, A
37	36	59.0	388	3	US-08-861-774E-94	Sequence 94, Appl1
38	36	59.0	409	4	US-09-252-991A-17910	Sequence 17910, A
39	36	59.0	533	4	US-09-508-370A-6	Sequence 6, Appl1
40	36	59.0	534	4	US-09-508-370A-5	Sequence 5, Appl1
41	36	59.0	621	4	US-09-270-767-43417	Sequence 43417, A
42	35	57.4	60	4	US-09-248-796A-14557	Sequence 14557, A
43	35	57.4	90	6	5220013-24	Patent No. 5220013
44	35	57.4	90	6	5220013-24	Patent No. 5220013
45	35	57.4	147	4	US-09-252-991A-23997	Sequence 23997, A

ALIGNMENTS

RESULT 1

US-09-469-186-1
; Sequence 1, Application US/09469186
; Patent No. 6383484
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
; FILE REFERENCE: ACHEN et al-1064-44660
; CURRENT APPLICATION NUMBER: US/09/469,186
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 60/113,254
; EARLIER FILING DATE: 1998-12-21
; EARLIER APPLICATION NUMBER: 60/134,556
; EARLIER FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-469-186-1

Query Match 70.5%; Score 43; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVPLTSVP 10
Db 76 ISVPLTSVP 84
|||||

RESULT 2

US-09-469-185-1
; Sequence 1, Application US/09469185
; Patent No. 6531185
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
; FILE REFERENCE: ACHEN et al-1064-44660
; CURRENT APPLICATION NUMBER: US/09/469,185
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 60/113,254
; EARLIER FILING DATE: 1998-12-21
; EARLIER APPLICATION NUMBER: 60/134,556
; EARLIER FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1

; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-469-185-1

Query Match 70.5%; Score 43; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ISVPLTSVP 10
Db 76 ISVPLTSVP 84

RESULT 3

US-10-100-037-1
; Sequence 1, Application US/10100037
; Patent No. 6730489
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
; FILE REFERENCE: ACHEN et al-1064-44660
; CURRENT APPLICATION NUMBER: US/10/100,037
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/469,186
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/113,254
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/134,556
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-100-037-1

Query Match 70.5%; Score 43; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ISVPLTSVP 10
Db 76 ISVPLTSVP 84

RESULT 4

US-09-847-524-6
; Sequence 6, Application US/09847524
; Patent No. 6689352
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G
; APPLICANT: STACKER, Steven A
; TITLE OF INVENTION: A METHOD FOR ACTIVATING ONLY THE VASCULAR ENDOTHELIAL
; FILE REFERENCE: AchenStacker-mouse VEGF-D
; CURRENT APPLICATION NUMBER: US/09/847,524
; CURRENT FILING DATE: 2001-03-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-847-524-6

Query Match 70.5%; Score 43; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ISVPLTSVP 10

Db 77 ISVPLTSVP 85

RESULT 5

US-09-431-888-8
; Sequence 8, Application US/09431888A
; Patent No. 6541008
; GENERAL INFORMATION:
; APPLICANT: Wise, Lyn M
; APPLICANT: Mercer, Andrew A
; APPLICANT: Savory, Loreen J
; APPLICANT: Fleming, Stephen B
; APPLICANT: Stackner, Stephen
; TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
; FILE REFERENCE: RECEPTOR-2, AND USES THEREOF
; TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
; FILE REFERENCE: Sequence Listing for 09/431,833
; Patent No. 6541008
; CURRENT APPLICATION NUMBER: US/09/431,888A
; CURRENT FILING DATE: 1999-11-02
; EARLIER APPLICATION NUMBER: 60/106,689
; EARLIER FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/106,800
; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-431-888-8

Query Match 70.5%; Score 43; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ISVPLTSVP 10
Db 92 ISVPLTSVP 100

RESULT 6

US-08-915-795-9
; Sequence 9, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/915,795
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983


```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; TISSUE TYPE: Mouse Lung
; US-08-915-795-9

Query Match 70.5%; Score 43; DB 3; Length 321;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVPLTSVP 10
Db 168 ISVPLTSVP 176

RESULT 7
US-09-847-524-4
; Sequence 4, Application US/09847524
; Patent No. 6689352
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Steven A.
; APPLICANT: STACKER, Steven A.
; TITLE OF INVENTION: A METHOD FOR ACTIVATING ONLY THE VASCULAR ENDOTHELIAL
; FILE REFERENCE: Achen&stacker-mouse VEGF-D
; CURRENT APPLICATION NUMBER: US/09/847,524
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; US-09-847-524-4

Query Match 70.5%; Score 43; DB 4; Length 321;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVPLTSVP 10
Db 168 ISVPLTSVP 176

RESULT 8
US-09-296-275-9
; Sequence 9, Application US/09296275
; Patent No. 6689580
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/296,275
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/915,795
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; TISSUE TYPE: Mouse Lung
; US-09-296-275-9

Query Match 70.5%; Score 43; DB 4; Length 321;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVPLTSVP 10
Db 168 ISVPLTSVP 176

RESULT 9
US-08-915-795-3
; Sequence 3, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
```


NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Suite 700
CITY: Washington
STATE: DC
COUNTRY: United States of America
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/296,275
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/915,795
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/42983
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
TELEX: N/A
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: Human Lung

US-09-296-275-5

Query Match 70.5%; Score 43; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ISVPLTSVP 10
Db 168 ISVPLTSVP 176

RESULT 13
US-09-375-248-6
Sequence 6, Application US/09375248
Patent No. 6764820
GENERAL INFORMATION:
APPLICANT: Ferrell, Robert E.
APPLICANT: Alitalo, Kari
APPLICANT: Finggold, David N.
APPLICANT: Karkkainen, Marika
TITLE OF INVENTION: SCREENING AND THERAPY FOR LYMPHATIC DISORDERS INVOLVING
FILE REFERENCE: 28967/35255A
CURRENT APPLICATION NUMBER: US/09/375,248
CURRENT FILING DATE: 1999-08-16
EARLIER APPLICATION NUMBER: PCT/US99/06133
EARLIER FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 354
TYPE: PRT
ORGANISM: Homo sapiens

US-09-375-248-6

Query Match 70.5%; Score 43; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ISVPLTSVP 10
Db 168 ISVPLTSVP 176

RESULT 14
US-09-468-647A-109
Sequence 109, Application US/09468647A
Patent No. 6783953
GENERAL INFORMATION:
APPLICANT: Gordon, Robert D
APPLICANT: Sprengel, Jorg J
APPLICANT: Yon, Jeffery R
APPLICANT: Dijkmans, Josiena J.H.
APPLICANT: Gosiewska, Anna
APPLICANT: Dhanaraj, Sridevi N
APPLICANT: Xu, Jean
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-X
FILE REFERENCE: B0192.70011US00
CURRENT APPLICATION NUMBER: US/09/468,647A
CURRENT FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: GB 9828377.3
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 60/124,967
PRIOR FILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: US 60/164,131
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PatentIn version 3.2
SEQ ID NO 109
LENGTH: 354
TYPE: PRT
ORGANISM: Homo sapiens

US-09-468-647A-109

Query Match 70.5%; Score 43; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ISVPLTSVP 10
Db 168 ISVPLTSVP 176

RESULT 15
US-09-169-079-22
Sequence 22, Application US/09169079
Patent No. 6824777
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Kaipainen, Arja
APPLICANT: Valtola, Reija
APPLICANT: Jussila, Lotta
TITLE OF INVENTION: Flt4 (VEGFR-3) as a Target for Tumor Imaging and Anti-Tumor Therap
FILE REFERENCE: 28113/34891
CURRENT APPLICATION NUMBER: US/09/169,079
CURRENT FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: 08/901,710
EARLIER FILING DATE: 1997-07-28
EARLIER APPLICATION NUMBER: 08/340,011
EARLIER FILING DATE: 1994-11-14
EARLIER APPLICATION NUMBER: 08/257,754
EARLIER FILING DATE: 1994-07-09
EARLIER APPLICATION NUMBER: 07/959,951
EARLIER FILING DATE: 1992-10-09
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 354

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-169-079-22
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Query Match      70.5%; Score 43; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      2 ISVPLTSVP 10
      |||||
Db      168 ISVPLTSVP 176
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Search completed: April 1, 2005, 09:36:16
Job time : 25.411 secs
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OM protein - protein search, using sw model

Run on: April 1, 2005, 06:17:29 ; Search time 13.0685 Seconds
(without alignments)
66.262 Million cell updates/sec

Title: US-09-761-636A-10

Perfect score: 50

Sequence: 1 CSVPLTSVC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	86.0	1487	2 S48719	phospholipase-A(2)
2	41	82.0	349	2 AD0990	probable membrane
3	41	82.0	364	2 C86015	hypothetical prote
4	41	82.0	376	2 C91169	hypothetical prote
5	41	82.0	376	2 S47693	hypothetical 38.5K
6	39	78.0	432	2 F64484	probable transamin
7	38	76.0	22	2 B55538	uvrC protein - Pse
8	36	72.0	591	2 S54788	calcium-stimulated
9	36	72.0	2180	2 T29764	hypothetical prote
10	35	70.0	91	2 D97130	transcription regu
11	35	70.0	124	2 A37931	napin - Swedish tu
12	35	70.0	127	2 S65447	allergen Sin a I -
13	35	70.0	133	1 NWRP1	napin 1 precursor
14	35	70.0	145	2 S65481	allergen Sin a I (
15	35	70.0	145	2 S65482	allergen Sin a I (
16	35	70.0	145	2 S65480	allergen Sin a I (
17	35	70.0	145	2 S65478	allergen Sin a I (
18	35	70.0	152	2 T34649	hypothetical prote
19	35	70.0	155	2 PS0426	napin BG9 precursor
20	35	70.0	178	1 NWRP2	napin 2 precursor
21	35	70.0	178	2 S25130	2S storage protein
22	35	70.0	178	2 A25997	napin precursor (n
23	35	70.0	178	2 S07828	napin B - rape
24	35	70.0	178	2 S25134	2S storage protein
25	35	70.0	178	2 S25137	2S storage protein
26	35	70.0	180	2 S10018	napin (clone BngNA
27	35	70.0	180	2 S52025	napin (clones BNNW
28	35	70.0	621	1 YRNC	monophenol monooxy
29	34	68.0	92	2 S35592	major allergen lar

30	34	68.0	141	2 T12116	NADH2 dehydrogenas
31	34	68.0	178	2 S15382	napin napB - rape
32	34	68.0	192	2 B96583	hypothetical prote
33	34	68.0	265	2 T11729	NADH2 dehydrogenas
34	34	68.0	270	2 T11687	NADH2 dehydrogenas
35	34	68.0	273	2 T11702	NADH2 dehydrogenas
36	34	68.0	277	2 T11697	NADH2 dehydrogenas
37	34	68.0	278	2 T11731	NADH2 dehydrogenas
38	34	68.0	376	2 S70841	hypothetical trans
39	34	68.0	377	2 S77634	exopolysaccharide
40	34	68.0	386	2 A57066	prostaglycin recep
41	34	68.0	418	2 E71716	proline/betaine tr
42	34	68.0	565	2 T08794	hypothetical prote
43	34	68.0	659	1 JC4365	arginine-tRNA liga
44	34	68.0	661	1 JN0870	hypothetical prote
45	34	68.0	669	2 T17122	hypothetical prote

ALIGNMENTS

RESULT 1

S48719 phospholipase-A(2) receptor protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C:Accession: S48719

R:Higashino, K.; Ishizaki, J.; Kishino, J.; Ohara, O.; Arita, H.

Eur. J. Biochem. 225, 375-382, 1994

A>Title: Structural comparison of phospholipase-A(2)-binding regions in phospholipase-A(2)

A:Reference number: S48719; MUID:95010128; PMID:7925459

A:Accession: S48719

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1487 <HIG>

A:Cross-references: UNIPROT:Q62028; GB:D30779; NID:gl375042; PIDN:BA06443.1; PID:9691754

C:Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II re

F:181-222/Domain: fibronectin type II repeat homology <2F1>

F:380-503/Domain: C-type lectin homology <LCH>

Query Match 86.0%; Score 43; DB 2; Length 1487;
Best Local Similarity 77.8%; Pred. No. 8.2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9

Db 929 CSVPLPSIC 937

RESULT 2

AD0990

probable membrane protein STY4229 [imported] - Salmonella enterica subsp. enterica serov

C:Species: Salmonella enterica subsp. enterica serovar Typhi

A>Note: this species has also been called Salmonella typhi

C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C:Accession: AD0990

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AD0990

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-349 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD08048.1; PID:gl16505028; GSPDB:GN00176

C:Genetics:

A:Gene: STY4229

C:Superfamily: conserved hypothetical protein HI0338

Query Match 82.0%; Score 41; DB 2; Length 349;

Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVPLTSVC 9
DB 314 SVPLTSVC 321

RESULT 3
C86015
hypothetical protein yhhT [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: C86015
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: C86015
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-364 <STO>
A:Cross-references: GB:AE005174; NID:gl2518133; PIDN:AGS5853.1; GSPDB:GN00145; UWGP:Z48
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yhhT
C:Superfamily: conserved hypothetical protein HI0338

Query Match 82.0%; Score 41; DB 2; Length 364;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVPLTSVC 9
DB 329 SVPLTSVC 336

RESULT 4
C91169
hypothetical protein ECs4323 [imported] - Escherichia coli (strain O157:H7, substrain RI
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: C91169
R:Havashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: C91169
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-376 <HAV>
A:Cross-references: PIDN:BA037745.1; PID:gl3363797; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 050952
C:Genetics:
A:Gene: ECs4323
C:Superfamily: conserved hypothetical protein HI0338

Query Match 82.0%; Score 41; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVPLTSVC 9
DB 341 SVPLTSVC 348

RESULT 5
S47693
hypothetical 38.5K protein (ftsY-nika intergenic region) - Escherichia coli (strain K-12
N:Alternate names: hypothetical protein o376
C:Species: Escherichia coli
C:Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004

C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 01-Mar-2002
C:Accession: S47693; E65144
R:Plunkett, G.
submitted to the EMBL Data Library, March 1994
A:Reference number: S47666
A:Accession: S47693
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-376 <PLU>
A:Cross-references: EMBL:U00039; NID:9466582; PIDN:AAB18449.1; PID:gs912460
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: E65144
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-376 <BLAT>
A:Cross-references: GB:AE000423; GB:U00096; NID:gl789880; PIDN:AAC76499.1; PID:gl789885;
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: yhhT
A:Start codon: GTG
C:Superfamily: conserved hypothetical protein HI0338

Query Match 82.0%; Score 41; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVPLTSVC 9
DB 341 SVPLTSVC 348

RESULT 6
F64484
probable transaminase (EC 2.6.1.-) MJ1479 [similarity] - Methanococcus jannaschii
N:Alternate names: alanine aminotransferase 2
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: F64484
R:Buit, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, C.
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: F64484
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-432 <BUL>
A:Cross-references: UNIPROT:Q58874; GB:U67588; GB:L77117; NID:gl592111; PID:gl592118; TIC
C:Genetics:
A:Map position: FOR1449710-1451008
C:Superfamily: aspartate transaminase
C:Keywords: aminotransferase

Query Match 78.0%; Score 39; DB 2; Length 432;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
DB 389 CVVPLTSFC 397

RESULT 7
B55538
uvrC protein - Pseudomonas syringae pv. syringae (strain B728a) (fragment)
N:Alternate names: Pseudomonas syringae pv. syringae
C:Species: Pseudomonas syringae pv. syringae
C:Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004

C:Accession: B55538
 R:Rich, J.J.; Kinscherf, T.G.; Kitten, T.; Willis, D.K.
 J. Bacteriol. 176, 7468-7475, 1994
 A:Title: Genetic evidence that the gacA gene encodes the cognate response regulator for
 A:Reference number: A55538; MUID:95095914; PMID:8002569
 A:Accession: B55538
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-22 <RIC>
 A:Cross-references: UNIPROT:Q52377; GB:U09767
 C:Genetics:
 A:Gene: uvrC

Query Match 76.0%; Score 38; DB 2; Length 22;
 Best Local Similarity 66.7%; Pred. No. 1.6;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
 DB 13 CSVPLTSVC 21

RESULT 8
 S54788
 calcium-stimulated protein kinase - Chlamydomonas eugametos
 C:Species: Chlamydomonas eugametos
 C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
 C:Accession: S54788
 R:Siderius, M.H.
 submitted to the EMBL Data Library, May 1995
 A:Description: Cloning a CDPK from Chlamydomonas eugametos.
 A:Reference number: S54788
 A:Accession: S54788
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-591 <SID>
 A:Cross-references: UNIPROT:Q39485; EMBL:Z49233; NID:G806541; PIDN:CAA89202.1; PID:G8065
 C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin
 C:Keywords: ATP; calcium binding; EF hand; serine/threonine-specific protein kinase; tan
 F:150-410/Domain: protein kinase homology <KIN>
 F:158-166/Region: protein kinase ATP-binding motif
 F:453-485/Domain: calmodulin repeat homology <EF1>
 F:489-521/Domain: calmodulin repeat homology <EF2>
 F:525-557/Domain: calmodulin repeat homology <EF3>
 F:559-591/Domain: calmodulin repeat homology <EF4>

Query Match 72.0%; Score 36; DB 2; Length 591;
 Best Local Similarity 55.6%; Pred. No. 68;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
 DB 88 CKIPLTRAC 96

RESULT 9
 T29764
 hypothetical protein T21E3.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T29764
 R:Du, Z.; Le, T.T.
 submitted to the EMBL Data Library, May 1997
 A:Description: The sequence of C. elegans cosmid T21E3.
 A:Reference number: Z20681
 A:Accession: T29764
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-2180 <DUZ>
 A:Cross-references: UNIPROT:O01768; EMBL:AF003133; PIDN:AAB54138.1; GSPDB:GN00019; CESP:
 A:Experimental source: strain Bristol N2; clone T21E3
 C:Genetics:
 A:Gene: CESP:T21E3.3

A:Map position: 1
 A:Introns: 400/2; 1608/3; 1644/1; 1674/3; 1686/2; 1731/2; 2073/1; 2098/2; 2146/3
 F:15-49/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F:51-85/Domain: LDL receptor ligand-binding repeat homology <LDL2>
 F:90-132/Domain: LDL receptor ligand-binding repeat homology <LDL3>
 F:149-185/Domain: LDL receptor ligand-binding repeat homology <LDL4>
 F:190-225/Domain: LDL receptor ligand-binding repeat homology <LDL5>
 F:229-272/Domain: LDL receptor ligand-binding repeat homology <LDL6>
 F:285-316/Domain: LDL receptor ligand-binding repeat homology <LDL7>
 F:323-359/Domain: LDL receptor ligand-binding repeat homology <LDL8>
 F:369-405/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F:816-856/Domain: LDL receptor ligand-binding repeat homology <LDL10>
 F:861-903/Domain: LDL receptor ligand-binding repeat homology <LDL11>
 F:908-943/Domain: LDL receptor ligand-binding repeat homology <LDL12>
 F:948-987/Domain: LDL receptor ligand-binding repeat homology <LDL13>
 F:993-1027/Domain: LDL receptor ligand-binding repeat homology <LDL14>
 F:1031-1063/Domain: LDL receptor ligand-binding repeat homology <LDL15>
 F:1126-1165/Domain: LDL receptor ligand-binding repeat homology <LDL16>
 F:1172-1209/Domain: LDL receptor ligand-binding repeat homology <LDL17>
 F:1213-1246/Domain: LDL receptor ligand-binding repeat homology <LDL18>

Query Match 72.0%; Score 36; DB 2; Length 2180;
 Best Local Similarity 85.7%; Pred. No. 2.2e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 VPLTSVC 9
 DB 922 IPLTSVC 928

RESULT 10
 D97130
 transcription regulator (phage-related) (Xre family) [imported] - Clostridium acetobutyli
 C:Species: Clostridium acetobutylicum
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
 C:Accession: D97130
 R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4833-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: D97130
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-91 <KUR>
 A:Cross-references: UNIPROT:Q97HY9; GB:AE001437; PIDN:AAK79831.1; PID:gl5024845; GSPDB:G
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 A:Gene: CAC1867

Query Match 70.0%; Score 35; DB 2; Length 91;
 Best Local Similarity 66.7%; Pred. No. 20;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
 DB 54 CSIGYTSVC 62

RESULT 11
 A37931
 napin - Swedish turnip (fragments)
 C:Species: Brassica napus var. rapifera (Swedish turnip, rutabaga)
 C:Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 09-Jul-2004
 C:Accession: A37931
 R:Svendsen, I.; Nicolova, D.; Goehev, I.; Genov, N.
 Carlsberg Res. Commun. 54, 231-239, 1989
 A:Title: Isolation and characterization of a trypsin inhibitor from the seeds of kohlrabi
 A:Reference number: A37931; MUID:91282906; PMID:2490369
 A:Accession: A37931
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-124 <SVE>

A;Cross-references: UNIPROT:Q7M1PI
C;Superfamily: wheat alpha-amylase inhibitor

Query Match 70.0%; Score 35; DB 2; Length 124;
Best Local Similarity 55.6%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9

DB 106 CNIPQSVVC 114

RESULT 12

S65447 allergen Sin a I - white mustard

N;Alternate names: allergen Sin a I large chain
C;Species: Sinapis alba (white mustard)

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C;Accession: S65447; S01792

R;Gonzalez de la Pena, M.A.; Monsalve, R.I.; Batanero, E.; Villalba, M.; Rodriguez, R.

Eur. J. Biochem. 237, 827-832, 1996

A;Title: Expression in Escherichia coli of Sin a 1, the major allergen from mustard.

A;Reference number: S65447; MUID:96235251; PMID:8647131

A;Accession: S65447

A;Molecule type: protein

A;Residues: 1-127 <GON>

A;Cross-references: UNIPROT:PI5322

A;Experimental source: seed

R;Menendez-Arias, L.; Moneo, I.; Dominguez, J.; Rodriguez, R.

Eur. J. Biochem. 177, 159-166, 1988

A;Title: Primary structure of the major allergen of yellow mustard (Sinapis alba L.) see

A;Reference number: S01791; MUID:89030681; PMID:3181153

A;Accession: S01792

A;Molecule type: protein

A;Residues: 40-127 <MEN>

C;Superfamily: wheat alpha-amylase inhibitor

C;Keywords: seed; storage protein

Query Match 70.0%; Score 35; DB 2; Length 127;

Best Local Similarity 55.6%; Pred. No. 26;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9

DB 109 CNIPQSVVC 117

RESULT 13

NWRP1

napin 1 precursor - rape (fragment)

N;Alternate names: 1.7S seed storage protein

C;Species: Brassica napus (rape)

C;Date: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 09-Jul-2004

C;Accession: A01330

R;Crouch, M.L.; Tenbarge, K.M.; Simon, A.E.; Ferl, R.

J. Mol. Appl. Genet. 2, 273-283, 1983

A;Title: cDNA clones for Brassica napus seed storage proteins: evidence from nucleotide

A;Reference number: A92836; MUID:84113267; PMID:6689334

A;Accession: A01330

A;Molecule type: mRNA

A;Residues: 1-133 <CRO>

A;Cross-references: UNIPROT:P01091; GB:K01544; NID:G167174; PIDN:AAA33005.1; PID:G167175

A;Experimental source: cv. Tower

C;Superfamily: wheat alpha-amylase inhibitor

C;Keywords: seed; storage protein

F;1-30/Product: napin 1 small chain (fragment) #status predicted <SCH>

F;50-130/Product: napin 1 large chain #status predicted <LCH>

Query Match

Best Local Similarity 70.0%; Score 35; DB 1; Length 133;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9

DB 114 CNIPQSVVC 122

RESULT 14

S65481

allergen Sin a I (clone SIN3) - white mustard (fragment)

C;Species: Sinapis alba (white mustard)

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C;Accession: S65481

R;Gonzalez de la Pena, M.A.; Monsalve, R.I.; Batanero, E.; Villalba, M.; Rodriguez, R.

Eur. J. Biochem. 237, 827-832, 1996

A;Title: Expression in Escherichia coli of Sin a 1, the major allergen from mustard.

A;Reference number: S65447; MUID:96235251; PMID:8647131

A;Accession: S65481

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-145 <GON>

A;Cross-references: UNIPROT:Q41279; EMBL:X91801; NID:G1009437; PIDN:CAA62911.1; PID:G1009

A;Experimental source: seed

C;Genetics:

A;Gene: sin3

C;Superfamily: wheat alpha-amylase inhibitor

C;Keywords: seed; storage protein

Query Match 70.0%; Score 35; DB 2; Length 145;

Best Local Similarity 55.6%; Pred. No. 30;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9

DB 127 CNIPQSVVC 135

RESULT 15

S65482

allergen Sin a I (clone SIN4) - white mustard (fragment)

C;Species: Sinapis alba (white mustard)

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C;Accession: S65482

R;Gonzalez de la Pena, M.A.; Monsalve, R.I.; Batanero, E.; Villalba, M.; Rodriguez, R.

Eur. J. Biochem. 237, 827-832, 1996

A;Title: Expression in Escherichia coli of Sin a 1, the major allergen from mustard.

A;Reference number: S65447; MUID:96235251; PMID:8647131

A;Accession: S65482

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-145 <GON>

A;Cross-references: UNIPROT:Q41280; EMBL:X91802; NID:G1009439; PIDN:CAA62912.1; PID:G1009

A;Experimental source: seed

C;Genetics:

A;Gene: sin4

C;Superfamily: wheat alpha-amylase inhibitor

C;Keywords: seed; storage protein

Query Match 70.0%; Score 35; DB 2; Length 145;

Best Local Similarity 55.6%; Pred. No. 30;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9

DB 127 CNIPQSVVC 135

Search completed: April 1, 2005, 09:33:24

Job time : 13.0685 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 03:33:32 ; Search time 55.1096 Seconds
(without alignments)
83.628 Million cell updates/sec

Title: US-09-761-636A-10

Perfect score: 50

Sequence: 1 CSVPLTSVC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	43	86.0	1487	2	Q62028 mus musculus
2	41	82.0	349	1	YHHT_ECOLI
3	41	82.0	349	2	Q82258
4	41	82.0	349	2	Q82LE3
5	41	82.0	349	2	Q83J80
6	41	82.0	376	2	Q8FCN4
7	41	82.0	409	2	Q63791
8	41	82.0	434	2	Q6LXF5
9	41	82.0	750	2	Q6ZKN1
10	41	82.0	750	2	Q9ARC6
11	41	82.0	750	2	Q9ARC9
12	41	82.0	780	2	Q9ARF2
13	41	82.0	781	1	CLCF_ARATH
14	41	82.0	783	2	Q6Z673
15	40	80.0	440	2	Q69GZ6
16	39	78.0	432	1	YE79_METJA
17	38	76.0	76	2	Q659D4
18	38	76.0	150	1	UVRC_PSESY
19	38	76.0	323	2	Q8WVW3
20	38	76.0	491	2	Q9H6R1
21	38	76.0	677	2	Q6PFM9
22	38	76.0	742	2	Q6P0P1
23	38	76.0	786	2	Q9H747
24	38	76.0	802	2	Q8TB22
25	37	74.0	97	2	Q8CLM0
26	37	74.0	192	2	Q64BX2
27	37	74.0	247	2	Q8HZR8
28	37	74.0	334	2	Q6AK47
29	37	74.0	660	2	Q6SCJ7
30	37	74.0	718	2	Q94JF5
31	37	74.0	1977	2	Q9V6A0

32	36	72.0	124	2	Q9D179	Q9d179 mus musculus
33	36	72.0	168	2	Q96PA7	Q96pa7 homo sapien
34	36	72.0	192	2	Q64DG2	Q64dg2 uncultured
35	36	72.0	201	2	Q9H1K3	Q9h1k3 homo sapien
36	36	72.0	247	2	Q9BXN2	Q9bxn2 homo sapien
37	36	72.0	410	2	Q6NU92	Q6nu92 xenopus lae
38	36	72.0	443	2	Q6DHS0	Q6dhs0 brachydanio
39	36	72.0	525	2	Q7F0H9	Q7f0h9 oryza sativ
40	36	72.0	591	2	Q39485	Q39485 chlamydomon
41	36	72.0	1136	2	Q7QP23	Q7qp23 giardia lam
42	36	72.0	1172	2	Q7R3Q6	Q7r3q6 giardia lam
43	36	72.0	1217	2	Q9ULL5	Q9ull5 homo sapien
44	36	72.0	1581	2	Q6PDJ2	Q6pdj2 mus musculus
45	36	72.0	1848	2	Q69ZN8	Q69zn8 mus musculus

ALIGNMENTS

```
RESULT 1
Q62028 PRELIMINARY; PRT; 1487 AA.
AC Q62028;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Phospholipase A2 receptor precursor.
GN Name=Pla2g1br;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95010128; PubMed=7925459;
RA Higashino K., Ishizaki J., Kishino J., Ohara O., Arita H.;
RT "Structural comparison of phospholipase-A2-binding regions in
RT phospholipase-A2 receptors from various mammals.";
RL Eur. J. Biochem. 225:375-382(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Higashino K.-I.;
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; D30779; BAA06443.1; -.
DR PIR; S48719; S48719.
DR HSSP; P08253; 1J7M.
DR MGD; MGI:102468; Pla2g1br.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR008997; RicinB_like.
DR InterPro; IPR000772; RicinB_lectin.
DR Pfam; PF00040; fn2.1.
DR Pfam; PF00059; Lectin_C; 8.
DR PRINTS; PR00013; FNTYPEII.
DR ProDom; PD000995; FN_Type_II; 1.
DR SMART; SM00034; CLECT; 8.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00458; RICIN; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; UNKNOWN_2.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 8.
DR PROSITE; PS00023; FIBRONECTIN_2; 1.
DR PROSITE; PS0231; RICIN_B_LECTIN; 1.
KW Receptor; Signal.
FT SIGNAL 1 26 Potential.
SQ CHAIN 27 1487 phospholipase A2 receptor.
SQ SEQUENCE 1487 AA; 170511 MW; AD8D905859B0ED88 CRC64;
```

Query Match 86.0%; Score 43; DB 2; Length 1487;

Best Local Similarity 77.8%; Pred. No. 31;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 CSVPPLRSVC 9
DB 929 CSVPPLRSIC 937
|||||:|
|:|:|
|:|:|
|:|:|

RESULT 2
YHHT_ECOLI STANDARD; PRT; 349 AA.
ID YHHT_ECOLI
AC P37622; P76700; Q8X6P3;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Hypothetical UPF0118 protein yhht.
GN Names:yhht; OrderedLocusNames=b3474, z4848, ECs4323;
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OC NCBI_TaxID=562, 83334;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RC STRAIN=94316500; PubMed=8041620;
RX MEDLINE=94316500; PubMed=8041620;
RX Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
RT "Analysis of the Escherichia coli genome. V. DNA sequence of the
RT region from 76.0 to 81.5 minutes."
RT Nucleic Acids Res. 22:2576-2586(1994).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RC MEDLINE=21074935; PubMed=11206531; DOI=10.1038/35054089;
RX Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RX Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RX Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RX Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,
RX Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RX Welch R.A., Blattner F.R.;
RA "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RA Nature 409:529-533(2001).
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;
RC MEDLINE=21156231; PubMed=11258736;
RX Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RX Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RX Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RX Kihara S., Shiba T., Hattori M., Shingawa H.;
RA "Complete genome sequence of enterohaemorrhagic Escherichia coli
RA O157:H7 and genomic comparison with a laboratory strain K-12."
RA DNA Res. 8:11-22(2001).
CC CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC CC -1- SIMILARITY: Belongs to the UPF0118 (perM) family.
CC CC
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CC or send an email to license@isb-sib.ch).
CC CC
CC EMBL; U00039; AAB18449.1; ALT INIT.
CC ENBL; U00096; AAC76499.1; ALT INIT.
CC ENBL; AE005570; AGS58583.1; ALT INIT.
CC ENBL; AP002565; BAB37746.1; ALT INIT.
CC ECHOBASE; EB2134;
CC EcoGene; EG12220; yhht.
CC InterPro; IPR002549; UPF0118.
CC Pfam; PF01594; UPF0118; 1.
KW Complete proteome; Hypothetical protein; Transmembrane.
FT TRANSMEM 11 31 Potential.
FT TRANSMEM 33 53 Potential.
FT TRANSMEM 63 83 Potential.

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DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative PerM family permease.
GN Name=yhhT; OrderedLocusNames=STM3582;
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UT2;
RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2."
RL Nature 413:852-856(2001).
DR EMBL; AE008865; AAL22442.1; -.
DR Pfam; PF01594; UPF0118; 1.
KW Complete proteome.
SQ SEQUENCE 349 AA; 38301 MW; 21A55D9F2C5FDB9A CRC64;

Query Match 82.0%; Score 41; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVPLTSVC 9
DB 314 SVPLTSVC 321

RESULT 5
Q83J80 PRELIMINARY; PRT; 349 AA.
ID Q83J80 Q7BYV3;
AC Q83J80;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein yhhT.
GN Name=yhhT; OrderedLocusNames=S4271, SF3492;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157."
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=2457T;
RX MEDLINE=22590274; PubMed=12704152;
RX DOI=10.1128/JAI.71.5.2775-2786.2003;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T."
RT Infect. Immun. 71:2775-2786(2003).
DR EMBL; AE015357; AAN44951.1; -.

DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative PerM family permease.
GN Name=yhhT; OrderedLocusNames=STM3582;
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UT2;
RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2."
RL Nature 413:852-856(2001).
DR EMBL; AE008865; AAL22442.1; -.
DR Pfam; PF01594; UPF0118; 1.
KW Complete proteome.
SQ SEQUENCE 349 AA; 38301 MW; 21A55D9F2C5FDB9A CRC64;

Query Match 82.0%; Score 41; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVPLTSVC 9
DB 314 SVPLTSVC 321

RESULT 5
Q83J80 PRELIMINARY; PRT; 349 AA.
ID Q83J80 Q7BYV3;
AC Q83J80;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein yhhT.
GN Name=yhhT; OrderedLocusNames=S4271, SF3492;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157."
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=2457T;
RX MEDLINE=22590274; PubMed=12704152;
RX DOI=10.1128/JAI.71.5.2775-2786.2003;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T."
RT Infect. Immun. 71:2775-2786(2003).
DR EMBL; AE015357; AAN44951.1; -.

DR EMBL; AE016992; AAP19231.1; -.
DR InterPro; IPR002549; UPF0118.
DR Pfam; PF01594; UPF0118; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 349 AA; 38464 MW; 935ADBA85BD65651 CRC64;

Query Match 82.0%; Score 41; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVPLTSVC 9
DB 314 SVPLTSVC 321

RESULT 6
Q8FCN4 PRELIMINARY; PRT; 376 AA.
ID Q8FCN4 Q8FCN4;
AC Q8FCN4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein yhhT.
GN Name=yhhT; OrderedLocusNames=c4267;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:HI / CFT073 / ATCC 700928 / UPEC;
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli."
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR EMBL; AE016768; AAN83703.1; -.
DR InterPro; IPR002549; UPF0118.
DR Pfam; PF01594; UPF0118; 1.
KW Complete proteome.
SQ SEQUENCE 376 AA; 41438 MW; 6B39C765A5D7315A CRC64;

Query Match 82.0%; Score 41; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVPLTSVC 9
DB 341 SVPLTSVC 348

RESULT 7
Q63791 PRELIMINARY; PRT; 409 AA.
ID Q63791 Q63791;
AC Q63791;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phospholipase A2 receptor (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Smooth muscle;
RX MEDLINE=95010128; PubMed=7925459;
RA Higashino K., Ishizaki J., Kishino J., Ohara O., Arita H.;
RT "Structural comparison of phospholipase-A2-binding regions in
RT phospholipase-A2 receptors from various mammals.";
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RL Eur. J. Biochem. 225:375-382 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Smooth muscle;
RA Higashino K.-I.;
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; D30781; BAA06445.1; -.
DR HSSP; P22030; 11UK.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; Lectin C; 3.
DR SMART; SM00034; CLECT; 3.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 3.
KW Receptor.
FT NON_TER 1
FT NON_TER 409
SQ SEQUENCE 409 AA; 47740 MW; 56D957D2DCA00AD8 CRC64;

Query Match 82.0%; Score 41; DB 2; Length 409;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
Db |||||:|:|
396 CSVMPSPIC 404

RESULT 8
Q6LXFS PRELIMINARY; PRT; 434 AA.
AC Q6LXFS;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Amino transferase (Subgroup I) (EC 2.6.1.-).
GN OrderedLocustNames=MMF1396;
OS Methanococcus maripaludis.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcaceae; Methanococcus.
OX NCBI_TaxID=39152;
RN [1]_TaxID=39152;
RP SEQUENCE FROM N.A.
RC STRAIN=S2 / L1;
RA Hendrickson E.L., Kaul R., Zhou Y., Bovee D., Chapman P., Chung J.,
RA Conway de Macario E., Dodsworth J., Gillett W., Graham D.E.,
RA Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T.,
RA Moore B., Porat I., Overbeek R., Palneiri A., Rouse G.,
RA Saenphimmachak C., Soll D., Whitman W.B., Larimer F.W., Olson M.V.,
RA Leigh J.A.;
RT "Complete genome sequence of the mesophilic hydrogenotrophic
methanogen Methanococcus maripaludis.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX957222; CAF30952.1; -.
DR GO; GO:0016844; F:1-aminocyclopropane-1-carboxylate synthase . . .; IEA.
DR GO; GO:0008483; F:transaminase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR InterPro; IPR001176; ACC synthase.
DR Pfam; PF00155; Aminotran 1,2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
KW Complete proteome.
SQ SEQUENCE 434 AA; 49487 MW; 3596D870353CEB04 CRC64;

Query Match 82.0%; Score 41; DB 2; Length 434;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
Db |||||:|:|
389 CGVPLTSFC 397

RESULT 9
Q6ZKN1 PRELIMINARY; PRT; 750 AA.
AC Q6ZKN1;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Putative CLC-F chloride channel protein.
GN Name=OJ118_A06.1;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]_TaxID=39947;
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003873; BAD08801.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005247; F:voltage-gated chloride channel activity; IEA.
DR GO; GO:0006821; P:chloride transport; IEA.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR001807; Cl-channel_volt.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00654; Voltage_CLC; 1.
DR PRINTS; PR00762; CLCHANNEL.
DR SMART; SM00116; CBS; 2.
SQ SEQUENCE 750 AA; 80236 MW; F5272D1A5611EAB2 CRC64;

Query Match 82.0%; Score 41; DB 2; Length 750;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSVPLTSV 8
Db |||||:|:|
473 CSVPLTSV 480

RESULT 10
Q9ARC6 PRELIMINARY; PRT; 750 AA.
AC Q9ARC6;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]_TaxID=4081;
RP SEQUENCE FROM N.A.
RX MEDLINE=1178822; PubMed=11283350;
RA Rossberg M., Theres K., Acarkan A., Herrero R., Schmitt T.,
RA Schumacher K., Schmitz G., Schmidt R.;
RT "Comparative sequence analysis reveals extensive microcolinearity in
the lateral suppressor regions of the tomato, Arabidopsis and Capsella
genomes.";
RT Plant Cell; 13:979-988 (2001).
DR EMBL; AJ303345; CAC36403.1; -.
DR HSSP; Q8ZRP8; 1KPL.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005247; F:voltage-gated chloride channel activity; IEA.
DR GO; GO:0006821; P:chloride transport; IEA.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR001807; Cl-channel_volt.
DR Pfam; PF00571; CBS; 2.
DR PRINTS; PR00762; CLCHANNEL.
DR SMART; SM00116; CBS; 2.
KW Hypothetical protein.
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SQ SEQUENCE 750 AA; 79985 MW; 92856D1EE2E5FCD4 CRC64;
Query Match 82.0%; Score 41; DB 2; Length 750;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSVPLTSV 8
Db 474 CSVPLTSV 481

RESULT 11
Q9ARF2 PRELIMINARY; PRT; 750 AA.
AC Q9ARF2
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21178822; PubMed=11283350;
RA Rosberg M., Theres K., Acarkan A., Herrero R., Schmitt T.,
RA Schumacher K., Schmitz G., Schmidt R.;
RT "Comparative sequence analysis reveals extensive microcolinearity in
the lateral suppressor regions of the tomato, Arabidopsis and Capsella
genomes.";
RL Plant Cell 13:979-988(2001).

RESULT 12
Q9ARF2 PRELIMINARY; PRT; 780 AA.
AC Q9ARF2
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Capsella rubella.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Brassicales; Brassicaceae; Capsella.
OX NCBI_TaxID=81985;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21178822; PubMed=11283350;
RA Rosberg M., Theres K., Acarkan A., Herrero R., Schmitt T.,

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RA Schumacher K., Schmitz G., Schmidt R.;
RT "Comparative sequence analysis reveals extensive microcolinearity in
the lateral suppressor regions of the tomato, Arabidopsis and Capsella
genomes.";
RL Plant Cell 13:979-988(2001).

RN [2]
RP SEQUENCE FROM N.A.
RA Schmidt R.H.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005247; F:voltage-gated chloride channel activity; IEA.
DR GO: GO:0006821; P:chloride transport; IEA.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR001807; Cl-channel_volt.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00654; Voltage CLC; 1.
DR PRINTS: PR00762; CLCHANNEL.
DR SMART: SM00116; CBS; 2.
KW Hypothetical protein.
SQ SEQUENCE 780 AA; 83811 MW; 5718FA7E2AE81FB CRC64;

Query Match 82.0%; Score 41; DB 2; Length 780;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSVPLTSV 8
Db 513 CSVPLTSV 520

RESULT 13
CLCF ARATH STANDARD; PRT; 781 AA.
AC Q8XR2; Q9ARM3; Q9LG04;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chloride channel protein CLC-f (AtCLC-f).
GN Name=CLC-F; OrderedLocusNames=At1G55620; ORFNames=F20N2.5;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=cv. Columbia;
RX MEDLINE=21178822; PubMed=11283350;
RA Rosberg M., Theres K., Acarkan A., Herrero R., Schmitt T.,
RA Schumacher K., Schmitz G., Schmidt R.;
RT "Comparative sequence analysis reveals extensive microcolinearity in
the lateral suppressor regions of the tomato, Arabidopsis, and
Capsella genomes.";
RL Plant Cell 13:979-988(2001).

RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=cv. Columbia; TISSUE=Aerial parts;
RX MEDLINE=21178822; PubMed=11283350;
RA Vinauger-Douard M., Charon C., Lapous D., Allot M., Granier F.,
Bouchez D., Barbier-Brygoo H., Ephritikhine G.;
RT "Molecular and functional characterization of AtCLC-f, a putative new
Arabidopsis chloride channel.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=cv. Columbia;
RX MEDLINE=21178822; PubMed=11283350; DOI=10.1038/35048500;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
Dunn P., Etku P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

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RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana";
RL Nature 408:816-820(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=cv. Columbia;
RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari P.,
RA Arakawa T., Banno F., Bowser L., Brooks S.Y., Carninci Y.,
RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the Arabidopsis
RT genome";
RL Science 302:842-846(2003).
CC -!- FUNCTION: Voltage-gated chloride channel.
CC -!- SUBUNIT: Homodimer (by similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q8RXR2-1; Sequence=Displayed;
CC Name=2;
CC Note=May be due to a competing acceptor splice site. No
CC experimental confirmation available;
CC -!- SIMILARITY: Belongs to the chloride channel (TC 1.A.11) family.
CC -!- SIMILARITY: Contains 2 CBS domains.
CC -!- CAUTION: Ref.3 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ303348; CAC36386.1; -;
CC EMBL; AF363368; AAK53291.1; -;
CC EMBL; AC00328; AAF79509.1; ALT_SEQ.
CC EMBL; AY080722; AAL86324.1; -;
CC GeneFarm; 2843; 272.
CC InterPro; IPR000644; CBS.
CC InterPro; IPR001807; Cl-channel_volt.
CC Pfam; PF00571; CBS; 2.
CC Pfam; PF00654; Voltage_CLC; 1.
CC PRINTS; PR00762; CLCHANNEL.
CC SMART; SM00116; CBS; 2.
CC Alternative splicing; CBS domain; Chloride; Chloride channel;
CC Ion transport; Ionic channel; Repeat; Transmembrane;
CC Voltage-gated channel.
CC TRANSMEM 129 149 1 (Potential).
CC TRANSMEM 184 204 2 (Potential).
CC TRANSMEM 221 241 3 (Potential).
CC FT

FT TRANSMEM 250 270 4 (Potential).
FT TRANSMEM 279 299 5 (Potential).
FT TRANSMEM 314 334 6 (Potential).
FT TRANSMEM 350 370 7 (Potential).
FT TRANSMEM 388 408 8 (Potential).
FT TRANSMEM 433 453 9 (Potential).
FT TRANSMEM 457 477 10 (Potential).
FT TRANSMEM 502 522 11 (Potential).
FT TRANSMEM 523 543 12 (Potential).
FT TRANSMEM 726 746 13 (Potential).
FT DOMAIN 619 672 CBS 1.
FT DOMAIN 697 758 CBS 2.
FT VARSPLIC 1 196 Missing (in isoform 2).
FT CONFLICT 643 643 /FTId=VSP_009325.
FT SEQUENCE 781 AA; 83548 MW; BE9DEB3603D9E0D8 CRC64;
SQ
Query Match 82.0%; Score 41; DB 1; Length 781;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSVPLTSV 8
Db 514 CSVPLTSV 521
RESULT 14
Q6Z673 PRELIMINARY; PRT; 783 AA.
AC Q6Z673;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE putative chloride channel protein.
GN Name=P0654B04.5; Synonyms=OJ1008.D06.20;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, PAC
RT clone:P0654B04.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, BAC
RT clone:OJ1008.D06.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005052; BAD12997.1; -;
DR EMBL; AP004040; BAD12877.1; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005247; F:voltage-gated chloride channel activity; IEA.
DR GO; GO:0006821; P:chloride transport; IEA.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR001807; Cl-channel_volt.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00654; Voltage_CLC; 1.
DR PRINTS; PR00762; CLCHANNEL.
SQ SEQUENCE 783 AA; 83561 MW; 1DA7D7EE91260802 CRC64;
Query Match 82.0%; Score 41; DB 2; Length 783;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSVPLTSV 8
Db 510 CSVPLTSV 517

RESULT 15

Q69GZ6 PRELIMINARY; PRT; 440 AA.
 AC Q69GZ6;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Aspartate aminotransferase-like protein.
 OS Methanococcus voltae.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanococcaceae; Methanococcus.
 OX NCBI_TaxID=2188;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PS;
 RA Feldman R., Overbeek R., Whitman W.;
 RT "Chromosomal segregation protein SMC."
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY289521; AAC91885.1; -;
 DR GO; GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . .; IEA.
 DR GO; GO:0008483; F:transaminase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0009058; P:biosynthesis; IEA.
 DR InterPro; IPR001176; ACC synthase.
 DR InterPro; IPR004839; Aminotrans_I/II.
 DR Pfam; PF00155; Aminotran_1_2; 1.
 DR PRINTS; PRO0753; ACCSYNTHASE.
 DR KW Aminotransferase; Transferase.
 SQ SEQUENCE 440 AA; 49619 MW; 144638E000595831 CRC64;

Query Match 80.0%; Score 40; DB 2; Length 440;

Best Local Similarity 77.8%; Pred.No. 33;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9

Db 394 CNVPLTSC 402

Search completed: April 1, 2005, 09:26:01
 Job time : 57.1096 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 03:27:37 ; Search time 67.9315 Seconds
(without alignments)
51.240 Million cell updates/sec

Title: US-09-761-636A-10

Perfect score: 50

Sequence: 1 CSVPLTSVC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	9	AAU04529	AAU04529 VEGF base
2	43	86.0	1487	AAB23826	AAB23826 Murine ph
3	41	82.0	422	ABO64325	ABO64325 Klebsiell
4	39	78.0	73	AAU63687	AAU63687 Propionib
5	39	78.0	73	ABM60206	ABM60206 Propionib
6	39	78.0	88	AAU53277	AAU53277 Propionib
7	39	78.0	88	ABM49796	ABM49796 Propionib
8	39	78.0	432	ADN18428	ADN18428 Bacteri
9	38	76.0	101	AAU43894	AAU43894 Propionib
10	38	76.0	101	ABM40413	ABM40413 Propionib
11	38	76.0	121	AAU74551	AAU74551 Human pro
12	38	76.0	225	ABG11475	ABG11475 Novel hum
13	38	76.0	742	ABU74693	ABU74693 Human pro
14	38	76.0	802	AAE01782	AAE01782 Human gen
15	38	76.0	802	ABG64141	ABG64141 Human alb
16	38	76.0	802	ADA56848	ADA56848 Human sec
17	38	76.0	802	ADA40695	ADA40695 Human sec
18	38	76.0	802	ABR47707	ABR47707 Human sec
19	38	76.0	802	ADC74086	ADC74086 Human sec
20	38	76.0	802	ADD37860	ADD37860 Human sec
21	38	76.0	802	ADL77406	ADL77406 Albumin f
22	37	74.0	9	ABJO4424	ABJO4424 Stem cell
23	37	74.0	86	AAU58469	AAU58469 Propionib
24	37	74.0	86	ABM54988	ABM54988 Propionib
25	37	74.0	1929	ABB67846	ABB67846 Drosophila

26	36	72.0	53	5	ABP06465	Abp06465 Human ORF
27	36	72.0	90	4	AAU74036	AAU74036 Human col
28	36	72.0	133	4	AAU21569	AAU21569 Novel hum
29	36	72.0	133	4	AAU19674	AAU19674 Human nov
30	36	72.0	133	4	AAU43498	AAU43498 Human pol
31	36	72.0	133	4	ABU10143	ABU10143 Human CDN
32	36	72.0	133	4	AAU18408	AAU18408 Human end
33	36	72.0	133	5	ABP47894	ABP47894 Human pol
34	36	72.0	133	5	ABP66730	ABP66730 Human pol
35	36	72.0	133	7	ADC10856	ADC10856 Human ext
36	36	72.0	133	7	ADM46210	ADM46210 Human neo
37	36	72.0	133	8	ADM24519	ADM24519 Human PRO
38	36	72.0	168	7	ABO71618	ABO71618 Pseudomon
39	36	72.0	201	2	AAW52837	AAW52837 Human C-t
40	36	72.0	201	2	AAU27449	AAU27449 Human CDC
41	36	72.0	201	2	AAU41764	AAU41764 Human PRO
42	36	72.0	201	2	AAW73888	AAW73888 Human DC3
43	36	72.0	201	3	AAU44320	AAU44320 Human PRO
44	36	72.0	201	4	AAU29077	AAU29077 Human PRO
45	36	72.0	201	5	ABB90372	ABB90372 Human pol

ALIGNMENTS

RESULT 1
AAU04529
ID AAU04529 standard; peptide; 9 AA.
XX
AC AAU04529;
XX
DT 26-SEP-2001 (first entry)
XX
DE VEGF based monocyclic peptide 7.
XX
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..9 /note= "This bond cyclises the peptide"
XX
PN WO200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2000; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX
(LUDW-) LUDWIG INST CANCER RES.
XX
PI Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR WPI; 2001-442248/47.
XX
PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.
XX
PS Claim 49; Page 32; 102pp; English.
XX
CC The sequence represents a monomeric monocyclic peptide of the invention,
CC whose 3-dimensional structure is modelled on the expose loop of human
CC VEGF (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis.
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSVPLTSVC 9
 |||||
 DB 1 CSVPLTSVC 9

RESULT 2
 AAB23826
 ID AAB23826 standard; protein; 1487 AA.
 AC AAB23826;
 DT 15-JAN-2001 (first entry)
 DE Murine phospholipase A2 receptor protein SEQ ID NO:7.
 KW Endocytic C lectin family; E-selectin; type C lectin; identification.
 OS Mus sp.
 XX US6117977-A.
 XX 12-SEP-2000.
 XX 24-APR-1997; 97US-00840062.
 XX 24-APR-1996; 96US-0052524P.
 XX 24-APR-1996; 96US-00637021.
 XX (GETH) GENENTECH INC.
 XX Wu K, Lasky LA;
 XX WPI; 1997-535838/49.
 XX Human and mouse type C lectin(s) - useful as competitive inhibitor of
 XX lectin activity and as molecular markers for tissues that express them.
 XX Example; Fig 3; 72pp; English.

XX The present invention describes an isolated type C lectin polypeptide (I)
 CC comprising amino acid residues 37-1393, 37-174, 175-229, 234-360, 381-
 CC 507, 520-645, 667-809, 824-951, 970-1108, 1110-1243, or 1259-1393 of the
 CC protein sequence given in AAB23822. The first 2 polypeptides are capable
 CC of binding to a carbohydrate residue, and the rest of the polypeptides

CC are useful for producing antibodies capable of binding to these 2
 CC polypeptides. Polynucleotide sequence encoding the polypeptides of the
 CC invention are useful in the identification and purification of their
 CC native ligands, and as molecular markers of the tissues in which they are
 CC expressed. They provide valuable sequence motifs, which can be inserted
 CC or substituted into other native members of the endocytic type C lectins,
 CC and provide hybridisation probes for searching cDNA and genomic libraries
 CC for the coding sequence of other type C lectins. Variants of type C
 CC lectins may be used therapeutically as competitive inhibitors of the
 CC biological activity of native type C lectins. The present sequence
 CC represents a murine phospholipase A2 receptor protein which is homologous
 CC to a type C lectin
 XX
 SQ Sequence 1487 AA;

Query Match 86.0%; Score 43; DB 2; Length 1487;
 Best Local Similarity 77.8%; Pred. No. 1.7e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CSVPLTSVC 9
 |||||
 DB 929 CSVPLPSIC 937

RESULT 3
 ABO64325
 ID ABO64325 standard; protein; 422 AA.

AC ABO64325;
 DT 29-JUL-2004 (first entry)
 DE Klebsiella pneumoniae polypeptide seqid 10842.

KW Recombinant expression vector; transcription regulatory element;
 KW Klebsiella pneumoniae protein; antibacterial; vaccine.

OS Klebsiella pneumoniae.

XX US6610836-B1.

XX 26-AUG-2003.

XX 27-JAN-2000; 2000US-00489039.

XX 29-JAN-1999; 99US-0117747P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Breton GL, Osborne M;

XX WPI; 2003-895346/82.

XX N-PSDB; ACH97876.

XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
 XX preparing a vaccine composition against Klebsiella pneumoniae.

XX Disclosure; SEQ ID NO 10842; 932pp; English.

XX The invention describes a new isolated nucleic acid encoding a Klebsiella
 CC pneumoniae polypeptide. Also described are: a recombinant expression
 CC vector comprising the nucleic acid, operably linked to a transcription
 CC regulatory element; and a cell comprising the recombinant expression
 CC vector. The nucleic acid is useful for preparing a vaccine composition
 CC against Klebsiella pneumoniae. This is the amino acid sequence of a
 CC Klebsiella pneumoniae polypeptide of the invention
 XX
 SQ Sequence 422 AA;

Query Match 82.0%; Score 41; DB 7; Length 422;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVPLTSVC 9
 Db 387 SVPLTSVC 394

RESULT 4
 AAU63687
 ID AAU63687 standard; protein; 73 AA.
 XX
 AC AAU63687;
 DT 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #24583.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertostis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 XX dermatological; osteopathic; neuroprotectant.
 OS
 PN Propionibacterium acnes.
 XX
 PN WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-US012865.
 XX
 PR 21-APR-2000; 2000US-0199047P.
 PR 02-JUN-2000; 2000US-0208941P.
 PR 07-JUL-2000; 2000US-0216747P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 DR WPI; 2001-616774/71.
 DR N-PSDB; AAS59634.
 XX
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.
 XX
 PS Example 1; SEQ ID NO 24882; 1069pp; English.
 XX
 CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertostis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 73 AA;
 Query Match 78.0%; Score 39; DB 4; Length 73;
 Best Local Similarity 66.7%; Pred. No. 43;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
 Db 35 CRAPITSVC 43

RESULT 5
 ABM60206
 ID ABM60206 standard; protein; 73 AA.
 XX
 AC ABM60206;
 DT 20-OCT-2003 (first entry)
 XX
 DE Propionibacterium acnes predicted ORF-encoded polypeptide #24882.
 XX
 KW Acne vulgaris; antisborrheic; dermatological; antibacterial;
 KW immunostimulant; immune response; vaccine.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO2003033515-A1.
 XX
 PD 24-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032727.
 XX
 PR 15-OCT-2001; 2001US-00978825.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Vallieue-Douglass J;
 XX
 DR WPI; 2003-381789/36.
 DR N-PSDB; ACF64563.
 XX
 PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX
 PS Example 1; SEQ ID NO 24882; 1481pp; English.
 XX
 CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 73 AA;

Query Match		78.0%;	Score 39;	DB 6;	Length 73;			
Best Local Similarity		66.7%;	Pred. No. 43;					
Matches 6;		Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;			
QY	1 CSVPLTVC 9							
		: :						
DB	35 CRAPITVC 43							
RESULT 6								
ID	AAU53277							
XX	AAU53277 standard; protein; 88 AA.							
AC	AAU53277;							
DT	27-FEB-2002 (first entry)							
DE	Propionibacterium acnes immunogenic protein #14173.							
KW	SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.							
OS	Propionibacterium acnes.							
XX	WO200181581-A2.							
PD	01-NOV-2001.							
XX	20-APR-2001; 2001WO-US012865.							
PR	21-APR-2000; 2000US-0199047P.							
PR	02-JUN-2000; 2000US-0208841P.							
PR	07-JUL-2000; 2000US-0216747P.							
XX	(CORI-) CORIXA CORP.							
PI	Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;							
PI	L'maisonneuve J, Zhang Y, Jen S, Carter D;							
DR	WPI: 2001-616774/71.							
DR	N-PSDB; AAS59559.							
XX	Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.							
PS	Example 1; SEQ ID NO 14472; 1069pp; English.							
CC	Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences							
XX	Sequence 88 AA;							
SQ								

Query Match		78.0%;	Score 39;	DB 4;	Length 88;			
Best Local Similarity		66.7%;	Pred. No. 51;					
Matches 6;		Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;			
QY	1 CSVPLTVC 9							
		: :						
DB	43 CSIFLTVC 51							
RESULT 7								
ID	ABM49796							
XX	ABM49796 standard; protein; 88 AA.							
AC	ABM49796;							
DT	20-OCT-2003 (first entry)							
DE	Propionibacterium acnes predicted ORF-encoded polypeptide #14472.							
KW	Acne vulgaris; anti-seborrheic; dermatological; antibacterial; immunostimulant; immune response; vaccine.							
XX	Propionibacterium acnes.							
PN	WO2003033515-A1.							
XX	24-APR-2003.							
PF	11-OCT-2002; 2002WO-US032727.							
XX	15-OCT-2001; 2001US-00978825.							
PA	(CORI-) CORIXA CORP.							
PI	Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;							
PI	Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;							
PI	Barth B, Vallieve-Douglass J;							
DR	WPI: 2003-381789/36.							
DR	N-PSDB; ACF64488.							
XX	New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.							
PS	Example 1; SEQ ID NO 14472; 1481pp; English.							
CC	The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polynucleotide of the invention; antibodies against polypeptides of the invention; fusion proteins comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. The polynucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly							

CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 88 AA;
SQ

Query Match 78.0%; Score 39; DB 6; Length 88;
Best Local Similarity 66.7%; Pred. No. 51;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
||:|||||
DB 43 CSIPLTGPC 51

RESULT 8
ADN18428
ID ADN18428 standard; protein; 432 AA.
XX
AC ADN18428;
XX
DT 02-DEC-2004 (first entry)
DE Bacterial polypeptide #1081.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 1081; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or

CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 432 AA;
XX

Query Match 78.0%; Score 39; DB 8; Length 432;
Best Local Similarity 77.8%; Pred. No. 2; 4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
||:|||||
DB 389 CVPPLTSFC 397

RESULT 9
AAU43894
ID AAU43894 standard; protein; 101 AA.
XX
AC AAU43894;
XX
DT 13-FEB-2002 (first entry)
DE Propionibacterium acnes immunogenic protein #4790.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN WO200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001WO-US012865.
XX
PR 21-APR-2000; 2000US-0199047P.
PR 02-JUN-2000; 2000US-0208841P.
PR 07-JUL-2000; 2000US-0216747P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI; 2001-616774/71.
DR N-PSDB; AAS59521.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
XX
PS Example 1; SEQ ID NO 5089; 1069pp; English.
XX
CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies

CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ

Sequence 101 AA;

Query Match 76.0%; Score 38; DB 4; Length 101;
Best Local Similarity 66.7%; Pred. No. 86;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
|:|||||
Db 16 CNLPLTLC 24

RESULT 10

ID ABM40413 standard; protein; 101 AA.

XX ABM40413;

DT 20-OCT-2003 (first entry)

XX Propionibacterium acnes predicted ORF-encoded polypeptide #5089.

DE Acne vulgaris; antiseborrheic; dermatological; antibacterial;

KW immunostimulant; immune response; vaccine.

XX Propionibacterium acnes.

XX WO2003033515-A1.

XX 24-APR-2003.

PF 11-OCT-2002; 2002WO-US032727.

PR 15-OCT-2001; 2001US-00978825.

XX (CORI-) CORIXA CORP.

XX Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;

PI Zhang Y, Wang S, Jen S, Lodes WD, Benson DR, Jones R, Carter D;

PI Barth B, Valliave-Dougllass J;

XX WPI; 2003-381789/36.

DR N-PSDB; ACF64450.

XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
PT or for stimulating an immune response specific for a P. acnes protein.

XX Example 1; SEQ ID NO 5089; 148pp; English.

XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
CC encoding a Propionibacterium acnes protein. The invention also relates to
CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
CC immunogenic fragments of P. acnes polypeptides. The invention
CC additionally encompasses expression vectors and host cells comprising a
CC polynucleotide of the invention; antibodies against polypeptides of the
CC invention; fusion proteins comprising a polypeptide of the invention; a
CC method for stimulating an immune response specific for a P. acnes
CC polypeptide and an isolated T cell population comprising P. acnes polypeptides,
CC via this method; a vaccine composition (comprising P. acnes polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations, or
CC antigen-presenting cells that express the polypeptide); a method and kit
CC for detecting or determining the presence or absence of P. acnes in a
CC patient; and a method for inhibiting the development of P. acnes in a
CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion

CC proteins, T cell populations or antigen-presenting cells that express the
CC polypeptides are useful for diagnosing, preventing or treating acne
CC vulgaris, or for stimulating an immune response specific for a P. acnes
CC protein. The polynucleotides can also be used as probes or primers for
CC nucleic acid hybridisation. The vaccine composition is useful for the
CC stimulation of an immune response against P. acnes, or for treating acne,
CC and the kit is useful for performing a diagnostic assay. The present
CC sequence represents a polypeptide predicted to be encoded by an ORF (open
CC reading frame) contained within the P. acnes polynucleotides of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX

Sequence 101 AA;

Query Match 76.0%; Score 38; DB 6; Length 101;
Best Local Similarity 66.7%; Pred. No. 86;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
|:|||||
Db 16 CNLPLTLC 24

RESULT 11

ID AAU74551 standard; protein; 121 AA.

XX AAU74551;

DT 08-MAY-2002 (first entry)

XX Human protein phosphatase 13.31 polypeptide.

XX Human; protein phosphatase 13.31; enzyme; malignant tumour; cancer;
KW embryonic developmental abnormality; autoimmune disease; anti-
KW gynaecological; cytostatic; immunosuppressant; gene therapy.

XX Homo sapiens.

XX WO200212457-A1.

XX 14-FEB-2002.

PF 02-JUL-2001; 2001WO-CN001118.

PR 07-JUL-2000; 2000CN-00117017.

XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2002-172153/22.

DR N-PSDB; ABK14072.

XX Human protein phosphatase 13.31 and encoding polynucleotide, used in
PT diagnosis and treatment of malignant tumors, autoimmune disease and
PT embryonic development abnormality.

XX Claim 1; Page 30; 34pp; Chinese.

XX The invention relates to an isolated polypeptide of human protein
CC phosphatase 13.31 and its associated polynucleotide. The sequences are
CC used in diagnosis and treatment of malignant tumour, embryonic
CC developmental abnormality and autoimmune disease and for studying human
CC anti-
CC antineoplastic. This sequence represents human protein phosphatase 13.31

XX Sequence 121 AA;

Query Match 76.0%; Score 38; DB 5; Length 121;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPLTVC 9
Db |||||
105 CSVPTDPC 113

RESULT 12
ABG11475
ID ABG11475 standard; protein; 225 AA.
XX
AC ABG11475;
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #11466.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS75662.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 41834; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activities. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences. The invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 225 AA;
SQ

Query Match 76.0%; Score 38; DB 4; Length 225;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPLTVC 9
Db |||||

RESULT 13
AAB74693
ID AAB74693 standard; protein; 742 AA.
XX
AC AAB74693;
DT 12-JUN-2001 (first entry)
XX
DE Human protease and protease inhibitor PPIM-26.
XX
KW Human; protease; protease inhibitor; protease and protease inhibitor;
KW PPIM; identification; diagnosis; anti-human immunodeficiency virus; HIV;
KW antidiabetic; immunostimulant; immunomodulator; antiinflammatory;
KW antithyroid; immunosuppressive; nephrotropic; antigout; thyromimetic;
KW cytostatic; antibacterial; fungicide; protozoacide; antiarteriosclerotic;
KW antiatherosclerotic; antipsoriatic; virucide; hepatotropic; antiatherosclerotic;
KW autoimmune disorder; inflammatory disease; AIDS; DiGeorge's syndrome;
KW severe combined immunodeficiency disease; SCID; Chediak-Higashi syndrome;
KW Cushing's disease; Addison's disease; autoimmune thyroiditis; gout;
KW Crohn's disease; diabetes mellitus; Good pasture's syndrome; infection;
KW Grave's disease; Hashimoto's thyroiditis; Sjogren's syndrome; cancer;
KW Werner's syndrome; cell proliferative disorder; arteriosclerosis;
KW atherosclerosis; cirrhosis; hepatitis; psoriasis.
XX
OS Homo sapiens.
XX
PN WO200110903-A2.
XX
PD 15-FEB-2001.
XX
PF 09-AUG-2000; 2000WO-US021878.
XX
PR 09-AUG-1999; 99US-0147986P.
PR 21-OCT-1999; 99US-0160807P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Yue H, Lal P, Tang YT, Bandman O, Baughn MR, Azimzai Y, Lu DM;
PI Yang J;
XX
DR WPI; 2001-202760/20.
DR N-PSDB; AAF81739.
XX
PT New protease (inhibitors) useful for diagnosis and treatment of
PT autoimmune/inflammatory disorders such as acquired immunodeficiency
PT syndrome, Cushing's disease, Addison's disease and cell proliferative
PT disorders such as cancer.
XX
PS Claim 1; Page 114-115; 134pp; English.

CC AAF81714 to AAF81740 encode the human proteases and protease inhibitors
CC (PPIMs) given in AAB74693 to AAB74694. The PPIMs can have activities such
CC as: anti-human immunodeficiency virus (HIV); antidiabetic; antithyroid;
CC immunostimulant; immunomodulator; antiinflammatory; immunosuppressive;
CC nephrotropic; antigout; thyromimetic; cytostatic; antibacterial;
CC fungicide; protozoacide; antiarteriosclerotic; antiatherosclerotic;
CC virucide; antipsoriatic; and hepatotropic. PPIM polynucleotide and
CC protein sequences can be used in the diagnosis, treatment and prevention
CC of autoimmune/inflammatory disorders such as AIDS, DiGeorge's syndrome,
CC severe combined immunodeficiency disease (SCID), Chediak-Higashi
CC syndrome, Cushing's disease, Addison's disease, autoimmune thyroiditis,
CC Crohn's disease, diabetes mellitus, Good pasture's syndrome, gout,
CC Grave's disease, Hashimoto's thyroiditis, Sjogren's syndrome, Werner's
CC syndrome, viral, bacterial, fungal, parasitic, protozoal, and helminthic
CC infections and cell proliferative disorder such as arteriosclerosis,
CC atherosclerosis, cirrhosis, hepatitis, psoriasis and cancer. PPIM
CC polynucleotide sequences can be used in somatic or germline gene therapy
CC and in diagnosis of diseases. They can also be used in generating
CC hybridisation probes useful in mapping the naturally occurring genomic
CC sequences and in molecular biology techniques

XX SQ Sequence 742 AA;
Query Match 76.0%; Score 38; DB 4; Length 742;
Best Local Similarity 66.7%; Pred. No. 6.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 CSVPPLTSSVC 9
|||||:
Db 726 CSVPITDPC 734
RESULT 14
AAE01782
ID AAE01782 standard; protein; 802 AA.
XX AAE01782;
AC AAE01782;
XX
DT 17-JUL-2001 (first entry)
XX
DE Human gene 13 encoded secreted protein HDPNW93, SEQ ID NO:103.
XX
KW Human; secreted protein; proliferative disorder; cancer; tumour;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiogenic disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder; gene therapy;
KW endocrine disorder; infection; wound healing; vulnery; cell culture;
KW chemotaxis; food additive; chromosome 17; binding partner identification.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Signal_peptide
FT Protein 20..802
FT /label= Human_mature_secretated_protein
FT
XX WO200134627-A1.
XX
XX
PD 17-MAY-2001.
XX
XX 08-NOV-2000; 2000WO-US030628.
XX
PR 12-NOV-1999; 99US-0164744P.
PR 30-JUN-2000; 2000US-0215140P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Komatsoulis GA, Baker KP, Young PE;
XX WPI; 2001-316491/33.
DR N-PSDB; AAD05591.
XX
XX New nucleic acid molecules encoding human secreted proteins, used in
PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
PT Parkinson's diseases and cancers.
XX
XX Claim 11; Page 492-494; 567pp; English.
XX
XX AAD05579-AAD05658 represent cDNAs corresponding to 28 human secreted
CC protein genes and AAE01770-AAE01849 represent the proteins they encode.
CC AAE01850-AAE01860 represent human secreted protein fragments or variants.
CC The genes and their secreted proteins are useful for preventing, treating
CC or ameliorating medical conditions, e.g., by protein or gene therapy.
CC Pathological conditions can be diagnosed by determining the amount of the
CC new protein in a sample or by determining the presence of mutations in
CC the new genes. Specific uses are described for each of the 28 genes,
CC based on the tissues in which they are most highly expressed, and include
CC developing products for the diagnosis or treatment of proliferative

CC disorders, cancer, tumours, foetal and developmental abnormalities,
CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
CC angiogenic disorders, kidney disorders, gastrointestinal disorders,
CC pregnancy-related disorders, endocrine disorders, and infections. The
CC proteins can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues, to identify their cognate ligands or binding
CC partners, and in chemotaxis, and can be used as a food additive or
CC preservative to modify storage properties. Antibodies specific for a
CC protein of the invention can be used in alleviating symptoms associated
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The
CC present sequence represents a human secreted protein of the invention
XX
SQ Sequence 802 AA;
Query Match 76.0%; Score 38; DB 4; Length 802;
Best Local Similarity 66.7%; Pred. No. 6.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 CSVPPLTSSVC 9
|||||:
Db 786 CSVPITDPC 794
RESULT 15
ABG64141
ID ABG64141 standard; protein; 802 AA.
XX
XX AC ABG64141;
XX
XX 27-AUG-2002 (first entry)
XX Human albumin fusion protein #816.
XX
XX Albumin fusion protein; therapeutic protein X; human albumin; HA;
KW human serum albumin; HSA; cancer; reproductive disorder;
KW digestive disorder; immune disorder; endocrine disorder;
KW haematopoietic disorder; neural disorder; connective disorder;
KW cytostatic; antiinfertility; antinflammatory; antiulcer;
KW immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
KW osteopathic; antiarthritic.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200177137-A1.
XX
XX 18-OCT-2001.
XX
XX 12-APR-2001; 2001WO-US011988.
XX
XX 12-APR-2000; 2000US-0229358P.
PR 25-APR-2000; 2000US-0199184P.
PR 21-DEC-2000; 2000US-0256931P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Rosen CA, Haseltine WA;
PI
XX WPI; 2002-010886/01.
XX
XX New fusion protein for treating disease e.g. diabetes comprises an
PT albumin fused to a therapeutic protein.
XX
XX Claim 1; Page 1035-1037; 2102pp; English.
XX

CC The present invention relates to albumin fusion proteins comprising a
CC therapeutic protein X and human albumin (HA, also known as human serum
CC albumin, HSA). The proteins are useful for treating a disease or disorder
CC that may be modulated by therapeutic protein X. The albumin extends the
CC shelf-life of protein X, and may increase its biological in vitro/in vivo
CC activity. The protein is useful for treating and diagnosing disorders
CC such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's
CC disease, ulcerative colitis), immune disorders (e.g. acquired
CC immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),
CC haematopoietic disorders, neural disorders (e.g. Alzheimer's,
CC Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,
CC schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).
CC ABG63326-ABG65518 represent albumin fusion proteins of the invention
XX
SQ Sequence 802 AA;

Query Match 76.0%; Score 38; DB 5; Length 802;
Best Local Similarity 66.7%; Pred. No. 6.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CSVPLTSCV 9
Db 786 CSVPIITDPC 794

Search completed: April 1, 2005, 09:18:18
Job time : 69.9315 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 09:26:18 ; Search time 221.178 Seconds
(without alignments)
13.493 Million cell updates/sec

Title: US-09-761-636A-10

Perfect score: 50

Sequence: 1 CSVPLTSVC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
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18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	42	84.0	154	US-10-424-599-241613	Sequence 241613,
3	42	84.0	194	US-10-424-599-241616	Sequence 241616,
4	41	82.0	149	US-10-424-599-206581	Sequence 206581,
5	41	82.0	178	US-10-767-701-54625	Sequence 54625, A
6	41	82.0	359	US-10-424-599-174316	Sequence 174316,
7	41	82.0	549	US-10-424-599-205890	Sequence 205890,
8	41	82.0	565	US-10-425-114-69391	Sequence 69391, A
9	41	82.0	883	US-10-437-963-133870	Sequence 133870,
10	39	78.0	63	US-10-424-599-276101	Sequence 276101,
11	39	78.0	432	US-10-369-493-1081	Sequence 1081, Ap
12	38	76.0	67	US-10-767-701-51825	Sequence 51825, A
13	38	76.0	802	US-09-833-245-888	Sequence 888, App

14	37	74.0	82	15	US-10-424-599-169061	Sequence 169061,
15	37	74.0	95	15	US-10-424-599-276082	Sequence 276082,
16	37	74.0	167	15	US-10-424-599-243236	Sequence 243236,
17	37	74.0	215	15	US-10-425-114-56269	Sequence 56269, A
18	37	74.0	267	15	US-10-424-599-236212	Sequence 236212,
19	37	74.0	269	15	US-10-425-114-39180	Sequence 39180, A
20	37	74.0	718	16	US-10-437-963-160508	Sequence 160508,
21	36	72.0	90	14	US-10-106-698-4810	Sequence 4810, Ap
22	36	72.0	133	9	US-09-764-870-324	Sequence 324, App
23	36	72.0	133	9	US-09-764-853-451	Sequence 451, App
24	36	72.0	133	14	US-10-125-540-324	Sequence 324, App
25	36	72.0	133	14	US-10-103-313-296	Sequence 296, App
26	36	72.0	133	15	US-10-158-057-176	Sequence 176, App
27	36	72.0	201	9	US-09-978-295A-477	Sequence 477, App
28	36	72.0	201	9	US-09-978-697-477	Sequence 477, App
29	36	72.0	201	9	US-09-978-192A-477	Sequence 477, App
30	36	72.0	201	9	US-09-999-832A-477	Sequence 477, App
31	36	72.0	201	10	US-09-978-189-477	Sequence 477, App
32	36	72.0	201	10	US-09-978-608A-477	Sequence 477, App
33	36	72.0	201	10	US-09-978-585A-477	Sequence 477, App
34	36	72.0	201	10	US-09-978-191A-477	Sequence 477, App
35	36	72.0	201	10	US-09-978-403A-477	Sequence 477, App
36	36	72.0	201	10	US-09-978-564A-477	Sequence 477, App
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39	36	72.0	201	10	US-09-978-824-477	Sequence 477, App
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42	36	72.0	201	10	US-09-978-423A-477	Sequence 477, App
43	36	72.0	201	10	US-09-978-193A-477	Sequence 477, App
44	36	72.0	201	10	US-09-999-830A-477	Sequence 477, App
45	36	72.0	201	10	US-09-978-757A-477	Sequence 477, App

ALIGNMENTS

RESULT 1
US-09-761-636A-10
; Sequence 10, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-10

Query Match 100.0%; Score 50; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
DB 1 CSVPLTSVC 9

RESULT 2
US-10-424-599-241613

; Sequence 241613, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 241613
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_60203C.1.pap
US-10-424-599-241613

Query Match 84.0%; Score 42; DB 15; Length 154;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
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Db 22 CSSPITSVC 30

RESULT 3

US-10-424-599-241616
; Sequence 241616, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 241616
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_60206C.1.pap
US-10-424-599-241616

Query Match 84.0%; Score 42; DB 15; Length 194;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
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Db 66 CSSPITSVC 74

RESULT 4

US-10-424-599-206581
; Sequence 206581, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 206581
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_28570C.1.pap
US-10-424-599-206581

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Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSVPLTSVC 9
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Db 57 CSSPITSVC 65

RESULT 5

US-10-767-701-54625
; Sequence 54625, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 54625
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 14570883.pap
US-10-767-701-54625

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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSVPLTSV 8
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Db 11 CSVPLTSV 18

RESULT 6

US-10-424-599-174316
; Sequence 174316, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 174316
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure

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; LOCATION: (1)...(359)
; OTHER INFORMATION: unsure at all Xaa locations
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_128426C.1.pep
US-10-424-599-174316

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Best Local Similarity 100.0%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CSVPLTSVC 8
DB      151 CSVPLTSVC 158

RESULT 7
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; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 205890
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_27947C.1.pep
US-10-424-599-205890

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Best Local Similarity 66.7%; Pred. No. 76;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 CSVPLTSVC 9
DB      66 CSSPITSIC 74

RESULT 8
US-10-425-114-69391
; Sequence 69391, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 69391
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-GMROPIC11B04_FLI.pep
US-10-425-114-69391

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Best Local Similarity 66.7%; Pred. No. 78;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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RESULT 9
US-10-437-963-133870
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; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 133870
; LENGTH: 883
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_3569C.1.pep
US-10-437-963-133870

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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CSVPLTSVC 8
DB      655 CSVPLTSVC 662

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; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 276101
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_91339C.1.pep
US-10-424-599-276101

Query Match      78.0%; Score 39; DB 15; Length 63;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 CSVPLTSVC 9
DB      111 CSSPITSIC 111
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Db          9  CSSPLSSIC 17

RESULT 11
US-10-369-493-1081
; Sequence 1081, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1081
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Methanococcus jannaschii
US-10-369-493-1081

Query Match      78.0%; Score 39; DB 15; Length 432;
Best Local Similarity 77.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  CSVPLTSVC 9
Db      389  CVPPLTSFC 397

RESULT 12
US-10-767-701-51825
; Sequence 51825, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 51825
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB5048-009-R1-XP1-B3.pep
US-10-767-701-51825

Query Match      76.0%; Score 38; DB 16; Length 67;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1  CSVPLTSVC 9
Db      56  CSSPLTALC 64

RESULT 13
US-09-833-245-888
; Sequence 888, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.

; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PFS46PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 888
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-888

Query Match      76.0%; Score 38; DB 11; Length 802;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1  CSVPLTSVC 9
Db      786  CSVPLTDEC 794

RESULT 14
US-10-424-599-169061
; Sequence 169061, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 169061
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_123677C.1.pep
US-10-424-599-169061

Query Match      74.0%; Score 37; DB 15; Length 82;
Best Local Similarity 66.7%; Pred. No. 58;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1  CSVPLTSVC 9
Db      50  CSPPLTATC 58

RESULT 15
US-10-424-599-276082
; Sequence 276082, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
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; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 276082
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(95)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_91321C.1.pap
US-10-424-599-276082

Query Match          74.0%; Score 37; DB 15; Length 95;
Best Local Similarity 66.7%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 CSVPLTSVC 9
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Db      1 CSVPTGLC 9

Search completed: April 1, 2005, 10:36:34
Job time : 222.178 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 06:17:29 ; Search time 15.9726 Seconds
(without alignments)
66.262 Million cell updates/sec

Title: US-09-761-636A-7
Perfect score: 61
Sequence: 1 CISVPLTSVPC 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: Pirl: *
2: Pirl2: *
3: Pirl3: *
4: Pirl4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	39	63.9	151	2 PQ0506	hypothetical prote
2	39	63.9	169	2 A72466	hypothetical prote
3	39	63.9	207	2 I47061	collagenase inhibi
4	39	63.9	925	2 T29311	hypothetical prote
5	39	63.9	1062	2 T46444	hypothetical prote
6	38	62.3	324	2 T31992	hypothetical prote
7	38	62.3	503	2 S62018	probable membrane
8	38	62.3	616	2 T29234	hypothetical prote
9	38	62.3	1829	2 T34239	hypothetical prote
10	37	60.7	184	2 B96814	hypothetical prote
11	37	60.7	527	2 H85135	hypothetical prote
12	37	60.7	583	2 F70592	probable lipq8 prot
13	37	60.7	788	2 G64707	cation-transportin
14	37	60.7	788	2 E71813	probable component
15	37	60.7	1787	2 T20160	hypothetical prote
16	36	59.0	165	2 B72727	hypothetical prote
17	36	59.0	174	2 JV0046	hypothetical 18K p
18	36	59.0	261	2 T16392	hypothetical prote
19	36	59.0	533	2 T46975	lysine-tRNA ligase
20	36	59.0	534	2 C64367	hypothetical prote
21	36	59.0	954	2 G711496	hypothetical prote
22	35	57.4	112	2 E72785	hypothetical prote
23	35	57.4	119	2 A59047	phospholipase A2 (
24	35	57.4	207	1 A35685	metalloproteinase
25	35	57.4	207	2 I46964	metalloproteinase
26	35	57.4	296	2 T34460	hypothetical prote
27	35	57.4	302	2 B81696	4-hydroxybenzoate
28	35	57.4	308	2 T29756	hypothetical prote
29	35	57.4	342	2 T25143	hypothetical prote

30	35	57.4	354	2 T31861	hypothetical prote
31	35	57.4	363	2 T02522	origin recognition
32	35	57.4	403	2 C75405	streptomycin biosy
33	35	57.4	410	2 T19995	hypothetical prote
34	35	57.4	457	2 B84725	probable glucosylt
35	35	57.4	537	2 T48599	hypothetical prote
36	35	57.4	756	2 T20109	hypothetical prote
37	35	57.4	790	2 T25095	hypothetical prote
38	35	57.4	970	2 D59435	Gem-interacting pr
39	35	57.4	1099	2 T16283	hypothetical prote
40	35	57.4	3014	1 JC5620	genome polypoteine
41	34.5	56.6	1246	2 T00826	hypothetical prote
42	34.5	56.6	1816	2 A84845	probable ABC trans
43	34	55.7	61	2 H90901	probable lipoprote
44	34	55.7	61	2 C90971	probable lipoprote
45	34	55.7	76	2 JE0003	hypothetical 8.6K

ALIGNMENTS

RESULT 1

PQ0506
hypothetical protein 151 - fowlpox virus (fragment)
N:Alternate names: ORF3 protein
C:Species: fowlpox virus
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C:Accession: PQ0506; S27935
R:Ogawa, R.; Calvert, J.G.; Yanagida, N.; Nazarian, K.
J. Gen. Virol. 74, 55-64, 1993
A:Title: Insertional inactivation of a fowlpox virus homologue of the vaccinia virus F121
A:Reference number: JQ1894; MUID:93139784; PMID:8380837
A:Accession: PQ0506
A:Molecule type: DNA
A:Residues: 1-151 <OGA>
A:Cross-references: UNIPROT:P36700; GB:M88588; NID:G333522; PIDN:AAA47188.1; PID:G333525
A:Note: submitted to the EMBL Data Library, May 1992

Query Match 63.9%; Score 39; DB 2; Length 151;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 CISVPLTSVP 10
||:|:|:
DB 90 CINTPIDSIP 99

RESULT 2

A72466
hypothetical protein APE2372 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: A72466
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kawa
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: A72466
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-169 <KAW>
A:Cross-references: UNIPROT:Q9Y9B5; DDBJ:AP000064; NID:G5105945; PIDN:BAA81385.1; PID:d1
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE2372

Query Match 63.9%; Score 39; DB 2; Length 169;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CISVPLTSVP 10
||:|:|:

Db 57 CIGIPVASVP 66

RESULT 3

I47061
collagenase inhibitor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C:Accession: I47061
R:Tanaka, T.; Andoh, N.; Takeya, T.; Sato, E.
Mol. Cell. Endocrinol. 83, 65-71, 1992
A:Title: Differential screening of ovarian cDNA libraries detected the expression of the
A:Reference number: I47061; MUID:92201478; PMID:1312961
A:Accession: I47061
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-207 <TAN>
A:Cross-references: UNIPROT:P35624; GB:S96211; NID:g247729; PIDN:AA821865.1; PID:g247730
C:Superfamily: metalloproteinase inhibitor

Query Match 63.9%; Score 39; DB 2; Length 207;
Best Local Similarity 54.5%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CISVPLTSVPC 11
| | | | |
Db 150 CTVFPCTSIPT 160

RESULT 4

T29311
hypothetical protein F36D4.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T29311
R:Pauley, A.; Gattung, S.
submitted to the EMBL Data Library, March 1996
A:Description: The sequence of C. elegans cosmid F36D4.
A:Reference number: Z20603
A:Accession: T29311
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-925 <PAU>
A:Cross-references: EMBL:U53181; PIDN:AAA93485.1; GSPDB:GN00023; CESP:F36D4.3
A:Experimental source: strain Bristol N2; clone F36D4
C:Genetics:
A:Gene: CESP:F36D4.3
A:Map position: 5
A:Introns: 24/3; 56/2; 103/3; 187/1; 387/2; 429/3; 455/3; 516/1; 555/1; 782/2; 882/3

Query Match 63.9%; Score 39; DB 2; Length 925;
Best Local Similarity 50.0%; Pred. No. 64;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVPLTSVPC 11
| | | | |
Db 2 VSLPMSNVPC 11

RESULT 5

T46444
hypothetical protein DKFZp434N1427.1 - human
C:Species: Homo sapiens (man)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46444
R:Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wienann, S.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23032
A:Accession: T46444
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1062 <AAA>
A:Cross-references: UNIPROT:Q9NSW2; EMBL:AL137701

A:Experimental source: adult testis; clone DKFZp434N1427
C:Genetics:
A:Note: DKFZp434N1427.1

Query Match 63.9%; Score 39; DB 2; Length 1062;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SVPLTSVPC 11
| | | | |
Db 25 SIPLSSTPC 33

RESULT 6

T31992
hypothetical protein C49D10.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31992
R:Henkhaus, J.; Wohldmann, P.; Beck, C.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid C49D10.
A:Reference number: Z21108
A:Accession: T31992
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-324 <HEN>
A:Cross-references: UNIPROT:O16608; EMBL:AF016665; PIDN:AAC71178.1; GSPDB:GN00020; CESP:(
A:Experimental source: strain Bristol N2; clone C49D10
C:Genetics:
A:Gene: CESP:C49D10.3
A:Map position: 2
A:Introns: 105/1
C:Superfamily: Caenorhabditis hypothetical protein C49G7.2

Query Match 62.3%; Score 38; DB 2; Length 324;
Best Local Similarity 54.5%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CISVPLTSVPC 11
| | | | |
Db 70 CIGVYLHPC 80

RESULT 7

S62018
probable membrane protein YDR539w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein D3703.2
C:Species: Saccharomyces cerevisiae
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: S62018
R:Dietrich, F.S.; Mulligan, J.; Allen, E.; Araujo, R.; Aviles, E.; Berno, A.; Carpenter, H.; Lin, D.; Mosedale, D.; Nakahara, K.; Namath, A.; Oefner, P.; Oh, C.; Petel, F.X.; Ro
W.
submitted to the EMBL Data Library, December 1995
A:Reference number: S62017
A:Accession: S62018
A:Molecule type: DNA
A:Residues: 1-503 <DIE>
A:Cross-references: UNIPROT:Q03034; EMBL:U43834; NID:g1165292; PID:g1165294; GSPDB:GN0000
C:Genetics:
A:Gene: MIPS:YDR539w
A:Cross-references: SGD:S0002947
A:Map position: 4R
C:Superfamily: conserved hypothetical protein sll0936
C:Keywords: transmembrane protein
F:210-226/Domain: transmembrane #status predicted <TMM>

Query Match 62.3%; Score 38; DB 2; Length 503;
Best Local Similarity 60.0%; Pred. No. 54;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISVPLTSVPC 11
 Db 115 IIVPVSSAPC 124

RESULT 8
 T29234
 hypothetical protein F55G1.13 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T29234
 R:Murray, J.; Le, T.T.
 submitted to the EMBL Data Library, May 1996
 A:Description: The sequence of C. elegans cosmid F55G1.
 A:Reference number: Z20591
 A:Accession: T29234
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-616 <MUR>
 A:Cross-references: UNIPROT:Q20852; EMBL:U58750; PIDN:AAB00653.1; GSPDB:GN000022; CESP:F55G1
 A:Experimental source: strain Bristol N2; clone F55G1
 C:Genetics:
 A:Gene: CESP:F55G1.13
 A:Map position: 4
 A:Introns: 98/1; 136/1; 230/1; 256/1; 363/1; 401/1; 443/1; 484/1; 528/2; 551/3

Query Match 62.3%; Score 38; DB 2; Length 616;
 Best Local Similarity 54.5%; Pred. No. 65;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CISVPLTSVPC 11
 Db 362 CVGNPCTSEPC 372

RESULT 9
 T34239
 hypothetical protein F26F12.7 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T34239
 R:Wilson, R.; Bentley, D.; Gattung, S.
 submitted to the EMBL Data Library, April 1996
 A:Description: The sequence of C. elegans cosmid F26F12.
 A:Reference number: Z21493
 A:Accession: T34239
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-1829 <WIL>
 A:Cross-references: UNIPROT:Q19815; EMBL:U55373; PIDN:AAC25894.1; GSPDB:GN000023; CESP:F26F12
 A:Experimental source: strain Bristol N2; clone F26F12
 C:Genetics:
 A:Gene: CESP:F26F12.7
 A:Map position: 5
 A:Introns: 110/3; 441/3; 801/2; 1244/3; 1693/2; 1784/1

Query Match 62.3%; Score 38; DB 2; Length 1829;
 Best Local Similarity 70.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CISVPLTSVPC 10
 Db 343 CIDPPLTEVP 352

RESULT 10
 B96814
 hypothetical protein T30F21.11 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana [mouse-ear cross]
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: B96814
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Palmer, N.A.; Kaul, S.; White, O.; Alonso, J.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.-C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: B96814
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-184 <STO>
 A:Cross-references: UNIPROT:Q9SYM6; GB:AE005173; NID:g4836878; PIDN:AAD30581.1; GSPDB:GN000023
 C:Genetics:
 A:Gene: T30F21.11
 A:Map position: 1

Query Match 60.7%; Score 37; DB 2; Length 184;
 Best Local Similarity 85.7%; Pred. No. 30;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLTSVPC 11
 Db 150 PLTAVPC 156

RESULT 11
 H85135
 hypothetical protein AT4G12650 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cross)
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C:Accession: H85135
 R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Harbor Laboratory
 A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
 A:Reference number: A85001; MUID:20083488; PMID:10617198
 A:Accession: H85135
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-527 <STO>
 A:Cross-references: UNIPROT:Q9SU21; GB:NC_001268; NID:g7267967; PIDN:CAB78308.1; GSPDB:GN000023
 C:Genetics:
 A:Gene: AT4G12650
 A:Map position: 4

Query Match 60.7%; Score 37; DB 2; Length 527;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CISVPLT 7
 Db 344 CISVPLT 350

RESULT 12
 F70592
 probable lpgB protein - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C:Accession: F70592
 R:Col, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.
 A:Reference number: A70500; MUID:98295987; PMID:9634230
 A:Accession: F70592
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-583 <COL>
 A:Cross-references: UNIPROT:O05989; GB:Z95121; GB:AL123456; NID:g3261742; PIDN:CAB08345.1

A:Experimental source: strain H37Rv

C:Genetics:

A:Gene: lpqB

Query Match 60.7%; Score 37; DB 2; Length 583;
Best Local Similarity 70.0%; Pred. No. 93;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CISVPLTSVP 10
|||||
Db 16 CASVPSTAP 25

RESULT 13

G64707
cation-transporting ATPase, P-type - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: G64707
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; PMID:97394467; PMID:9252185
A:Accession: G64707
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-788 <TOM>
A:Cross-references: UNIPROT:Q26033; GB:AE000648; GB:AE000511; NID:G2314570; PIDN:AAD0853
C:Superfamily: Enterococcus copper-transporting ATPase copA; ATPase nucleotide-binding domain F218-547/Domain: ATPase transduction domain homology <ATT>
F:612-750/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 60.7%; Score 37; DB 2; Length 788;
Best Local Similarity 63.6%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CISVPLTSVPC 11
|||||

Db 456 CISVLVISCPC 466

RESULT 14

E71813
probable component of cation transport for cbb3-type oxidase - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: E71813
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Werberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.
A:Reference number: A71800; PMID:99120557; PMID:9923682
A:Accession: E71813
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-788 <ARN>
A:Cross-references: UNIPROT:Q9ZJB7; GB:AE001561; GB:AE001439; NID:G4156000; PIDN:AAD0696
A:Experimental source: strain J99
C:Genetics:
A:Gene: fixI

C:Superfamily: Enterococcus copper-transporting ATPase copA; ATPase nucleotide-binding domain F:612-750/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 60.7%; Score 37; DB 2; Length 788;
Best Local Similarity 63.6%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CISVPLTSVPC 11
|||||

Db 456 CISVLVISCPC 466

RESULT 15

T20160
hypothetical protein T14G8.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T20160; T24924
R:McMurray, A.
submitted to the EMBL Data Library, November 1995
A:Reference number: Z19231
A:Accession: T20160
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1787 <WIL>
A:Cross-references: UNIPROT:Q22516; EMBL:Z67881; PIDN:CAA91798.1; GSPDB:GN00028; CESP:T14
A:Experimental source: clone C52G5
R:Matthews, P.
submitted to the EMBL Data Library, November 1995
A:Reference number: Z19955
A:Accession: T24924
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1787 <WI2>
A:Cross-references: EMBL:Z67884; PIDN:CAA91810.1; GSPDB:GN00028; CESP:T14G8.1
A:Experimental source: clone T14G8
C:Genetics:
A:Gene: CESP:T14G8.1
A:Map position: X
A:Introns: 112/3; 453/3; 597/3; 815/2; 1258/3; 1682/2; 1709/3; 1764/1

Query Match 60.7%; Score 37; DB 2; Length 1787;
Best Local Similarity 60.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CISVPLTSVP 10
|||||

Db 354 CIDPPLTEIP 363

Search completed: April 1, 2005, 09:33:24

Job time : 17.9726 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 03:33:32 ; Search time 67.3562 Seconds
(without alignments)
83.628 Million cell updates/sec

Title: US-09-761-636A-7

Perfect score: 61

Sequence: 1 CISVPLTSVPC 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	43	70.5	2 Q9GLX1	Q9GLX1 bos taurus
2	43	70.5	123 Q695V0	Q695V0 felis silve
3	43	70.5	2 Q8QGD7	Q8QGD7 gallus gall
4	43	70.5	4 VEGD RAT	O35251 rattus norv
5	43	70.5	2 Q91ZE4	Q91ZE4 rattus norv
6	43	70.5	354 Q43915	Q43915 homo sapien
7	43	70.5	1 VEGD_MOUSE	P97946 mus musculu
8	42	68.9	2 Q9GUB7	Q9GUB7 caenorhabdi
9	41	67.2	2 Q8C7W1	Q8C7W1 mus musculu
10	40	65.6	80 Q6UVX0	Q6UVX0 homo sapien
11	40	65.6	2 Q9NFP3	Q9NFP3 leishmania
12	40	65.6	346 Q6YUH8	Q6YUH8 oryza sativ
13	40	65.6	474 Q8VIA1	Q8VIA1 mus musculu
14	40	65.6	631 Q6CD98	Q6CD98 yarrowia li
15	40	65.6	782 Q921H6	Q921H6 mus musculu
16	40	65.6	2 Q8VDF2	Q8VDF2 mus musculu
17	39	63.9	169 Q9Y9B5	Q9Y9B5 aeropyrum p
18	39	63.9	207 Q1M1_PIG	P35624 sus scrofa
19	39	63.9	278 Q6W040	Q6W040 mus musculu
20	39	63.9	2 Q9PY69	Q9PY69 soybean mos
21	39	63.9	326 Q7R5W3	Q7R5W3 giardia lam
22	39	63.9	366 Q7U7P2	Q7U7P2 synechococ
23	39	63.9	386 Q7V6T2	Q7V6T2 prochloroco
24	39	63.9	451 Q1V10_FOMPV	P36700 fowlpox vir
25	39	63.9	451 Q2OH45	Q2OH45 fowlpox vir
26	39	63.9	500 Q8NA51	Q8NA51 homo sapien
27	39	63.9	524 Q6PF16	Q6PF16 homo sapien
28	39	63.9	2 Q9XQ05	Q9XQ05 oryza sativ
29	39	63.9	665 Q69F01	Q69F01 oryza sativ
30	39	63.9	707 Q8BW61	Q8BW61 m mus muscu
31	39	63.9	737 Q8BW83	Q8BW83 m mus muscu

32	39	63.9	817 Q7NUH5	Q7NUH5 chromobacte
33	39	63.9	925 Q8HXK6	Q8HXK6 macaca fasc
34	39	63.9	1062 Q9NSW2	Q9NSW2 homo sapien
35	39	63.9	1411 Q96QW6	Q96QW6 homo sapien
36	39	63.9	1513 Q9HDV4	Q9HDV4 schizosacch
37	39	63.9	1723 Q9V4K1	Q9V4K1 homo sapien
38	38	62.3	91 Q7T3K0	Q7T3K0 oncorhynch
39	38	62.3	207 Q09411	Q09411 arthroderma
40	38	62.3	318 Q86691	Q86691 hepatitis c
41	38	62.3	324 Q16608	Q16608 caenorhabdi
42	38	62.3	362 Q76LA9	Q76LA9 spinacia ol
43	38	62.3	425 Q8L424	Q8L424 arabidopsis
44	38	62.3	461 Q7Q5T5	Q7Q5T5 anopheles g
45	38	62.3	503 QY39_YEAST	QY39_YEAST

ALIGNMENTS

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RESULT 1
Q9GLX1
ID Q9GLX1 PRELIMINARY; PRT; 122 AA.
AC Q9GLX1;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Vascular endothelial growth factor-D (Fragment).
GN Name=VEGF-D;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Mandriota S.J., Pepper M.S.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF099135; AAG29747.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR0004153; P:cell growth and/or maintenance; IEA.
DR Pfam; PF03128; CXCXC; 2.
DR ProDom; PD001629; PD_growth_factor; 1.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 13820 MW; CC504B00E29D54EB CRC64;

Query Match 70.5%; Score 43; DB 2; Length 122;
Best Local Similarity 100.0%; Pred.No. 6.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVPLTSVP 10
Db |||||
1 ISVPLTSVP 9

RESULT 2
Q695V0
ID Q695V0 PRELIMINARY; PRT; 123 AA.
AC Q695V0;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DE C-fos induced growth factor (Fragment).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
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QY      2  ISVPLTSVP 10
Db      173 ISVPLTSVP 181

RESULT 5
Q91ZE4  PRELIMINARY; PRT; 326 AA.
ID Q91ZE4
AC Q91ZE4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE VEGF-D.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21541129; PubMed=11683876;
RA Kirkin V., Mazitschek R., Krishnan J., Steffen A., Waltenberger J.,
RA Pepper M.S., Giannis A., Sleeman J.P.;
RT "Characterization of indolinones which preferentially inhibit VEGF-C-
RT and VEGF-D-induced activation of VEGFR-3 rather than VEGFR-2.";
RL Eur. J. Biochem. 268:5530-5540(2001).
CC -!- SIMILARITY: Belongs to the PDGFR/VEGF growth factor family.
DR EMBL; AY032728; AAK96008.1; -.
DR HSSP; P01127; 1PDG.
DR GO; GO:0016020; Cmembrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF_1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Growth factor; Mitogen.
SQ SEQUENCE 326 AA; 37106 MW; D7CAEBA6C9FABB7D CRC64;

Query Match 70.5%; Score 43; DB 2; Length 326;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  ISVPLTSVP 10
Db      173 ISVPLTSVP 181

RESULT 6
VEGD_HUMAN
ID VEGD_HUMAN STANDARD; PRT; 354 AA.
AC O43915;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
DE growth factor) (FIGF).
GN Name=FIGF; Synonyms=VEGFD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=97349118; PubMed=9205122; DOI=10.1006/geno.1997.4774;
RA Yamada Y., Nezu J.-I., Shimane M., Hirata Y.;
RT "Molecular cloning of a novel vascular endothelial growth factor,
RT VEGF-D.";
RL Genomics 42:483-488(1997).

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RN SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=98140120; PubMed=9479493; DOI=10.1006/geno.1997.5079;
RA Rocchigiani M., Lestingi M., Luddi A., Orlandini M., Franco B.,
RA Rosi E., Ballabio A., Zuffardi O., Oliviero S.;
RT "Human FIGF: cloning, gene structure, and mapping to chromosome Xp22.1
RT between the FIGA and the GRPR genes.";
RL Genomics 47:207-216(1998).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98118549; PubMed=9435229; DOI=10.1073/pnas.95.2.548;
RA Achen M.G., Jeltsch M., Kukk E., Mäkinen T., Vitali A., Wilks A.F.,
RA Altalero K., Stacker S.A.;
RT "Vascular endothelial growth factor D (VEGF-D) is a ligand for the
RT tyrosine kinases VEGF receptor 2 (Flk1) and VEGF receptor 3 (Flt4).";
RL Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
RA Schenck A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP PROCESSING, AND SEQUENCE OF 89-94; 100-105 AND 206-213.
RX MEDLINE=20011413; PubMed=10542248; DOI=10.1074/jbc.274.45.32127;
RA Stacker S.A., Stenvers K.L., Caesar C., Vitali A., Domagala T.,
RA Nice E.C., Roufail S., Simpson R.J., Moritz R., Karpanen T.,
RA Alitalo K., Achen M.G.;
RT "Biosynthesis of vascular endothelial growth factor-D involves
RT proteolytic processing which generates non-covalent homodimers.";
RL J. Biol. Chem. 274:32127-32136(1999).
CC -!- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
CC and endothelial cell growth, stimulating their proliferation and
CC migration and also has effects on the permeability of blood
CC vessels. May function in the formation of the venous and lymphatic
CC vascular systems during embryogenesis, and also in the maintenance
CC of differentiated lymphatic endothelium in adults. Binds and
CC activates VEGFR-2 (Flk1) and VEGFR-3 (Flt4) receptors.
CC -!- SUBUNIT: Homodimer; non-covalent and antiparallel.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Highly expressed in lung, heart, small
CC intestine and fetal lung, and at lower levels in skeletal muscle,
CC colon, and pancreas.
CC -!- PTM: Undergoes a complex proteolytic maturation which generates a
CC variety of processed secreted forms with increased activity toward
CC VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer
CC linked by disulfide bonds before secretion. The fully processed
CC VEGF-D is composed mostly of two VEGF homology domains (VHDs)
CC bound by non-covalent interactions.
CC -!- SIMILARITY: Belongs to the PDGFR/VEGF growth factor family.
CC -----
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CC -----
DR EMBL; D89630; BAA24264.1; -.
DR EMBL; Y12863; CAAT73370.1; -.
DR EMBL; Y12864; CAAT73371.1; -.
DR EMBL; Y12865; CAAT73371.1; JOINED.
DR EMBL; Y12866; CAAT73371.1; JOINED.
DR EMBL; Y12867; CAAT73371.1; JOINED.
DR EMBL; Y12868; CAAT73371.1; JOINED.
DR EMBL; Y12869; CAAT73371.1; JOINED.
DR EMBL; Y12870; CAAT73371.1; JOINED.
DR EMBL; AJ000185; CAA03942.1; -.
DR EMBL; BC027948; AAH27948.1; -.
DR HSSP; P01127; 1PDG.
DR Genew; HGNC:3708; FIGF.
DR H-InvdB; HIX0016668; -.
DR MIM; 300091; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005161; F:platelet-derived growth factor receptor bin. .; TAS.
DR GO; GO:0005102; F:receptor binding; TAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR InterPro; IPR0004153; CXKCXC_repeat.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF03128; CXKC; 3.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS02278; PDGF_2; 1.
DR Angiogenesis; Cleavage on pair of basic residues;
KW Direct protein sequencing; Glycoprotein; Growth factor; Mitogen;
KW Multigene family; Repeat; Signal.
FT SIGNAL 1 21
FT PROPEP 22 88
FT CHAIN 89 205
FT PROPEP 206 354
FT DOMAIN 222 318
FT REPEAT 222 237
FT REPEAT 258 273
FT REPEAT 277 293
FT REPEAT 301 318
FT DISULFID 111 153
FT DISULFID 142 189
FT DISULFID 146 191
FT DISULFID 136 136
FT DISULFID 145 145
FT CARBOHYD 155 155
FT CARBOHYD 185 185
FT CARBOHYD 287 287
SQ SEQUENCE 354 AA; 40444 MW; 2048D769D735173E CRC64;

Query Match 70.5%; Score 43; DB 1; Length 354;
Best Local Similarity 100.0%; Pred.No. 21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVPLTSVP 10
DB 168 ISVPLTSVP 176

RESULT 7
VEGD_MOUSE
ID VEGD_MOUSE STANDARD; PRT; 358 AA.
AC P97946;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Vascular endothelial growth factor D precursor (VEGFD-D) (c-fos induced
PE growth factor) (FIGF).

```

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GN Name=Figf; Synonym=Vegfd;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Fibroblast;
RC MEDLINE=97030254; PubMed=8876195; DOI=10.1073/pnas.93.21.11675;
RA Orlandini M., Marconcini L., Ferruzzi R., Oliviero S.;
RT "Identification of a c-fos-induced gene that is related to the
RT platelet-derived growth factor/vascular endothelial growth factor
RT family.";
RT Proc. Natl. Acad. Sci. U.S.A. 93:11675-11680(1996).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Lung;
RC MEDLINE=97349118; PubMed=9205122; DOI=10.1006/geno.1997.4774;
RA Yamada Y., Nezu J.-I., Shimane M., Hirata Y.;
RT "Molecular cloning of a novel vascular endothelial growth factor,
RT VEGF-D.";
RT Genomics 42:483-488(1997).
[3]
RN DEVELOPMENTAL STAGE.
RP MEDLINE=98288130; PubMed=9622638; DOI=10.1016/S0925-4773(98)00049-5;
RA Avantaggiato V., Orlandini M., Acampora D., Oliviero S., Simeone A.;
RT "Embryonic expression pattern of the murine figf gene, a growth factor
RT belonging to platelet-derived growth factor/vascular endothelial
RT growth factor family.";
RT Mech. Dev. 73:221-224(1998).
[4]
RN RECEPTOR SPECIFICITY.
RP MEDLINE=21276411; PubMed=11279005; DOI=10.1074/jbc.M100097200;
RA Baldwin M.E., Catimel B., Nice E.C., Roufail S., Hall N.E.,
RA Stevens K.L., Karhainen M.J., Alitalo K., Stacker S.A., Achen M.G.;
RT "The specificity of receptor binding by vascular endothelial growth
RT factor-d is different in mouse and man.";
RT J. Biol. Chem. 276:19166-19171(2001).
CC -!- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
CC and endothelial cell growth, stimulating their proliferation and
CC migration and also has effects on the permeability of blood
CC vessels. May function in the formation of the venous and lymphatic
CC vascular systems during embryogenesis, and also in the maintenance
CC of differentiated lymphatic endothelium in adults. Binds and
CC activates VEGFR-3 (Flt4) receptor.
CC -!- SUBUNIT: Homodimer; non-covalent and antiparallel.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Highly expressed in fetal and adult lung.
CC -!- DEVELOPMENTAL STAGE: Expressed in a dynamic pattern in several
CC body structures and organs of the embryo such as limb buds,
CC acoustic ganglion, teeth, heart, anterior pituitary as well as
CC lung and kidney mesenchyme, liver, derma, and perosteum of the
CC vertebral column.
CC -!- INDUCTION: By the transcription factor c-fos.
CC -!- PTM: Undergoes a complex proteolytic maturation which generates a
CC variety of processed secreted forms with increased activity toward
CC VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer
CC linked by disulfide bonds before secretion. The fully processed
CC VEGF-D is composed mostly of two VEGF homology domains (VHDs)
CC bound by non-covalent interactions (By similarity).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
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or send an email to license@isb-sib.ch).
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EMBL; X99572; CAA67892.1; -.
EMBL; D89628; BAA14002.1; -.
HSSP; P01127; 1PDG.

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DR PMMA-2DPAGE; P97946; -.
DR MGD; MGI:108037; Figf.
DR GO; GO:0005576; C:extracellular; IDA.
DR GO; GO:0008083; F:growth factor activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0008283; P:cell proliferation; IDA.
DR InterPro; IPR004153; CXKC repeat.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF03128; CXKC; 2.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Angiogenesis; Cleavage on pair of basic residues; Glycoprotein;
KW Growth factor; Mitogen; Multigene family; Repeat; Signal.
FT SIGNAL 1 21
FT PROPEP 22 93
FT CHAIN 94 210
FT PROPEP 211 358
FT DOMAIN 227 323
FT REPEAT 227 242
FT REPEAT 263 278
FT REPEAT 282 298
FT REPEAT 306 323
FT DISULFID 116 158
FT DISULFID 147 194
FT DISULFID 151 196
FT DISULFID 141 141
FT DISULFID 150 150
FT CARBOHYD 160 160
FT CARBOHYD 190 190
FT CARBOHYD 292 292
SQ SEQUENCE 358 AA; 40908 MW; 6636B17FBF07037C CRC64;

Query Match 70.5%; Score 43; DB 1; Length 358;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVPLTSVP 10
DB 173 ISVPLTSVP 181
ID Q9GUB7 PRELIMINARY; PRT; 348 AA.
AC Q9GUB7
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Serpentine receptor, class h protein 92.
GN Name=arh-92; ORFNames=F25E5.13;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R., Bradshaw H.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
[3]

RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF078157; AAG24081.1; -.
DR WormBase; WBGene00005313; F25E5.13.
DR WormPep; F25E5.13; CE24915.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003003; 7TM_chemrecept.
DR InterPro; IPR000168; Nm7TM_chemrecept.
DR Pfam; PF01604; 7tm_5; 1.
KW Receptor.
SQ SEQUENCE 348 AA; 39882 MW; 456DEC8833CF3176 CRC64;

Query Match 68.9%; Score 42; DB 2; Length 348;
Best Local Similarity 54.5%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CISVPLTSVPC 11
DB 33 CISVPLTSVPC 43
ID Q8C7W1 PRELIMINARY; PRT; 118 AA.
AC Q8C7W1
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mus musculus ES cells cDNA, RIKEN full-length enriched library,
DE clone:C330008L01 product:hypothetical protein, full insert
DE sequence.
GN Name=C330008L01rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA The FANTOM Consortium,

```

RESULT 12	
Q6YUH8	
ID	Q6YUH8
AC	PRELIMINARY; PRT; 346 AA.
DT	Q6YUH8; 2004
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Hypothetical protein P066E12.10 (Hypothetical protein
DE	P0459B01.2).

GN Name=P0666E12.10; Synonyms=P0459B01.2;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF005868; BAD08173.1; -;
DR EMBL; AF004778; BAD07857.1; -;
KW Hypothetical protein.
SQ SEQUENCE 346 AA; 37266 MW; 411ED95C7021A216 CRC64;
Query Match 65.6%; Score 40; DB 2; Length 346;
Best Local Similarity 63.6%; Pred. No. 72;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 CISVPLTSVPC 11
DB 197 CANVPLVSVSC 207
RESULT 13
QVIAL PRELIMINARY; PRT; 474 AA.
ID Q8VIAL;
AC Q8VIAL;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE NP95 (Fragment).
GN Name=np95;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22206529; PubMed=12084726; DOI=10.1074/jbc.M205199200;
RA Muto M., Kanari Y., Kubo E., Takabe T., Kurihara T., Fujimori A.,
RA Tatsumi K.;
RT "Targeted disruption of Np95 gene renders murine embryonic stem cells
RT hypersensitive to DNA damaging agents and DNA replication blocks.";
RL J. Biol. Chem. 277:34549-34555(2002).
DR EMBL; AB066245; BAB79496.1; -;
DR HSP; Q9UIG0; 1F62.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF00628; PHD; 1.
DR Pfam; PF02240; ubiquitin; 1.
DR Pfam; PF02182; YDC_SRA; 1.
DR PRINTS; PR00348; UBIQUITIN.
DR SMART; SM00249; PHD; 1.
DR SMART; SM00213; UBQ; 1.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
DR PROSITE; PS00053; UBIQUITIN_2; 1.
DR PROSITE; PS01359; ZF_PHD_1; UNKNOWN_1.
DR PROSITE; PS00016; ZF_PHD_2; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
FT NON TER 474 474
SQ SEQUENCE 474 AA; 53685 MW; 0EAE841CCD8C7FEA CRC64;
Query Match 65.6%; Score 40; DB 2; Length 474;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 CISVPLTSVP 10
DB 349 CLKPLTSVP 358
RESULT 14
Q6CD98 PRELIMINARY; PRT; 631 AA.
AC Q6CD98;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Yarrowia lipolytica chromosome C of strain CL1899 of Yarrowia
DE lipolytica.
GN ORFNames=YALIO02541g;
OS Yarrowia lipolytica CL1899.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CL1899;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swenene D., Tekaiia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpetti C., Gaillardin C., Weissenbach J.,
RA Winkler P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CL1899;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382129; CAG81663.1; -; F81FBCB97476B6EB CRC64;
SQ SEQUENCE 631 AA; 70478 MW; F81FBCB97476B6EB CRC64;
Query Match 65.6%; Score 40; DB 2; Length 631;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 CISVPLTSVP 10
DB 243 CITVFWVSIP 252
RESULT 15
Q9ZIH6 PRELIMINARY; PRT; 782 AA.
AC Q9ZIH6;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Nuclear protein np95 (Nuclear zinc finger protein Np95).
GN Name=Uhrfl; Synonyms=Np95;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE-Pre-Tcell;
 RX MEDLINE=9909250; PubMed=9880673;
 RA Fujimori A., Matsuda Y., Takemoto Y., Hashimoto Y., Kubo E., Araki R.,
 RA Fukumura R., Mita K., Tatsumi K., Muto M.;
 RT "Cloning and mapping of Np95 gene which encodes a novel nuclear
 RT protein associated with cell proliferation.";
 RL Mamm. Genome 9:1032-1035(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Davenport J.W., Fernandes E.R., Neale G.A.M., Goorha R.M.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; D87908; BAA74579.1; -;
 DR EMBL; AF274046; AAK55743.1; -;
 DR HSP; Q9UIG0; IF62.
 DR MGD; MGI:133889; Uhrfl.
 DR GO; GO:0005634; C:nucleus; TAS.
 DR GO; GO:0008283; P:cell proliferation; TAS.
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR011011; FYVE_PHD_Znf.
 DR InterPro; IPR002345; Lipocalin.
 DR InterPro; IPR003105; SRA_YDG.
 DR InterPro; IPR006266; Ubiquitin.
 DR InterPro; IPR001965; Znf PHD.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00628; PHD; 1.
 DR Pfam; PF00240; ubiquitin; 1.
 DR Pfam; PF02182; YDG_SRA; 1.
 DR PRINTS; PR00348; UBIQUITIN.
 DR SMART; SM00249; PHD; 1.
 DR SMART; SM00184; RING; 2.
 DR SMART; SM00466; SRA; 1.
 DR SMART; SM00213; UBQ; 1.
 DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
 DR PROSITE; PS00053; UBIQUITIN_2; 1.
 DR PROSITE; PS01359; ZF_PHD_1; UNKNOWN_1.
 DR PROSITE; PS00016; ZF_PHD_2; 1.
 DR PROSITE; PS00518; ZF_RING_1; UNKNOWN_1.
 DR PROSITE; PS00089; ZF_RING_2; 2.
 KW Nuclear protein.
 SQ SEQUENCE 782 AA; 88303 MW; DCSEEDFCDF69619B CRC64;

Query Match 65.6%; Score 40; DB 2; Length 782;
 Best Local Similarity 70.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CISVPLTSVP 10
 | : |||||
 Db 349 CLKPLTSVP 358

Search completed: April 1, 2005, 09:25:59
 Job time : 69.3562 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 03:27:37 ; Search time 83.0274 Seconds
(without alignments)
51.240 Million cell updates/sec

Title: US-09-761-636A-7

Perfect score: 61

Sequence: 1 CTSVPLTSVPC 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	11	AAU04526	Aau04526 VEGF base
2	59	96.7	11	AAU04542	Aau04542 VEGF base
3	57	93.4	11	AAU04545	Aau04545 VEGF base
4	54	88.5	11	AAU04543	Aau04543 VEGF base
5	52	85.2	11	AAU04544	Aau04544 VEGF base
6	45.5	74.6	10	AAU04532	Aau04532 VEGF base
7	43	70.5	96	AAU04520	Aau04520 Human VEG
8	43	70.5	109	AAU04520	Aau04520 Human VEG
9	43	70.5	109	AAU04520	Aau04520 Human VEG
10	43	70.5	109	AAU04520	Aau04520 Human VEG
11	43	70.5	109	AAU04520	Aau04520 Human VEG
12	43	70.5	110	AAU04520	Aau04520 Human VEG
13	43	70.5	178	AAU08287	Aay08287 Human gro
14	43	70.5	287	ABG73779	Abg73779 Human NVR
15	43	70.5	321	AAW53243	Aaw53243 Mus muscu
16	43	70.5	321	AAW47931	Aam47931 Mouse VEG
17	43	70.5	325	AAW53240	Aaw53240 Homo sapi
18	43	70.5	325	AAW53240	Aaw53240 Homo sapi
19	43	70.5	326	AAW44236	Aaw44236 Rat vascu
20	43	70.5	337	AAU08286	Aay08286 Human gro
21	43	70.5	354	AAW44233	Aaw44233 Human vas
22	43	70.5	354	AAW49036	Aaw49036 Human zve
23	43	70.5	354	AAW53241	Aaw53241 Homo sapi
24	43	70.5	354	AAW53241	Aaw53241 Homo sapi
25	43	70.5	354	AAU10649	Aab10649 Human VEG
				AAU07050	Human VEG

26	43	70.5	354	3	AAV70983	Aay70983 Human vas
27	43	70.5	354	3	AAE29049	Aab29049 Human VEG
28	43	70.5	354	4	AAE37606	Aab37606 Human VEG
29	43	70.5	354	4	AAE37606	Aab37606 Human vas
30	43	70.5	354	4	AAE37606	Aay37606 Human VEG
31	43	70.5	354	4	AAU08441	Aau08441 Polypepti
32	43	70.5	354	5	ABG33055	Abg33055 Human vas
33	43	70.5	354	5	ABG32046	Abg32046 Human Flt
34	43	70.5	354	6	ABE84623	Abb84623 Human VEG
35	43	70.5	354	7	ADD08950	Adn08950 Human VEG
36	43	70.5	354	7	ADN95941	Adn95941 Human VEG
37	43	70.5	354	8	ADQ20886	Adq20886 Human sof
38	43	70.5	354	8	ADO71602	Ado71602 A human v
39	43	70.5	354	8	ADR31436	Adr31436 Human vas
40	43	70.5	358	2	AAW14992	Aaw14992 Murine c-
41	43	70.5	358	2	AAW44295	Aaw44295 Mouse vas
42	43	70.5	358	2	AAW53242	Aaw53242 Mus muscu
43	43	70.5	358	5	AAW47930	Aam47930 Mouse VEG
44	43	70.5	620	2	AAW14994	Aaw14994 Mouse c-F
45	42	68.9	39	2	AAU07909	Aay07909 Human sec

ALIGNMENTS

RESULT 1

AAU04526
ID AAU04526 standard; peptide; 11 AA.

XX

AC AAU04526;

XX

DT 26-SEP-2001 (first entry)

XX

DE VEGF based monocyclic peptide 3.

XX

KW Human; VEGF; vascular endothelial growth factor; angiogenesis;

KW neovascularisation; lymphangiogenesis; psoriasis; tumour;

KW diabetes induced neovascular sequelae; rheumatoid arthritis;

KW diabetic retinopathy; chronic inflammation; cyclic.

XX

OS Synthetic.

XX

EH Key Location/Qualifiers

FT Disulfide-bond 1..11

FT /note= "This bond cyclises the peptide"

XX

XX WO200152875-A1.

XX

PD 26-JUL-2001.

XX

PF 18-JAN-2001; 2001WO-US001533.

XX

PR 18-JAN-2000; 2000US-0176293P.

XX

PR 16-MAY-2000; 2000US-0204590P.

XX

XX (LUDW-) LUDWIG INST CANCER RES.

PA

XX Achen MG, Hughes RA, Stackner S, Cendron A;

XX

XX WPI; 2001-442248/47.

XX

PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

XX

PS Claim 49; Page 32; 102pp; English.

XX

XX The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGF (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTSVPLTSVPC 11
 DB 1 CTSVPLTSVPC 11

RESULT 2
 AAU04542
 ID AAU04542 standard; peptide; 11 AA.
 XX
 AC AAU04542;
 DT 26-SEP-2001 (first entry)
 DE VEGF based monocyclic peptide 20.
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 1..11
 FT /note= "This bond cyclises the peptide"
 XX
 PN WO200152875-A1.
 XX
 PD 26-JUL-2001.
 XX
 XX 18-JAN-2001; 2001WO-US001533.
 XX
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 XX Achen MG, Hughes RA, Stacker S, Cendron A;
 FI WPI; 2001-442248/47.
 DR
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine

PT residues.
 XX Example 25; Page 47; 102pp; English.
 CC The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the exposed loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 11 AA;

Query Match 96.7%; Score 59; DB 4; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.0045;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTSVPLTSVPC 11
 DB 1 CTSVPLTSVPC 11

RESULT 3
 AAU04545
 ID AAU04545 standard; peptide; 11 AA.
 XX
 AC AAU04545;
 DT 26-SEP-2001 (first entry)
 DE VEGF based monocyclic peptide 23.
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 1..11
 FT /note= "This bond cyclises the peptide"
 XX
 PN WO200152875-A1.
 XX
 PD 26-JUL-2001.
 XX
 XX 18-JAN-2001; 2001WO-US001533.
 XX
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX

KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 XX diabetic retinopathy; chronic inflammation; cyclic.

XX Synthetic.

OS Key Location/Qualifiers

FH Disulfide-bond 1..11 /note= "This bond cyclises the peptide"

FT

XX WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

XX 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Hughes RA, Stacker S, Cendron A;

XX WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,

XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment

XX from an exposed loop of a growth factor protein by oxidizing the cysteine

XX residues.

XX Example 25; Page 47; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention,

XX whose 3-dimensional structure is modelled on the expose loop of human

XX VEGFD (vascular endothelial growth factor). The invention relates to a

XX method of producing a monomeric monocyclic peptide by a measuring beta-

XX beta carbon separation distances on opposite antiparallel strands of a

XX peptide loop fragment from an exposed loop of a growth factor protein and

XX cyclising the peptide by oxidising the cysteine residues. The monocyclic

XX peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic

XX peptides) and a cyclic peptide with at least one amino acid deleted prior

XX to cyclisation are used to interfere with angiogenesis,

XX neovascularisation or lymphangiogenesis in a mammal with a condition

XX characterised by angiogenesis, neovascularisation or lymphangiogenesis.

XX hemangioma, vascularised malignant or benign tumour, post-recovery

XX cerebrovascular accident, post-angioplasty restenosis, head, heat or cold

XX trauma, substance-induced neovascularisation of the liver, excessive

XX hormone-related angiogenic dysfunction, diabetes induced neovascular

XX sequelae, hypertension induced neovascular sequelae, or chronic liver

XX infection. The peptides are also used to modulate vascular permeability

XX in a mammal (the mammal has a condition characterised by fluid

XX accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,

XX or brain. The peptides are used to image blood vessels and lymphatic

XX vasculature. The monomeric and bicyclic peptides are used to interfere

XX with at least one biological activity induced by VEGF, VEGF-C or -D and

XX are also used in combination with an anti-inflammatory agent, to treat a

XX chronic inflammation, especially rheumatoid arthritis, psoriasis and

XX diabetic retinopathy

XX Sequence 11 AA;

Query Match 85.2%; Score 52; DB 4; Length 11;

Best Local Similarity 72.7%; Pred. No. 0.064;

Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTSVPLTSVPC 11

DB 1 CISLPISSVPC 11

RESULT 6

AAU04532

ID AAU04532 standard; peptide; 10 AA.

Query Match 74.6%; Score 45.5; DB 4; Length 10;

Best Local Similarity 90.9%; Pred. No. 0.69;

Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Sequence 10 AA;

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

AAU04532

standard; peptide; 10 AA.

</

QY 1 CISVPLTSVPC 11
 |||||
 Db 1 CISVPL-SVPC 10
 |||||

RESULT 7
 AAU04520
 ID AAU04520 standard; protein; 96 AA.
 XX
 AC AAU04520;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE Human VEGF-D amino acids Val101-PR0186.
 XX
 KW Human; VEGF-D; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200152875-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 18-JAN-2001; 2001WO-US001533.
 XX
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Achen MG, Hughes RA, Stacker S, Cendron A;
 XX
 DR WPI; 2001-442248/47.
 XX
 PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX
 PS Example 1; Page 89; 102pp; English.
 XX
 CC The sequence represents Human VEGF-D (vascular endothelial growth factor)
 CC amino acids Val101-PR0186. The sequence is used in a method of producing
 CC a monomeric monocyclic peptide by a measuring beta-beta carbon separation
 CC distances on opposite antiparallel strands of a peptide loop fragment
 CC from an exposed loop of a growth factor protein and cyclizing the peptide
 CC by oxidising the cysteine residues. The monocyclic peptides, dimeric
 CC bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic
 CC peptide with at least one amino acid deleted prior to cyclisation are
 CC used to interfere with angiogenesis, neovascularisation or
 CC lymphangiogenesis in a mammal with a condition characterised by
 CC angiogenesis, neovascularisation or lymphangiogenesis. The condition is
 CC diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised
 CC malignant or benign tumour, post-recovery cerebrovascular accident, post-
 CC angioplasty restenosis, head, heat or cold trauma, substance-induced
 CC neovascularisation of the liver, excessive hormone-related angiogenic
 CC dysfunction, diabetes induced neovascular sequelae, hypertension induced
 CC neovascular sequelae, or chronic liver infection. The peptides are also
 CC used to modulate vascular permeability in a mammal (the mammal has a
 CC condition characterised by fluid accumulation in peripheral limbs or in
 CC lungs, peritoneal cavity, pleura, or brain. The peptides are used to
 CC image blood vessels and lymphatic vasculature. The monomeric and bicyclic
 CC peptides are used to interfere with at least one biological activity
 CC induced by VEGF, VEGF-C or -D and are also used in combination with an
 CC anti-inflammatory agent, to treat a chronic inflammation, especially
 CC rheumatoid arthritis, psoriasis and diabetic retinopathy
 XX
 SQ Sequence 96 AA;

Query Match 70.5%; Score 43; DB 4; Length 96;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVPLTSVP 10
 |||||
 Db 68 ISVPLTSVP 76
 |||||

RESULT 8
 AAY23889
 ID AAY23889 standard; protein; 109 AA.
 XX
 AC AAY23889;
 XX
 DT 21-SEP-1999 (first entry)
 XX
 DE Human vascular endothelial growth factor (VEGF)-D.
 XX
 KW Vascular endothelial growth factor; VEGF; VEGF-D; malignant melanoma;
 KW tumour; psoriasis; angiogenesis; lymphangiogenesis; skin graft;
 KW wound healing; lymphedema; scleroderma; anhydrotic ectodermal dysplasia.
 XX
 OS Homo sapiens.
 XX
 PN WO9933485-A1.
 XX
 PD 08-JUL-1999.
 XX
 PF 23-DEC-1998; 98WO-US027373.
 XX
 PR 24-DEC-1997; 97AU-00001131.
 PR 29-MAY-1998; 98US-0087392P.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Achen MG, Stacker SA, Alitalo K;
 XX
 DR WPI; 1999-405368/34.
 XX
 PT A human cell line stably expressing vascular endothelial growth factor D,
 PT useful for treating melanomas or tumors expressing VEGF-D.
 XX
 PS Claim 6; Page 72; 79pp; English.
 XX
 CC The present sequence represents human vascular endothelial growth factor
 CC (VEGF)-D. The specification describes a human cell line which stably
 CC expresses VEGF-D, or fragments/analogs having VEGF-D biological
 CC activity. VEGF-D variants or antagonists, e.g. antisense nucleic acids or triplex
 CC DNA, VEGF-D variants or antibodies (especially chimeric antibodies), are
 CC useful for the treatment or alleviation of malignant melanomas, tumours
 CC or psoriasis. Angiogenesis and lymphangiogenesis stimulating amounts of
 CC VEGF-D can be administered to enhance the acceptance and/or healing of
 CC skin grafts or to stimulate the healing of a surgical or traumatic wound
 CC to the skin. Lymphangiogenesis stimulating amounts of VEGF-D can be used
 CC to treat lymphedema. Endothelial proliferation stimulating amounts of
 CC VEGF-D are used to treat scleroderma. Vascularisation stimulating amounts
 CC of VEGF-D can be used to treat anhydrotic ectodermal dysplasia. VEGF-D
 CC antibodies are useful for detecting tumours expressing VEGF-D. Fully-
 CC processed VEGF-D can be used to stimulate at least one VEGF-D bioactivity
 CC chosen from endothelial cell proliferation, migration, survival and
 CC differentiation and lymphangiogenesis without inducing vascular
 CC permeability
 XX
 SQ Sequence 109 AA;

Query Match 70.5%; Score 43; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVPLTSVP 10
 |||||
 Db 76 ISVPLTSVP 84
 |||||

RESULT 9
AAB11931
ID AAB11931 standard; protein; 109 AA.
XX AC AAB11931;
XX AC AAB11931;
XX 20-NOV-2000 (first entry)
XX Human truncated VEGF-D.
XX Truncated VEGF-D; vascular endothelial growth factor; human;
XX monoclonal antibody; VEGF receptor; VEGFR-2; VEGFR-3;
XX vascular permeability disorder; endothelial cell proliferative disorder;
XX angiogenic disorder; lymphangiogenic disorder;
XX neovascularisation disorder; endothelial cell differentiation disorder;
XX cancer; diabetic retinopathy; psoriasis; arthropathy; pulmonary oedema;
XX detection; diagnosis; imaging; lymphatic vasculature.
XX Homo sapiens.
OS WO200037025-A2.
PN 29-JUN-2000.
XX 21-DEC-1999; 99WO-US031332.
XX 21-DEC-1998; 98US-0113254P.
XX 17-MAY-1999; 99US-0134558P.
XX (LUDW-) LUDWIG INST CANCER RES.
XX Achen MG, Stacker SA;
XX WPI; 2000-442498/38.
XX Novel compositions comprising antibodies reactive to vascular endothelial
XX growth factor-D, useful for treating, e.g. angiogenesis, lymphangiogenesis
XX and neovascularization disorders.
XX Claim 1; Fig 1; 44pp; English.
XX This sequence represents a 109 amino acid truncated human VEGF-D
XX (vascular endothelial growth factor D), lacking both the N- and C-
XX terminal regions. The invention relates to a monoclonal antibody, or
XX fragments thereof, which is specifically reactive with the truncated
XX human VEGF-D, and methods of preparing the antibody. The antibody of the
XX invention interferes with the binding of VEGF-D to the VEGF receptors
XX VEGFR-2 and VEGFR-3, but does not interfere with the binding of VEGF to
XX these receptors and additionally is not reactive with VEGF-C. The
XX antibody may be used to treat disorders associated with vascular
XX permeability, endothelial cell proliferation, angiogenesis,
XX lymphangiogenesis, neovascularisation and endothelial cell
XX differentiation, especially cancer, diabetic retinopathy, psoriasis, and
XX arthropathies. The antibody may also be used to treat fluid accumulation
XX in the heart and/or lung via modulation of vascular permeability. It may
XX additionally be used to detect VEGF-D and may be used to image lymphatic
XX vasculature in tissue
XX Sequence 109 AA;
SQ
Query Match 70.5%; Score 43; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ISVPLTSVP 10
Db 76 ISVPLTSVP 84
RESULT 10
AAB84621
ID AAB84621 standard; protein; 109 AA.
XX AC AAB84621;
XX 01-APR-2003 (first entry)
XX Human wild-type VEGF-D monomer SEQ ID 3.
XX Human; single-chain; extracellular ligand-binding domain; VEGF;
XX vascular endothelial growth factor; VEGF type 2 receptor; KDR; Flt-4;
XX VEGF type 3 receptor; VEGF-C; VEGF-D; signal transduction; angiogenesis;
XX lymphangiogenesis.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Region 8..18
FT /note= "region of monomer likely to be modified by
FT mutation as described in claim 9"
FT Region 36..49
FT /note= "region of monomer likely to be modified by
FT mutation as described in claim 9"
FT Region 55..60
FT /note= "region of monomer likely to be modified by
FT mutation as described in claim 9"
FT Misc-difference 60
FT /note= "This residues is described as Gln in Claim 9"
FT Region 70..86
FT /note= "region of monomer likely to be modified by
FT mutation as described in claim 9"
XX WO200281520-A2.
XX 17-OCT-2002.
XX 08-APR-2002; 2002WO-DK000233.
XX 06-APR-2001; 2001DK-00000578.
XX 06-APR-2001; 2001US-0282239P.
XX (MAXY-) MAXYGEN HOLDINGS LTD.
XX Boesen TP, Halkier T;
XX WPI; 2003-058505/05.
XX Novel single-chain dimeric polypeptide for inhibiting angiogenesis, binds
XX to extracellular ligand-binding domain of vascular endothelial growth
XX factor type 2/type 3 receptor but does not activate the receptor.
XX Claim 9; Page 66; 71pp; English.
XX This invention describes a novel single-chain dimeric polypeptide which
XX binds to extracellular ligand-binding domain of vascular endothelial
XX growth factor (VEGFR) type 2 receptor (KDR) or VEGFR type 3 receptor (Flt-
XX 4). The polypeptide of the invention comprises two receptor-binding sites
XX of which one is capable of binding to a ligand-binding domain of the
XX receptor and one is incapable of effectively binding to a ligand-binding
XX domain of the receptor, and at least one monomer of the dimeric
XX polypeptide is derived from VEGF, VEGF-C or VEGF-D, where the polypeptide
XX is capable of binding to the receptor, but incapable of activating the
XX receptor. The polypeptide of the invention is useful for preparing a
XX medicament for preventing or treating a disease or condition involving
XX increased signal transduction from, or an increased activation of a VEGF
XX type 2 or type 3 receptor e.g. for inhibiting angiogenesis or
XX lymphangiogenesis. This sequence represents a human single-chain VEGF-D
XX monomer which can be modified and used in the construction of a VEGF-
XX based KDR antagonist described in the disclosure of the invention
XX Sequence 109 AA;
SQ
Query Match 70.5%; Score 43; DB 6; Length 109;
Best Local Similarity 100.0%; Pred. No. 21;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVPLTSVP 10
 Db 76 ISVPLTSVP 84

RESULT 11
 ABG73750
 ID ABG73750 standard; protein; 109 AA.
 XX AC ABG73750;
 XX DT 01-APR-2003 (first entry)
 XX DE Human VEGF-D monomer unit E57R variant.
 XX KW Human; single-chain; extracellular ligand-binding domain; VEGF;
 KW KW vascular endothelial growth factor; VEGF type 2 receptor; KDR; Flt-4;
 KW VEGF type 3 receptor; VEGF-C; VEGF-D; signal transduction; angiogenesis;
 KW lymphangiogenesis; mutant; mutein; variant.
 XX OS Homo sapiens.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 FT FT Misc-difference 10
 FT FT /note= "This wild-type residue is replaced by Arg or Glu
 FT in the first monomer unit of the VEGF-D dimer if the E57R
 FT mutation has not occurred (see Claim 16) and is
 FT optionally replaced if the E57R mutation has occurred.
 FT The claim describes this residue as Ser but is shown as
 FT Ile in the sequence listing"
 FT FT Misc-difference 37
 FT FT /note= "This wild-type Asn residue is optionally replaced
 FT by Arg in the second monomer unit of the VEGF-D dimer
 FT (See Claim 11)"
 FT FT Misc-difference 38
 FT FT /note= "This wild type Thr residue is optionally replaced
 FT by Arg or Glu in the second monomer unit of the VEGF-D
 FT dimer (see Claims 11 and 16)"
 FT FT Misc-difference 39
 FT FT /note= "This wild type Phe residue is optionally replaced
 FT by Arg or Glu in the second monomer unit of the VEGF-D
 FT dimer (see Claims 11 and 16)"
 FT FT Misc-difference 40
 FT FT /note= "This wild type Phe residue is optionally replaced
 FT by Arg in the second monomer unit of the VEGF-D dimer
 FT (see Claim 11)"
 FT FT Misc-difference 57
 FT FT /label= E57R
 FT /note= "wild type Gln is replaced by Arg in the first
 FT monomer unit of the VEGF-D dimer (See Claim 11) and is
 FT optionally replaced if the S10R/E mutation has occurred
 FT (see Claim 16)"
 FT FT Misc-difference 76
 FT FT /note= "This wild type Ile residue is optionally replaced
 FT by Arg or Glu in the second monomer unit of the VEGF-D
 FT dimer (see Claim 16)"
 XX WO200281520-A2.
 XX 17-OCT-2002.
 XX 08-APR-2002; 2002WO-DK000233.
 XX 06-APR-2001; 2001DK-00000578.
 PR 06-APR-2001; 2001US-0282239P.
 XX (MAXY-) MAXYGEN HOLDINGS LTD.
 PA Boesen TP, Halkier T;
 XX

DR WPI; 2003-058505/05.
 XX Novel single-chain dimeric polypeptide for inhibiting angiogenesis, binds
 PT to extracellular ligand-binding domain of vascular endothelial growth
 PT factor type 2/type 3 receptor but does not activate the receptor.
 XX
 PS Claim 11; Page; 71pp; English.
 XX This invention describes a novel single-chain dimeric polypeptide which
 CC binds to extracellular ligand-binding domain of vascular endothelial
 CC growth factor (VEGF) type 2 receptor (KDR) or VEGF type 3 receptor (Flt-
 CC 4). The polypeptide of the invention comprises two receptor-binding sites
 CC of which one is capable of binding to a ligand-binding domain of the
 CC receptor and one is incapable of effectively binding to a ligand-binding
 CC domain of the receptor, and at least one monomer of the dimeric
 CC polypeptide is derived from VEGF, VEGF-C or VEGF-D, where the polypeptide
 CC is capable of binding to the receptor, but incapable of activating the
 CC receptor. The polypeptide of the invention is useful for preparing a
 CC medicament for preventing or treating a disease or condition involving
 CC increased signal transduction from, or an increased activation of a VEGF
 CC type 2 or type 3 receptor e.g. for inhibiting angiogenesis or
 CC lymphangiogenesis. This sequence represents a variant of the human VEGF-D
 CC monomer unit used in the construction of a VEGF-D dimer described in the
 CC disclosure of the invention. In one instance a polypeptide is claimed
 CC comprising a first monomer derived from VEGF-D having at least the
 CC mutation E57R and optionally comprising a second monomer derived from
 CC VEGF-D having at least one mutation selected from the group consisting of
 CC N37R, T38T, F39R and F40R. In a second instance a polypeptide is claimed
 CC comprising a first monomer containing a substitution consisting of S10R,
 CC S10E and E57R (although the residue at position 10 is an Ile), and/or in
 CC the other VEGF-D derived monomer at least one substitution selected from
 CC the group consisting of T38R, T38E, F39R, F39E, I76R and I76E. NOTE: This
 CC sequence is not represented in the body of the specification but has been
 CC constructed from the wild-type VEGF-D sequence represented in ABB84621

QY 2 ISVPLTSVP 10
 Db 76 ISVPLTSVP 84

Query Match 70.5%; Score 43; DB 6; Length 109;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
 AAM47933
 ID AAM47933 standard; protein; 110 AA.
 XX AC AAM47933;
 XX DT 28-FEB-2002 (first entry)
 XX DE Mouse VEGF-D VHD domain SEQ ID NO 6.
 XX KW Mouse; vascular endothelial growth factor-D; VEGF-D; proliferation;
 KW lymph vessel endothelial cell; VEGF receptor-3; neoplastic disease;
 KW VEGF-PDGF homology domain; VHD.
 XX OS Mus sp.
 XX PN WO200182870-A2.
 XX PD 08-NOV-2001.
 XX PF 03-MAY-2001; 2001WO-US014295.
 XX PR 03-MAY-2000; 2000US-0201421P.
 XX (LUDW-) LUDWIG INST CANCER RES.
 XX Achen MG, Stacker S;
 PI

XX WPI; 2002-049310/06.
DR N-PSDB; ABA05427.
XX
PT Specific activating of VEGF receptor-3, useful for stimulating
PT proliferation and/or maintaining of only lymph vessel endothelial cells,
PT by administration of a polypeptide having high sequence identity with the
PT mouse VEGF-D polypeptide.
XX
XX
PS Claim 1; Page 41; 41pp; English.
XX
CC The invention relates to a method for activating only vascular
CC endothelial growth factor (VEGF) receptor-3 comprising administering to a
CC cell bearing the receptor an active amount of a composition comprising a
CC polypeptide having at least 90%, preferably 95%, sequence identity with
CC the mouse VEGF-D polypeptide or its fragment. The polypeptide
CC specifically activates VEGF receptor-3 which results in proliferation of
CC lymph vessel endothelial cells. The polypeptide is useful for activating
CC only VEGF receptor-3 and is therefore useful for stimulating
CC proliferation and/or maintaining of only lymph vessel endothelial cells.
CC The polypeptide is also useful in the diagnosis of a neoplastic disease
CC characterized by an increase in lymph vessel endothelial cells. The mouse
CC VEGF-D has two isoforms. The longer amino acid sequence designated mVEGF-
CC D1 (AA47930) has an insertion of five amino acids (AA47932) after
CC residue 30 and diverges in the C-terminal sequence after residue 317
CC compared to the shorter isoform mVEGF-D2, which diverges after residue
CC 312. The present sequence is that of the VEGF-PDGF homology domain (VHD),
CC comprising residues 92-201 of the full length mouse VEGF-D2 protein of
CC the invention
XX
XX Sequence 110 AA;
SQ
Query Match 70.5%; Score 43; DB 5; Length 110;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ISVPLTSVP 10
Db 77 ISVPLTSVP 85
RESULT 13
AA08287
ID AAY08287 standard; protein; 178 AA.
XX
AC AAY08287;
XX
XX 14-JUL-1999 (first entry)
XX
XX Human growth factor protein fragment FIGF178 (VEGF-D178).
XX
XX Growth factor; human; dimer; cysteine knot; cellular inclusion body;
XX pharmaceutical.
XX
XX Homo sapiens.
XX
XX DE19748734-A1.
XX
XX 06-MAY-1999.
XX
XX 05-NOV-1997; 97DE-01048734.
XX
XX 05-NOV-1997; 97DE-01048734.
XX
XX (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
XX
XX Kaerst U, Mueller C, Rinas U, Weich H, Erdmann H;
XX WPI; 1999-278785/24.
XX
XX Preparing active growth factor dimers from inclusion bodies in high
XX yield.
XX

PS Claim 14; Page 9; 14pp; German.
XX
CC This invention describes the novel preparation of biologically active
CC dimers of recombinant human growth factors of the cysteine knot family
CC starting from cellular inclusion bodies. Such dimers are useful in
CC pharmaceutical compositions and the method provides yields of 31-39.7%,
CC in examples, compared with about 10% for the conventional method (see
CC Biochemistry, 28 (1989) 2956). AAY08278-Y08301 are human growth factor
CC protein fragments used in the method of the invention
XX
XX Sequence 178 AA;
SQ
Query Match 70.5%; Score 43; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ISVPLTSVP 10
Db 153 ISVPLTSVP 161
RESULT 14
ABG73779
ID ABG73779 standard; protein; 287 AA.
XX
AC ABG73779;
XX
XX 03-APR-2003 (first entry)
XX
XX Human NVR protein.
XX
XX NVR; human; endothelial growth factor; cytostatic; cancer; angiogenesis;
XX cell proliferation; revascularisation; amputation; vasculogenesis;
XX transplant; brain; breast; intestine; kidney; lung; ovary; pancreas;
XX prostate; uterus; gene therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 281
FT /note= "Encoded by TAA, an in frame stop codon which
FT interrupts the coding region as shown in Figure 1A-B.
FT This site is the end of the protein sequence represented
FT in SEQ ID 1 of the Sequence listing"
FT 282..287
FT Region /note= "Region not represented in SEQ ID 1 of the
FT Sequence listing"
XX
XX US2002155338-A1.
XX
XX 24-OCT-2002.
XX
XX 09-JAN-2002; 2002US-00044622.
XX
XX 23-JAN-1997; 97US-00788812.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Bandman O, Goli SK, Murry LE;
XX
XX WPI; 2003-182635/18.
XX
XX N-PSDB; ABQ77105.
XX
XX New endothelial growth factor polypeptide and polynucleotides, useful for
XX diagnosing, preventing, and treating cancer and other conditions or
XX diseases involving angiogenesis and cell proliferation.
XX
XX Claim 1; Fig 1A-B; 28pp; English.
XX
XX This invention describes a novel human endothelial growth factor
XX polypeptide which has cytostatic activity. The polypeptide and its
XX encoding polynucleotide are useful in the diagnosis, prevention, and
XX treatment of cancer and other conditions or diseases involving
XX

CC angiogenesis and cell proliferation. NVR may also be used to promote
 CC revascularisation following traumatic amputation and surgical
 CC reconstruction or added to a tissue culture to promote vasculogenesis in
 CC tissues for autologous or heterologous transplant. Antagonists or
 CC inhibitors of NVR may be used to suppress or prevent angiogenesis and
 CC thus prevent the growth and development of cancers such as cancer of the
 CC brain, breast, intestine, kidney, lung, ovary, pancreas, prostate or
 CC uterus. The products of the invention can be used for gene therapy. This
 CC sequence represents the human NVR protein described in the disclosure of
 CC the invention
 XX
 SQ Sequence 287 AA;

Query Match 70.5%; Score 43; DB 6; Length 287;

Best Local Similarity 100.0%; Pred. No. 58;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVPLTSVP 10

|||||

Db 168 ISVPLTSVP 176

RESULT 15

AAW53243

ID AAW53243 standard; protein; 321 AA.

XX AC AAW53243;

DT 03-AUG-1998 (first entry)

DE Mus musculus vascular endothelial growth factor D2 (VEGF-D2).

XX vascular endothelial growth factor; VEGF-D; angiogenesis; modification;
 KW acceleration; wound healing; tissue; organ; transplants;
 KW collateral circulation; infarction; arterial stenosis;
 KW coronary artery disease; inhibition; cancer; treatment;
 KW diabetic retinopathy; lung disorders; blood circulation;
 KW gaseous exchange; chronic obstructive airway disease;
 KW intestinal malabsorptive syndrome; biopsy; metastatic risk; detection;
 KW diagnosis; congestive heart failure.

XX Mus musculus.

XX WO9807832-A1.

XX 26-FEB-1998.

XX 21-AUG-1997; 97WO-US014696.

XX 23-AUG-1996; 96AU-00001825.

PR 23-AUG-1996; 96US-0023751P.

PR 11-NOV-1996; 96AU-00003554.

PR 14-NOV-1996; 96US-0031097B.

PR 05-FEB-1997; 97AU-00004954.

PR 10-FEB-1997; 97US-0038814P.

PR 19-JUN-1997; 97AU-00007435.

PR 01-JUL-1997; 97US-0051426P.

XX (LUDW-) LUDWIG INST CANCER RES.

PA (UYHE-) UNIV HELSINKI LICENSING LTD.

XX Achen MG, Wilks AF, Stacker SA, Alitalo K;

XX WPI; 1998-179057/16.

DR N-PSDB; AAV20809.

XX New isolated vascular endothelial growth factor-D - used to develop
 PT products for use in e.g. modifying angiogenesis or treating lung, heart
 PT or intestinal disorders.

PS Claim 16; Page 64-65; 101pp; English.

XX The sequence is that of mouse lung vascular endothelial growth factor D2

CC (VEGF-D2). VEGF-D2 can be used for e.g. acceleration of angiogenesis in
 CC wound healing, tissue or organ transplantation, or to establish
 CC collateral circulation in tissue infarction or arterial stenosis, such as
 CC coronary artery disease, and inhibition of angiogenesis in the treatment
 CC of cancer or of diabetic retinopathy. It can also be used in the
 CC treatment of lung disorders to improve blood circulation in the lung
 CC and/or gaseous exchange between the lungs and the blood stream or to
 CC improve blood circulation to the heart and O₂ gas permeability in cases
 CC of cardiac insufficiency, to improve blood flow and gaseous exchange in
 CC chronic obstructive airway disease, or to treat malabsorptive syndromes
 CC in the intestinal tract. Quantitation of VEGF-D in cancer biopsy
 CC specimens may be useful as an indicator of future metastatic risk.
 CC Antagonists can be used for treating e.g. conditions such as congestive
 CC heart failure, involving accumulations of fluid in the lung resulting
 CC from increases in vascular permeability. The products can also be used
 CC for detection and diagnosis

XX
 SQ Sequence 321 AA;

Query Match 70.5%; Score 43; DB 2; Length 321;

Best Local Similarity 100.0%; Pred. No. 65;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVPLTSVP 10

|||||

Db 168 ISVPLTSVP 176

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Job time : 83.0274 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 09:26:18 ; Search time 270.329 Seconds

(without alignments)
13.493 Million cell updates/sec

Title: US-09-761-636A-7

Perfect score: 61

Sequence: 1 CISVPLTSVPC 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	59	96.7	11	9	US-09-761-636A-23
3	57	93.4	11	9	US-09-761-636A-26
4	54	88.5	11	9	US-09-761-636A-24
5	52	85.2	11	9	US-09-761-636A-25
6	45.5	74.6	10	9	US-09-761-636A-13
7	43	70.5	49	13	US-10-139-876-11
8	43	70.5	81	13	US-10-086-623-18
9	43	70.5	81	14	US-10-260-539-18
10	43	70.5	96	9	US-09-761-636A-1
11	43	70.5	109	9	US-09-956-095-3
12	43	70.5	109	9	US-09-219-345A-1
13	43	70.5	109	16	US-10-779-731-1

14	43	70.5	110	10	US-09-847-524-6	Sequence 6, Appli
15	43	70.5	134	17	US-10-868-549-10	Sequence 10, Appli
16	43	70.5	197	15	US-10-352-153-8	Sequence 8, Appli
17	43	70.5	280	13	US-10-044-622-1	Sequence 1, Appli
18	43	70.5	321	10	US-09-847-524-4	Sequence 4, Appli
19	43	70.5	321	14	US-10-274-953-9	Sequence 9, Appli
20	43	70.5	321	14	US-10-161-694-9	Sequence 9, Appli
21	43	70.5	321	16	US-10-705-476-9	Sequence 9, Appli
22	43	70.5	325	14	US-10-274-953-3	Sequence 3, Appli
23	43	70.5	325	14	US-10-161-694-3	Sequence 3, Appli
24	43	70.5	325	16	US-10-705-476-3	Sequence 3, Appli
25	43	70.5	354	9	US-09-956-095-2	Sequence 2, Appli
26	43	70.5	354	9	US-09-219-345A-11	Sequence 11, Appli
27	43	70.5	354	9	US-09-795-006A-119	Sequence 119, App
28	43	70.5	354	10	US-09-375-248-6	Sequence 6, Appli
29	43	70.5	354	11	US-09-765-534B-22	Sequence 22, Appli
30	43	70.5	354	14	US-10-262-538-26	Sequence 26, Appli
31	43	70.5	354	14	US-10-274-953-5	Sequence 5, Appli
32	43	70.5	354	14	US-10-161-694-5	Sequence 5, Appli
33	43	70.5	354	14	US-10-174-930-1	Sequence 1, Appli
34	43	70.5	354	15	US-10-661-740-6	Sequence 6, Appli
35	43	70.5	354	16	US-10-705-476-5	Sequence 5, Appli
36	43	70.5	354	17	US-10-868-577A-4	Sequence 4, Appli
37	43	70.5	354	17	US-10-868-549-4	Sequence 4, Appli
38	43	70.5	358	9	US-09-852-209A-13	Sequence 13, Appli
39	43	70.5	358	10	US-09-847-524-2	Sequence 2, Appli
40	43	70.5	358	13	US-10-139-876-2	Sequence 2, Appli
41	43	70.5	358	14	US-10-131-600-13	Sequence 13, Appli
42	43	70.5	358	14	US-10-274-953-8	Sequence 8, Appli
43	43	70.5	358	15	US-10-161-694-8	Sequence 8, Appli
44	43	70.5	358	15	US-10-303-997B-13	Sequence 13, Appli
45	43	70.5	358	15	US-10-439-337A-13	Sequence 13, Appli

ALIGNMENTS

RESULT 1
US-09-761-636A-7
; Sequence 7, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-7

Query Match 100.0%; Score 61; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CISVPLTSVPC 11
Db 1 CISVPLTSVPC 11

RESULT 2
US-09-761-636A-23

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; Sequence 23, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-23

Query Match          96.7%; Score 59; DB 9; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0046;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTSVPLTSVPC 11
Db 1 CLSVPLTSVPC 11

RESULT 3
US-09-761-636A-26
; Sequence 26, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-26

Query Match          93.4%; Score 57; DB 9; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.0098;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTSVPLTSVPC 11
Db 1 CTSVPLTSVPC 11

RESULT 4
US-09-761-636A-24
; Sequence 24, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
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; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-24

Query Match          88.5%; Score 54; DB 9; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.063;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTSVPLTSVPC 11
Db 1 CITIPLTSVPC 11

RESULT 5
US-09-761-636A-25
; Sequence 25, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-25

Query Match          85.2%; Score 52; DB 9; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.063;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTSVPLTSVPC 11
Db 1 CTSVPLTSVPC 11

RESULT 6
US-09-761-636A-13
; Sequence 13, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
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; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 13
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-13

Query Match 74.6%; Score 45.5; DB 9; Length 10;
Best Local Similarity 90.9%; Pred. No. 0.65;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 C1SVPLTSPVC 11
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Db 1 C1SVPL-SVPC 10
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RESULT 7
US-10-139-876-11
; Sequence 11, Application US/10139876
; Publication No. US20020123481A1
; GENERAL INFORMATION:
; APPLICANT: Oliviero, Salvatore
; TITLE OF INVENTION: C-Fos Induced Growth Factor (Figf) And Dna Encoding Same
; FILE REFERENCE: 35784/205172
; CURRENT APPLICATION NUMBER: US/10/139,876
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 09/043,476
; PRIOR FILING DATE: 1998-03-18
; PRIOR APPLICATION NUMBER: PCT/IB96/0113
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: GB9612368.2
; PRIOR FILING DATE: 1996-06-13
; PRIOR APPLICATION NUMBER: GB9519928.7
; PRIOR FILING DATE: 1995-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)...(48)
; OTHER INFORMATION: segment of FIGF
US-10-139-876-11

Query Match 70.5%; Score 43; DB 13; Length 49;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ISVPLTSPV 10
|||||
Db 23 ISVPLTSPV 31
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RESULT 8
US-10-086-623-18
; Sequence 18, Application US/10086623
; Publication No. US20020164710A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne

; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES THE
; FILE REFERENCE: 1064/44833C2
; CURRENT APPLICATION NUMBER: US/10/086,623
; CURRENT FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: PDGF/VEGF-homology domain of VEGF-D
US-10-086-623-18

Query Match 70.5%; Score 43; DB 13; Length 81;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ISVPLTSPV 10
|||||
Db 58 ISVPLTSPV 66
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RESULT 9
US-10-260-539-18
; Sequence 18, Application US/10260539
; Publication No. US20030073637A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES THE
; FILE REFERENCE: 1064/44833C2
; CURRENT APPLICATION NUMBER: US/10/260,539
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US/10/086,623
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: PDGF/VEGF-homology domain of VEGF-D
US-10-260-539-18

Query Match          70.5%; Score 43; DB 14; Length 81;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ISVPLTSVP 10
Db 58 ISVPLTSVP 66

RESULT 10
US-09-761-636A-1
; Sequence 1, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Amino acid residues of V101-Pro196 of VEGF-D
US-09-761-636A-1

Query Match          70.5%; Score 43; DB 9; Length 96;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ISVPLTSVP 10
Db 68 ISVPLTSVP 76

RESULT 11
US-09-956-095-3
; Sequence 3, Application US/09956095
; Patent No. US20020102260A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; APPLICANT: STACKER, Steven A.
; TITLE OF INVENTION: METHODS FOR TREATING NEOPLASTIC DISEASE CHARACTERIZED BY
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR D EXPRESSION, FOR SCREENING
; TITLE OF INVENTION: FOR NEOPLASTIC DISEASE OR METASTATIC RISK AND FOR MAINTAINING
; TITLE OF INVENTION: VASCULARIZATION OF TISSUE
; FILE REFERENCE: 1064/48666PC
; CURRENT APPLICATION NUMBER: US/09/956,095
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 09/796,714
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/234,196

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1

Query Match          70.5%; Score 43; DB 9; Length 109;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ISVPLTSVP 10
Db 76 ISVPLTSVP 84

RESULT 12
US-09-219-345A-1
; Sequence 1, Application US/09219345A
; Patent No. US20020127222A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; TITLE OF INVENTION: EXPRESSION VECTORS AND CELL LINES EXPRESSING VASCULAR
; TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR D, AND METHOD OF TREATING
; FILE REFERENCE: 1064/44385 Marc ACHEN
; CURRENT APPLICATION NUMBER: US/09/219,345A
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: AU PP 1131
; PRIOR FILING DATE: 1997-12-24
; PRIOR APPLICATION NUMBER: US 60/087,392
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-09-219-345A-1

Query Match          70.5%; Score 43; DB 9; Length 109;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ISVPLTSVP 10
Db 76 ISVPLTSVP 84

RESULT 13
US-10-779-731-1
; Sequence 1, Application US/10779731
; Publication No. US20040141917A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; APPLICANT: STACKER, Steve A.
; TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
; FILE REFERENCE: ACHEN et al-1064-44660
; CURRENT APPLICATION NUMBER: US/10/779,731
; CURRENT FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: US/10/100,037
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/469,186
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/113,254
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/134,556
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
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Search completed: April 1, 2005, 10:36:33
Job time : 270.329 secs

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; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-779-731-1

Query Match      70.5%; Score 43; DB 16; Length 109;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVPLTSVP 10
DB 76 ISVPLTSVP 84

RESULT 14
US-09-847-524-6
; Sequence 6, Application US/09847524
; Publication No. US20030166523A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G
; APPLICANT: STACKER, Steven A
; TITLE OF INVENTION: A METHOD FOR ACTIVATING ONLY THE VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR RECEPTOR-3 AND USES THEREOF
; FILE REFERENCE: Achen&Stacker-mouse VEGF-D
; CURRENT APPLICATION NUMBER: US/09/847,524
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-847-524-6

Query Match      70.5%; Score 43; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVPLTSVP 10
DB 77 ISVPLTSVP 85

RESULT 15
US-10-868-549-10
; Sequence 10, Application US/10868549
; Publication No. US20050043235A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al.
; TITLE OF INVENTION: USE OF VEGF-C OR VEGF-D IN RECONSTRUCTIVE SURGERY
; FILE REFERENCE: 28967/39117A
; CURRENT APPLICATION NUMBER: US/10/868,549
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,114
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR FILING DATE: 2003-06-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-868-549-10

Query Match      70.5%; Score 43; DB 17; Length 134;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVPLTSVP 10
DB 101 ISVPLTSVP 109
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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 07:04:23 ; Search time 17.7534 Seconds
(without alignments)
33.638 Million cell updates/sec

Title: US-09-761-636A-6

Perfect score: 46

Sequence: 1 CNEESLIC 8

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	109	3	US-09-469-186-1
2	46	100.0	109	4	US-09-469-185-1
3	46	100.0	109	4	US-10-100-037-1
4	46	100.0	197	4	US-09-431-888-8
5	46	100.0	325	3	US-08-915-795-3
6	46	100.0	325	4	US-09-296-275-3
7	46	100.0	354	3	US-08-915-795-5
8	46	100.0	354	4	US-09-296-275-5
9	46	100.0	354	4	US-09-375-248-6
10	46	100.0	354	4	US-09-468-647A-109
11	46	100.0	354	4	US-09-169-079-22
12	46	100.0	354	4	US-09-214-982-1
13	46	100.0	362	4	US-09-949-016-11286
14	36	78.3	110	4	US-09-847-524-6
15	36	78.3	120	6	5194596-9
16	36	78.3	120	6	5219739-9
17	36	78.3	120	6	5194596-9
18	36	78.3	120	6	5219739-9
19	36	78.3	132	3	US-09-125-642C-15
20	36	78.3	132	4	US-09-431-888-11
21	36	78.3	133	4	US-09-431-888-2
22	36	78.3	164	6	5194596-17
23	36	78.3	164	6	5219739-17
24	36	78.3	164	6	5219739-18
25	36	78.3	164	6	5194596-17
26	36	78.3	164	6	5219739-17
27	36	78.3	164	6	5219739-18

28	36	78.3	190	6	5332671-3
29	36	78.3	190	6	5332671-3
30	36	78.3	321	3	US-08-915-795-9
31	36	78.3	321	4	US-09-847-524-4
32	36	78.3	321	4	US-09-296-275-9
33	36	78.3	358	3	US-08-915-795-8
34	36	78.3	358	4	US-09-847-524-2
35	36	78.3	358	4	US-09-296-275-8
36	36	78.3	358	4	US-09-438-046-15
37	34	73.9	1722	4	US-09-538-092-1033
38	33	71.7	102	4	US-09-248-796A-17550
39	33	71.7	146	3	US-08-586-0398-33
40	33	71.7	146	4	US-09-699-769-33
41	33	71.7	189	1	US-08-469-427A-15
42	33	71.7	190	2	US-08-563-083C-20
43	33	71.7	190	3	US-08-586-0398-31
44	33	71.7	190	4	US-09-699-769-31
45	33	71.7	214	3	US-08-586-0398-35

ALIGNMENTS

RESULT 1

US-09-469-186-1

; Sequence 1, Application US/09469186

; Patent No. 6383484

; GENERAL INFORMATION:

; APPLICANT: ACHEN, Marc G.

; APPLICANT: STACKER, Steve A.

; TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF

; FILE REFERENCE: ACHEN et al-1064-44660

; CURRENT APPLICATION NUMBER: US/09/469,186

; CURRENT FILING DATE: 1999-12-21

; EARLIER APPLICATION NUMBER: 60/113,254

; EARLIER FILING DATE: 1998-12-21

; EARLIER APPLICATION NUMBER: 60/134,556

; EARLIER FILING DATE: 1999-05-17

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 109

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-469-186-1

Query Match 100.0%; Score 46; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.46; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

Qy 1 CNEESLIC 8

Db 54 CNEESLIC 61

RESULT 2

US-09-469-185-1

; Sequence 1, Application US/09469185

; Patent No. 6531185

; GENERAL INFORMATION:

; APPLICANT: ACHEN, Marc G.

; APPLICANT: STACKER, Steve A.

; TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF

; FILE REFERENCE: ACHEN et al-1064-44660

; CURRENT APPLICATION NUMBER: US/09/469,185

; CURRENT FILING DATE: 1999-12-21

; EARLIER APPLICATION NUMBER: 60/113,254

; EARLIER FILING DATE: 1998-12-21

; EARLIER APPLICATION NUMBER: 60/134,556

; EARLIER FILING DATE: 1999-05-17

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

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; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-469-185-1

Query Match      100.0%; Score 46; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db 54 CNEESLIC 61

RESULT 3
US-10-100-037-1
; Sequence 1, Application US/10100037
; Patent No. 6730489
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; APPLICANT: STACKER, Steve A.
; TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
; FILE REFERENCE: ACHEN et al-1064-44660
; CURRENT APPLICATION NUMBER: US/10/100,037
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/469,186
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/113,254
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/134,556
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-100-037-1

Query Match      100.0%; Score 46; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db 54 CNEESLIC 61

RESULT 4
US-09-431-888-8
; Sequence 8, Application US/09431888A
; Patent No. 6541008
; GENERAL INFORMATION:
; APPLICANT: Wise, Lynn M
; APPLICANT: Mercer, Andrew A
; APPLICANT: Savory, Loreen J
; APPLICANT: Fleming, Stephen B
; APPLICANT: Stackler, Stephen
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
; TITLE OF INVENTION: VEGF-2, AND USES THEREOF
; FILE REFERENCE: Sequence Listing for 09/431,833
; Patent No. 6541008
; CURRENT APPLICATION NUMBER: US/09/431,888A
; CURRENT FILING DATE: 1999-11-02
; EARLIER APPLICATION NUMBER: 60/106,689
; EARLIER FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/106,800
; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 197

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-431-888-8

Query Match      100.0%; Score 46; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db 70 CNEESLIC 77

RESULT 5
US-08-915-795-3
; Sequence 3, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,795
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D. 26,269
; REGISTRATION NUMBER: 1064/42983
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Breast
US-08-915-795-3

Query Match      100.0%; Score 46; DB 3; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db 117 CNEESLIC 124

RESULT 6
US-09-296-275-3
; Sequence 3, Application US/09296275
; Patent No. 6689580
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; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/296,275
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/915,795
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Breast
; US-09-296-275-3

Query Match 100.0%; Score 46; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.3; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

Qy 1 CNEESLIC 8
Db 117 CNEESLIC 124

RESULT 7
US-08-915-795-5
; Sequence 5, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,795
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Lung
; US-08-915-795-5

Query Match 100.0%; Score 46; DB 3; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.5; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

Qy 1 CNEESLIC 8
Db 146 CNEESLIC 153

RESULT 8
US-09-296-275-5
; Sequence 5, Application US/09296275
; Patent No. 6689580
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/296,275
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/915,795
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Breast
; US-09-296-275-3
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; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Lung
US-09-296-275-5

Query Match 100.0%; Score 46; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.5; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

Qy 1 CNEESLIC 8
Db 146 CNEESLIC 153

RESULT 9

US-09-375-248-6
; Sequence 6, Application US/09375248
; Patent No. 6764820
; GENERAL INFORMATION:
; APPLICANT: Ferrell, Robert E.
; APPLICANT: Alitalo, Kari
; APPLICANT: Finegold, David N.
; APPLICANT: Karkkainen, Marika
; TITLE OF INVENTION: SCREENING AND THERAPY FOR LYMPHATIC DISORDERS INVOLVING
; TITLE OF INVENTION: THE FLT4 RECEPTOR TYROSINE KINASE (VEGFR-3)
; FILE REFERENCE: 28967735255A
; CURRENT APPLICATION NUMBER: US/09/375,248
; CURRENT FILING DATE: 1999-08-16
; EARLIER APPLICATION NUMBER: PCT/US99/06133
; EARLIER FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-375-248-6

Query Match 100.0%; Score 46; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.5; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

Qy 1 CNEESLIC 8
Db 146 CNEESLIC 153

RESULT 10

US-09-468-647A-109
; Sequence 109, Application US/09468647A
; Patent No. 6783953
; GENERAL INFORMATION:
; APPLICANT: Gordon, Robert D.
; APPLICANT: Sprengel, Joerg J.
; APPLICANT: Von, Jeffery R.
; APPLICANT: Dijkmans, Josiena J.H.
; APPLICANT: Gosiowska, Anna
; APPLICANT: Dhanaraj, Sri devi N
; APPLICANT: Xu, Jean
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-X
; FILE REFERENCE: B0192.70011US00
; CURRENT APPLICATION NUMBER: US/09/468,647A
; CURRENT FILING DATE: 1999-12-21

; PRIOR APPLICATION NUMBER: GB 9828377.3
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/124,967
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/164,131
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 109
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-468-647A-109

Query Match 100.0%; Score 46; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.5; Indels 0; Gaps 0;
Matches -8; Conservative 0; Mismatches 0;

Qy 1 CNEESLIC 8
Db 146 CNEESLIC 153

RESULT 11

US-09-169-079-22
; Sequence 22, Application US/09169079
; Patent No. 6824777
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Kaipainen, Arja
; APPLICANT: Valtola, Reija
; APPLICANT: Jussila, Lotta
; TITLE OF INVENTION: Flt4 (VEGFR-3) as a Target for Tumor Imaging and Anti-Tumor Therapi
; FILE REFERENCE: 28113/34891
; CURRENT APPLICATION NUMBER: US/09/169,079
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: 08/901,710
; EARLIER FILING DATE: 1997-07-28
; EARLIER APPLICATION NUMBER: 08/340,011
; EARLIER FILING DATE: 1994-11-14
; EARLIER APPLICATION NUMBER: 08/257,754
; EARLIER FILING DATE: 1994-07-09
; EARLIER APPLICATION NUMBER: 07/959,951
; EARLIER FILING DATE: 1992-10-09
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-169-079-22

Query Match 100.0%; Score 46; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.5; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

Qy 1 CNEESLIC 8
Db 146 CNEESLIC 153

RESULT 12

US-09-214-982-1
; Sequence 1, Application US/09214982
; Patent No. 6828426
; GENERAL INFORMATION:
; APPLICANT: Hirata, Yuichi
; APPLICANT: Nezu, Junichi
; TITLE OF INVENTION: No. 6828426el VEGF-like Factor
; FILE REFERENCE: 50026/014001
; CURRENT APPLICATION NUMBER: US/09/214,982
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 8-185216 Japan

EARLIER FILING DATE: 1996-07-15
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 354
TYPE: PRT
ORGANISM: Homo sapiens
US-09-214-982-1

Query Match 100.0%; Score 46; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNEESLIC 8
Db 146 CNEESLIC 153

RESULT 13
US-09-949-016-11286
Sequence 11286, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11286
LENGTH: 362
TYPE: PRT
ORGANISM: Human
US-09-949-016-11286

Query Match 100.0%; Score 46; DB 4; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNEESLIC 8
Db 154 CNEESLIC 161

RESULT 14
US-09-847-524-6
Sequence 6, Application US/09847524
Patent No. 6689352
GENERAL INFORMATION:
APPLICANT: ACHEN, Marc G
APPLICANT: STACKER, Steven A
TITLE OF INVENTION: A METHOD FOR ACTIVATING ONLY THE VASCULAR ENDOTHELIAL
GROWTH FACTOR RECEPTOR-3 AND USES THEREOF
FILE REFERENCE: Achen&Stacker-mouse VEGF-D
CURRENT APPLICATION NUMBER: US/09/847,524
CURRENT FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 110
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-09-847-524-6

Query Match 78.3%; Score 36; DB 4; Length 110;

Best Local Similarity 62.5%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CNEESLIC 8
Db 55 CNEEGVMC 62

RESULT 15
5194596-9
Patent No. 5194596
APPLICANT: TISCHER, EDMUND G.;ABRAHAM, JUDITH A.;FIDDES, JOHN
C.;MITCHELL, RICHARD L.
TITLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL
GROWTH FACTOR
NUMBER OF SEQUENCES: 32
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/450,883
FILING DATE: 14-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 387,545
FILING DATE: 27-JUL-1989
SEQ ID NO:9;
LENGTH: 120
5194596-9

Query Match 78.3%; Score 36; DB 6; Length 120;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CNEESLIC 8
Db 60 CNEESLEC 67

Search completed: April 1, 2005, 09:36:15
Job time : 18.7534 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 09:26:18 ; Search time 196.603 Seconds
(without alignments)
13.493 Million cell updates/sec

Title: US-09-761-636A-6

Perfect score: 46

Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	46	100.0	8	US-09-761-636A-6	Sequence 6, Appli
2	46	100.0	9	US-09-761-636A-9	Sequence 9, Appli
3	46	100.0	73	US-09-761-636A-3	Sequence 3, Appli
4	46	100.0	96	US-09-761-636A-1	Sequence 1, Appli
5	46	100.0	109	US-09-956-095-3	Sequence 3, Appli
6	46	100.0	109	US-09-219-345A-1	Sequence 1, Appli
7	46	100.0	109	US-10-779-731-1	Sequence 1, Appli
8	46	100.0	134	US-10-868-549-10	Sequence 10, Appli
9	46	100.0	197	US-10-352-153-8	Sequence 8, Appli
10	46	100.0	280	US-10-044-622-1	Sequence 1, Appli
11	46	100.0	325	US-10-274-953-3	Sequence 3, Appli
12	46	100.0	325	US-10-161-694-3	Sequence 3, Appli
13	46	100.0	325	US-10-705-476-3	Sequence 3, Appli

14	46	100.0	354	9	US-09-956-095-2	Sequence 2, Appli
15	46	100.0	354	9	US-09-219-345A-11	Sequence 11, Appli
16	46	100.0	354	9	US-09-795-006A-119	Sequence 119, Appli
17	46	100.0	354	10	US-09-375-248-6	Sequence 22, Appli
18	46	100.0	354	11	US-09-765-534B-22	Sequence 26, Appli
19	46	100.0	354	14	US-10-262-538-26	Sequence 5, Appli
20	46	100.0	354	14	US-10-274-953-5	Sequence 5, Appli
21	46	100.0	354	14	US-10-161-694-5	Sequence 5, Appli
22	46	100.0	354	15	US-10-661-740-6	Sequence 6, Appli
23	46	100.0	354	16	US-10-705-476-5	Sequence 5, Appli
24	46	100.0	354	17	US-10-868-577A-4	Sequence 4, Appli
25	46	100.0	354	17	US-10-868-549-4	Sequence 4, Appli
26	43	91.5	8	9	US-09-761-636A-20	Sequence 20, Appli
27	42	91.3	8	9	US-09-761-636A-22	Sequence 22, Appli
28	41	89.1	8	9	US-09-761-636A-19	Sequence 19, Appli
29	41	89.1	9	9	US-09-761-636A-33	Sequence 33, Appli
30	40	87.0	9	9	US-09-761-636A-34	Sequence 34, Appli
31	39	84.8	8	9	US-09-761-636A-21	Sequence 21, Appli
32	39	84.8	354	14	US-10-174-930-1	Sequence 1, Appli
33	39	84.8	362	13	US-10-139-876-4	Sequence 4, Appli
34	37	80.4	172	15	US-10-424-599-211285	Sequence 211285, Appli
35	36	78.3	49	13	US-10-139-876-11	Sequence 11, Appli
36	36	78.3	81	13	US-10-086-623-18	Sequence 18, Appli
37	36	78.3	81	14	US-10-260-539-18	Sequence 18, Appli
38	36	78.3	110	10	US-09-847-524-6	Sequence 6, Appli
39	36	78.3	132	9	US-09-795-006A-151	Sequence 151, Appli
40	36	78.3	132	15	US-10-352-153-11	Sequence 11, Appli
41	36	78.3	133	9	US-09-852-209A-11	Sequence 11, Appli
42	36	78.3	133	14	US-10-131-600-11	Sequence 11, Appli
43	36	78.3	133	15	US-10-352-153-2	Sequence 2, Appli
44	36	78.3	133	15	US-10-303-997B-11	Sequence 11, Appli
45	36	78.3	133	15	US-10-439-337A-11	Sequence 11, Appli

ALIGNMENTS

RESULT 1
US-09-761-636A-6
; Sequence 6, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-6

Query Match 100.0%; Score 46; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db 1 CNEESLIC 8

RESULT 2
US-09-761-636A-9

; Sequence 9, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: STACKER, Steven
; APPLICANT: ACHEN, Marc
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-9

Query Match 100.0%; Score 46; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
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Db 2 CNEESLIC 9

RESULT 3
US-09-761-636A-3
; Sequence 3, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Amino acid residues Vall01-Thr173 of VEGF-D
US-09-761-636A-3

Query Match 100.0%; Score 46; DB 9; Length 73;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
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Db 46 CNEESLIC 53

RESULT 4
US-09-761-636A-1
; Sequence 1, Application US/09761636A
; Patent No. US20020065218A1

; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Amino acid residues of Vall01-Pro196 of VEGF-D
US-09-761-636A-1

Query Match 100.0%; Score 46; DB 9; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
| | | | |
Db 46 CNEESLIC 53

RESULT 5
US-09-956-095-3
; Sequence 3, Application US/09956095
; Patent No. US20020102260A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; APPLICANT: STACKER, Steven A.
; TITLE OF INVENTION: METHODS FOR TREATING NEOPLASTIC DISEASE CHARACTERIZED BY
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR D EXPRESSION, FOR SCREENING
; TITLE OF INVENTION: FOR NEOPLASTIC DISEASE OR METASTATIC RISK AND FOR MAINTAINING
; FILE REFERENCE: 1064/48666PC
; CURRENT APPLICATION NUMBER: US/09/956,095
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 09/796,714
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/234,196
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-956-095-3

Query Match 100.0%; Score 46; DB 9; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
| | | | |
Db 54 CNEESLIC 61

RESULT 6
US-09-219-345A-1
; Sequence 1, Application US/09219345A
; Patent No. US2002012722A1
; GENERAL INFORMATION:

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; APPLICANT: ACHEN, Marc
; TITLE OF INVENTION: EXPRESSION VECTORS AND CELL LINES EXPRESSING VASCULAR
; TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR D, AND METHOD OF TREATING
; TITLE OF INVENTION: MELANOMAS
; FILE REFERENCE: 1064/44385 Marc ACHEN
; CURRENT APPLICATION NUMBER: US/09/219,345A
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: AU PP 1131
; PRIOR FILING DATE: 1997-12-24
; PRIOR APPLICATION NUMBER: US 60/087,392
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-219-345A-1

Query Match      100.0%; Score 46; DB 9; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CNEESLIC 8
Db      54 CNEESLIC 61

RESULT 7
US-10-779-731-1
; Sequence 1, Application US/10779731
; Publication No. US20040141917A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
; FILE REFERENCE: ACHEN et al-1064-44660
; CURRENT APPLICATION NUMBER: US/10/779,731
; CURRENT FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: US/10/100,037
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/469,186
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/113,254
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/134,556
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-779-731-1

Query Match      100.0%; Score 46; DB 16; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CNEESLIC 8
Db      54 CNEESLIC 61

RESULT 8
US-10-868-549-10
; Sequence 10, Application US/10868549
; Publication No. US20050043235A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al.
; TITLE OF INVENTION: USE OF VEGF-C OR VEGF-D IN RECONSTRUCTIVE SURGERY
; FILE REFERENCE: 28967/39117A
; CURRENT APPLICATION NUMBER: US/10/868,549

; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,114
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR FILING DATE: 2003-06-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-868-549-10

Query Match      100.0%; Score 46; DB 17; Length 134;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CNEESLIC 8
Db      79 CNEESLIC 86

RESULT 9
US-10-352-153-8
; Sequence 8, Application US/10352153
; Publication No. US20030211101A1
; GENERAL INFORMATION:
; APPLICANT: Wise, Lyn M
; APPLICANT: Mercer, Andrew A
; APPLICANT: Savory, Loreen J
; APPLICANT: Fleming, Stephen B
; APPLICANT: Stacker, Stephen
; TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
; TITLE OF INVENTION: VIRUS N22 BINDS AND ACTIVATES MAMMALIAN VEGF
; FILE OF INVENTION: RECEPTOR-2, AND USES THEREOF
; FILE REFERENCE: Sequence Listing for 09/431,833
; CURRENT APPLICATION NUMBER: US/10/352,153
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US/09/431,888A
; PRIOR FILING DATE: 1999-11-02
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/106,689
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/106,800
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-352-153-8

Query Match      100.0%; Score 46; DB 15; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CNEESLIC 8
Db      70 CNEESLIC 77

RESULT 10
US-10-044-622-1
; Sequence 1, Application US/10044622
; Publication No. US20020155538A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL ENDOTHELIAL GROWTH
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,622
FILING DATE: 09-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/788,812
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0185 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGAST01
CLONE: 873352
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-044-622-1

Query Match 100.0%; Score 46; DB 13; Length 280;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNEESLIC 8
Db 146 CNEESLIC 153

RESULT 11
US-10-274-953-3
; Sequence 3, Application US/10274953
; Publication No. US20030114658A1
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/274,953
; FILING DATE: 22-Oct-2002
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/296,275
; FILING DATE:
; APPLICATION NUMBER: 08/915,795
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Breast
; US-10-274-953-3
Query Match 100.0%; Score 46; DB 14; Length 325;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CNEESLIC 8
Db 117 CNEESLIC 124
RESULT 12
US-10-161-694-3
; Sequence 3, Application US/10161694
; Publication No. US20030125537A1
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,694
; FILING DATE: 05-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/296,275
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/915,795
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844

TELEX: N/A
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Breast
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-161-694-3

Query Match 100.0%; Score 46; DB 14; Length 325;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
DB 117 CNEESLIC 124

RESULT 13
US-10-705-476-3
; Sequence 3, Application US/10705476
; Publication No. US20040175730A1
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; Andrew F. WILKS
; Steven A. STACKER
; Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/705,476
; FILING DATE: 12-Nov-2003
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,694
; FILING DATE: 05-Jun-2002
; APPLICATION NUMBER: US/09/296,275
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/915,795
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A

INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO

; ORIGINAL SOURCE:
; TISSUE TYPE: Human Breast
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-705-476-3

Query Match 100.0%; Score 46; DB 16; Length 325;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
DB 117 CNEESLIC 124

RESULT 14
US-09-956-095-2
; Sequence 2, Application US/09956095
; Patent No. US20020102260A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; APPLICANT: STACKER, Steven A.
; TITLE OF INVENTION: METHODS FOR TREATING NEOPLASTIC DISEASE CHARACTERIZED BY
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR D EXPRESSION, FOR SCREENING
; TITLE OF INVENTION: FOR NEOPLASTIC DISEASE OR METASTATIC RISK AND FOR MAINTAINING
; TITLE OF INVENTION: VASCULARIZATION OF TISSUE
; FILE REFERENCE: 1064/48666PC
; CURRENT APPLICATION NUMBER: US/09/956,095
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 09/796,714
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/234,196
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-956-095-2

Query Match 100.0%; Score 46; DB 9; Length 354;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
DB 146 CNEESLIC 153

RESULT 15
US-09-219-345A-11
; Sequence 11, Application US/09219345A
; Patent No. US20020127222A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; TITLE OF INVENTION: EXPRESSION VECTORS AND CELL LINES EXPRESSING VASCULAR
; TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR D, AND METHOD OF TREATING
; TITLE OF INVENTION: MELANOMAS
; FILE REFERENCE: 1064/44385 Marc ACHEN
; CURRENT APPLICATION NUMBER: US/09/219,345A
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: AU PP 1131
; PRIOR FILING DATE: 1997-12-24
; PRIOR APPLICATION NUMBER: US 60/087,392
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-219-345A-11

Query Match 100.0%; Score 46; DB 9; Length 354;
 Best Local Similarity 100.0%; Pred. No. 4.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CNEESLIC 8
 Db 146 CNEESLIC 153

Search completed: April 1, 2005, 10:36:33
 Job time : 196.603 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 03:33:32 ; Search time 48.9863 Seconds

(without alignments)
83.628 Million cell updates/sec

Title: US-09-761-636A-6

Perfect score: 46

Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	46	100.0	354	1	VEGD_HUMAN	O43915 homo sapien
2	40	87.0	252	2	Q8QGD7	Q8QGD7 gallus gall
3	40	87.0	326	1	VEGD_RAT	O35251 rattus norv
4	40	87.0	326	1	Q91ZE4	Q91ZE4 rattus norv
5	40	87.0	1768	2	Q7RPD9	Q7RPD9 plasmodium
6	39	84.8	267	2	Q64VA6	Q64VA6 bacteroides
7	37	80.4	152	2	Q8B571	Q8B571 pseudocowpo
8	37	80.4	200	2	Q81XN1	Q81XN1 bacillus an
9	36	78.3	65	2	Q8MIN0	Q8MIN0 capra hircu
10	36	78.3	68	2	Q97500	Q97500 oryctolagus
11	36	78.3	75	2	O18843	O18843 oryctolagus
12	36	78.3	78	2	Q9N1S2	Q9N1S2 capreolus c
13	36	78.3	109	2	Q8MIN1	Q8MIN1 capra hircu
14	36	78.3	118	2	Q9M2B1	Q9M2B1 ovis aries
15	36	78.3	120	2	Q866G4	Q866G4 oryctolagus
16	36	78.3	123	2	Q9N1S1	Q9N1S1 capreolus c
17	36	78.3	131	2	Q8MT86	Q8MT86 capreolus c
18	36	78.3	132	2	Q772M8	Q772M8 orf virus s
19	36	78.3	132	2	Q9YMF3	Q9YMF3 orf virus.
20	36	78.3	133	1	VEGH_ORFN2	P52584 orf virus (
21	36	78.3	136	2	Q8QGE8	Q8QGE8 orf virus.
22	36	78.3	137	2	Q6TVW8	Q6TVW8 orf virus.
23	36	78.3	146	1	VEGA_SHEEP	P50412 ovis aries
24	36	78.3	148	2	O42571	O42571 xenopus lae
25	36	78.3	152	2	Q6TVI2	Q6TVI2 bovine papu
26	36	78.3	157	2	Q6R5A5	Q6R5A5 bovine papu
27	36	78.3	164	1	VEGA_CAVPO	P26561 cavia porce
28	36	78.3	190	1	VEGA_BOVIN	P15691 bos taurus
29	36	78.3	190	2	O77643	O77643 ovis aries
30	36	78.3	194	2	O42572	O42572 xenopus lae
31	36	78.3	267	2	Q8VU11	Q8VU11 bacteroides

32	36	78.3	358	1	VEGD_MOUSE	P97946 mus musculu
33	36	78.3	421	2	Q95TI0	Q95TI0 drosophila
34	36	78.3	502	2	Q9VFF4	Q9VFF4 drosophila
35	36	78.3	864	2	Q8IZZ3	Q8IZZ3 homo sapien
36	36	78.3	1115	2	Q27764	Q27764 plasmodium
37	36	78.3	1136	2	Q7RCK5	Q7RCK5 plasmodium
38	36	78.3	1778	2	Q96J14	Q96J14 homo sapien
39	35	76.1	83	2	Q81RL5	Q81RL5 bacillus an
40	35	76.1	86	2	Q73BP6	Q73BP6 bacillus ce
41	35	76.1	138	2	Q6H4N2	Q6H4N2 oryza sativ
42	35	76.1	227	2	Q891A7	Q891A7 clostridium
43	35	76.1	268	2	Q6NE37	Q6NE37 leptospira
44	35	76.1	282	2	Q7QBU9	Q7QBU9 anopheles g
45	35	76.1	435	2	Q8N5U8	Q8N5U8 homo sapien

ALIGNMENTS

RESULT 1
VEGD_HUMAN
ID VEGD_HUMAN STANDARD; PRT; 354 AA.
AC O43915;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced growth factor) (FIGF).
DE Name=FIGF; Synonyms=VEGFD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=97349118; PubMed=9205122; DOI=10.1006/geno.1997.4774;
RA Yamada Y., Nezu J.-I., Shimane M., Hirata Y.;
RT "Molecular cloning of a novel vascular endothelial growth factor, VEGF-D.";
RL Genomics 42:483-488(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=98140120; PubMed=9479493; DOI=10.1006/geno.1997.5079;
RA Rocchigiani M., Lestingi M., Luddi A., Orlandini M., Franco B., Rossi E., Ballabio A., Zuffardi O., Oliviero S.;
RT "Human FIGF: cloning, gene structure, and mapping to chromosome Xp22.1 between the FIGA and the GRPR genes.";
RL Genomics 47:207-216(1998).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98118549; PubMed=94353229; DOI=10.1073/pnas.95.2.548;
RA Achen M.G., Jeltsch M., Kuk E., Maekinen T., Vitali A., Wilks A.F., Allitalo K., Stacker S.A.;
RT "Vascular endothelial growth factor D (VEGF-D) is a ligand for the tyrosine kinases VEGF receptor 2 (Flk1) and VEGF receptor 3 (Flt4).";
Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RP PROCESSING, AND SEQUENCE OF 89-94; 100-105 AND 206-213.
RX MEDLINE=20011413; PubMed=10542248; DOI=10.1074/jbc.274.45.32127;
RA Stacker S.A., Stenvers K.L., Caesar C., Vitali A., Domagala T.,
RA Nice E.C., Roufail S., Simpson R.J., Moritz R., Karpanen T.,
RA Alitalo K., Achen M.G.;
RT "Biosynthesis of vascular endothelial growth factor-D involves
proteolytic processing which generates non-covalent homodimers.";
RL J. Biol. Chem. 274:32127-32136 (1999).
CC -!- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
and endothelial cell growth, stimulating their proliferation and
migration and also has effects on the permeability of blood
vessels. May function in the formation of the venous and lymphatic
vascular systems during embryogenesis, and also in the maintenance
of differentiated lymphatic endothelium in adults. Binds and
activates VEGFR-2 (Flk1) and VEGFR-3 (Flt4) receptors.
CC -!- SUBUNIT: Homodimer; non-covalent and antiparallel.
CC -!- TISSUE SPECIFICITY: Highly expressed in lung, heart, small
intestine and fetal lung, and at lower levels in skeletal muscle,
colon, and pancreas.
CC -!- PTM: Undergoes a complex proteolytic maturation which generates a
variety of processed secreted forms with increased activity toward
VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer
linked by disulfide bonds before secretion. The fully processed
VEGF-D is composed mostly of two VEGF homology domains (VHDs)
bound by non-covalent interactions.
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
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CC -----
DR EMBL; D89630; BAA24264.1; -;
DR EMBL; Y12863; CAA73370.1; -;
DR EMBL; Y12864; CAA73371.1; -;
DR EMBL; Y12865; CAA73371.1; JOINED.
DR EMBL; Y12866; CAA73371.1; JOINED.
DR EMBL; Y12867; CAA73371.1; JOINED.
DR EMBL; Y12868; CAA73371.1; JOINED.
DR EMBL; Y12869; CAA73371.1; JOINED.
DR EMBL; Y12870; CAA73371.1; JOINED.
DR EMBL; AJ000185; CAA03942.1; -;
DR EMBL; BC027948; AAB27948.1; -;
DR HSSP; P01127; 1PDG.
DR Genew; HGNC:3708; FTGF.
DR H-INVD; HIX0016668; -;
DR MIM; 300091; -;
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005161; F:platelet-derived growth factor receptor bin. .; TAS.
DR GO; GO:0005102; F:receptor binding; TAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR InterPro; IPR004153; CXXC-repeat.
DR Pfam; PF03128; CXXC; 3.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS00278; PDGF_2; 1.

KW Angiogenesis; Cleavage on pair of basic residues;
KW Direct protein sequencing; Glycoprotein; Growth factor; Mitogen;
KW Multigene family; Repeat; Signal.
FT SIGNAL 1 21 Potential.
FT PROPEP 22 88 Or 99 (in a minor form).
FT CHAIN 89 205 Vascular endothelial growth factor D.
FT PROPEP 206 354
FT DOMAIN 222 318 4 X 16 AA repeats of C-X(10)-C-X-C-
X(1,3)-C.
FT REPEAT 222 237 1 (approximate).
FT REPEAT 258 273 2.
FT REPEAT 277 293 3.
FT REPEAT 301 318 4.
FT DISULFID 111 153 By similarity.
FT DISULFID 142 189 By similarity.
FT DISULFID 146 191 By similarity.
FT DISULFID 136 136 Interchain (By similarity).
FT DISULFID 145 145 Interchain (By similarity).
FT CARBOHYD 155 155 N-linked (GlcNAc...) (potential).
FT CARBOHYD 185 185 N-linked (GlcNAc...) (potential).
FT CARBOHYD 287 287 N-linked (GlcNAc...) (potential).
SQ SEQUENCE 354 AA; 40444 MW; 2048D769D735173E CRC64;
Query Match 100.0%; Score 46; DB 1; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CNEESLIC 8
Db 146 CNEESLIC 153
RESULT 2
Q8QGD7 PRELIMINARY; PRT; 252 AA.
ID Q8QGD7
AC Q8QGD7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vascular endothelial growth factor D.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Diaz-Irelles R., Rodriguez-Leon J., Kawakami Y.,
RA Izpisua-Belmonte J.C.;
RT "Expression of the chick vascular endothelial growth factor D gene
during limb development.";
RL Mech. Dev. 0:0-0(2002).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AF479650; AAM12733.1; -;
DR HSSP; P49763; 1RV6.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS00278; PDGF_2; 1.
KW Growth factor; Mitogen.
SQ SEQUENCE 252 AA; 28768 MW; 643475DAB2E72F27 CRC64;
Query Match 87.0%; Score 40; DB 2; Length 252;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 CNEESLIC 8

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Db 146 CNEESLSC 153
|||||
RESULT 3
VEGD RAT STANDARD; PRT; 326 AA.
AC Q35251.
DT 28-FEB-2003 (Rel. 41, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
DE growth factor) (FIGF).
GN Name=Figf; Synonyms=Vegfd;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; Nezu J., Shimane M.;
RA Yamada Y., Hirata Y., to the EMBL/GenBank/DBJ databases.
RL Submitted (JUL-1997)
CC -!- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
CC and endothelial cell growth, stimulating their proliferation and
CC migration and also has effects on the permeability of blood
CC vessels. May function in the formation of the venous and lymphatic
CC vascular systems during embryogenesis, and also in the maintenance
CC of differentiated lymphatic endothelium in adults. Binds and
CC activates VEGFR-3 (Flt4) receptor (By similarity).
CC -!- SUBUNIT: Homodimer; non-covalent and antiparallel (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- PTM: Undergoes a complex proteolytic maturation which generates a
CC variety of processed secreted forms with increased activity toward
CC VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer
CC linked by disulfide bonds before secretion. The fully processed
CC VEGF-D is composed mostly of two VEGF homology domains (VHDS)
CC bound by non-covalent interactions (By similarity).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; AF014827; AAB66557.1; -.
CC HSSP; P01127; IPDG.
CC RGD; 620695; Figf.
CC InterPro; IPR000072; PD_growth_factor.
CC Pfam; PF00341; PDGF; 1.
CC ProDom; PD001629; PD_growth_factor; 1.
CC SMART; SM00141; PDGF; 1.
CC PROSITE; PS00249; PDGF_1; 1.
CC PROSITE; PS0278; PDGF_2; 1.
CC Angiogenesis; Cleavage on pair of basic residues; Glycoprotein;
KW Growth factor; Mitogen; Multigene family; Repeat; Signal.
FT SIGNAL 1 21 Potential.
FT PROPEP 22 93 Potential.
FT CHAIN 94 210 Vascular endothelial growth factor D.
FT PROPEP 211 326 Potential.
FT DOMAIN 227 317 X(1,3)-C.
FT FT 227 242 1 (approximate).
FT REPEAT 263 278 2.
FT REPEAT 282 298 3.
FT REPEAT 306 317 4 (incomplete).
FT DISULFID 116 158 By similarity.
FT DISULFID 147 194 By similarity.
FT DISULFID 151 196 By similarity.
FT DISULFID 141 141 Interchain (By similarity).
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FT DISULFID 150 150 Interchain (By similarity).
FT CARBOHYD 160 160 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 190 190 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 292 292 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 326 AA; 37112 MW; 1261AFA373596C00 CRC64;

Query Match 87.0%; Score 40; DB 1; Length 326;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db 151 CNEESVMC 158
|||||

RESULT 4
Q912E4 PRELIMINARY; PRT; 326 AA.
AC Q912E4.
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE VEGF-D.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21541129; PubMed=11683876;
RA Kirkin V., Mazitschek R., Krishnan J., Steffen A., Waltenberger J.,
RA Pepper M.S., Giannis A., Szeeman J.P.;
RT "Characterization of indolinones which preferentially inhibit VEGF-C-
RT and VEGF-D-induced activation of VEGFR-3 rather than VEGFR-2.";
RL Eur. J. Biochem. 268:5530-5540(2001).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
CC EMBL; AY032728; AAK96008.1; -.
CC HSSP; P01127; IPDG.
CC RGD; GO:0016020; C:membrane; IEA.
CC GO; GO:0008083; F:growth factor activity; IEA.
CC GO; GO:0008283; P:cell proliferation; IEA.
CC GO; GO:0000074; P:regulation of cell cycle; IEA.
CC Pfam; PF00341; PDGF; 1.
CC ProDom; PD001629; PD_growth_factor; 1.
CC SMART; SM00141; PDGF; 1.
CC PROSITE; PS00249; PDGF_1; 1.
CC PROSITE; PS0278; PDGF_2; 1.
CC Growth factor; Mitogen.
KW SEQUENCE 326 AA; 37106 MW; D7CAEBA6C9FABB7D CRC64;

Query Match 87.0%; Score 40; DB 2; Length 326;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db 151 CNEESVMC 158
|||||

RESULT 5
Q7RPD9 PRELIMINARY; PRT; 1768 AA.
AC Q7RPD9.
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Strong similarity to unknown protein-related.
GN Name=PY01520;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallow S.J., van Aken S.E., Riedmuller S.B., Feidblum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Flossens L., Yates F.R. III, Raine J.D., Sindén R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519 (2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC Preliminary data.
DR EMBL: AABL01000404; EAA20861.1; -.
DR InterPro: IPR008532; DUF814.
DR Pfam: PF05670; DUF814; 1.
SQ SEQUENCE 1768 AA; 205674 MW; 127CB4EA11658448 CRC64;

Query Match 87.0%; Score 40; DB 2; Length 1768;
Best Local Similarity 75.0%; Pred. No. 88;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db |||:|:|
359 CNEENVIC 366

RESULT 6
Q64VA6 PRELIMINARY; PRT; 267 AA.
AC Q64VA6;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=BF1825;
OS Bacteroides fragilis.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YCH46;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuhara S., Hattori M., Hayashi T., Ohnishi Y.;
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation."
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
RW EMBL: AF06841; BAD48572.1; -.
KW Hypothetical protein.
SQ SEQUENCE 267 AA; 30102 MW; 30267558B52E078A CRC64;

Query Match 84.8%; Score 39; DB 2; Length 267;
Best Local Similarity 62.5%; Pred. No. 21;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db |||:|:|
133 CNEEKIVC 140

RESULT 7
Q8B571 PRELIMINARY; PRT; 152 AA.
ID Q8B571;
AC Q8B571;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)

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DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Vascular endothelial growth factor-like protein.
GN Name=VEGF;
OS Pseudocowpox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Parapoxvirus.
OX NCBI_TaxID=129726;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VR634;
RX MEDLINE=22462882; PubMed=12573575; DOI=10.1006/viro.2002.1750;
RA Ueda N., Wise L.M., Stacker S.A., Fleming S.B., Mercer A.A.;
RT "Pseudocowpox virus encodes a homolog of vascular endothelial growth
RT factor."
RL Virology 305:298-309(2003).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL: AF542070; AAO16216.1; -.
DR HSPF; Q9UH58; 1FLT.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0008083; F:growth factor activity; IEA.
DR GO: GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR000072; PD_growth_factor.
DR Pfam: PF00341; PDGF; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR ProDom: PD001629; PD_growth_factor; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS50278; PDGF_2; 1.
KW Growth factor.
SQ SEQUENCE 152 AA; 16202 MW; F4B3956D60B37A3D CRC64;

Query Match 80.4%; Score 37; DB 2; Length 152;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db |||:|:|
89 CNDESQIC 96

RESULT 8
Q81XN1 PRELIMINARY; PRT; 200 AA.
ID Q81XN1; QGHRF8; Q6KK55;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=BA5202, BA54838, GBAA5202;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA Deboy R.T., Madupu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / isolate 0581;

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RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.,
RT "Bacillus anthracis comparative genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Strep;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Rice H.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017040; AAP28871.1; -
DR EMBL; AE017334; AAP24333.1; -
DR EMBL; AE017225; AAT57131.1; -
DR DR TIGR; BA5202; -
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 200 AA; 23905 MW; 70B8DD90E5DBA7A0 CRC64;

Query Match 80.4%; Score 37; DB 2; Length 200;
Best Local Similarity 62.5%; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
DB 52 CNDKMIC 59

RESULT 9
OSMINO PRELIMINARY; PRT; 65 AA.
ID Q8MINO;
AC Q8MINO;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Vascular endothelial growth factor 121 (Fragment).
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Corpus luteum;
RA Kawate N., Tsuji M., Tamada H., Inaba T., Sawada T.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AY114353; RAM76674.1; -
DR HSP; Q9UH58; IFLT.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Growth factor; Mitogen.
FT NON_TER 1
SQ SEQUENCE 65 AA; 7562 MW; BA3E384364B0583 CRC64;

Query Match 78.3%; Score 36; DB 2; Length 65;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
DB 5 CNDKMIC 12

RESULT 10
OSMINO PRELIMINARY; PRT; 65 AA.
ID Q18843
AC Q18843;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Vascular endothelial growth factor (Fragment).
GN Name=VEGF;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White New Zealand; TISSUE=Skeletal muscle;
RX MEDLINE=98191144; PubMed=9530113;
RA Skorjanc D., Jaschinski F., Heine G., Pette D.;
RT "Sequential increases in capillarization and mitochondrial enzymes in low-frequency-stimulated rabbit muscle.";
RL Am. J. Physiol. 274:C810-C818(1998).
CC -1- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AF022179; AAC15469.1; -
DR HSP; Q9UH58; IBJ1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR000072; PD_growth_factor.

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O97500 PRELIMINARY; PRT; 68 AA.
ID O97500;
AC O97500;
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Vascular endothelial growth factor (Fragment).
GN Name=VEGF;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Inoue K., Kawabe Y., Kodama T.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AB020216; BAA36949.1; -
DR HSP; Q9UH58; IBJ1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS0249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Growth factor; Mitogen.
FT NON_TER 1
FT NON_TER 68
FT NON_TER 68
SQ SEQUENCE 68 AA; 7819 MW; 687638661E98DEE0 CRC64;

Query Match 78.3%; Score 36; DB 2; Length 68;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
DB 41 CNDKMIC 48

RESULT 11
O18843 PRELIMINARY; PRT; 75 AA.
ID O18843;
AC O18843;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Vascular endothelial growth factor (Fragment).
GN Name=VEGF;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White New Zealand; TISSUE=Skeletal muscle;
RX MEDLINE=98191144; PubMed=9530113;
RA Skorjanc D., Jaschinski F., Heine G., Pette D.;
RT "Sequential increases in capillarization and mitochondrial enzymes in low-frequency-stimulated rabbit muscle.";
RL Am. J. Physiol. 274:C810-C818(1998).
CC -1- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AF022179; AAC15469.1; -
DR HSP; Q9UH58; IBJ1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR000072; PD_growth_factor.

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DR Pfam; PF00341; PDGF; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR Growth factor; Mitogen.
FT NON TER 1 1
FT NON TER 75 75
SQ SEQUENCE 75 AA; 8720 MW; DDCE2C5B29BE69359 CRC64;

Query Match 78.3%; Score 36; DB 2; Length 75;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db 29 CNDESLEC 36

RESULT 12
Q9N1S2 PRELIMINARY; PRT; 78 AA.
AC Q9N1S2;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Vascular endothelial growth factor isoform 121 (Fragment).
GN Name=VEGF;
OS Capreolus capreolus (Roeder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Odocoileinae; Capreolus.
OX NCBI_TaxID=9858;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Wagener A., Blotner S., Goritz F., Fickel J.;
RT "Detection of growth factors in the testis of roe deer (Capreolus capreolus).";
RL Anim. Reprod. Sci. 64:65-75 (2000).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AF152593; AAF73232.1; -.
DR HSSP; Q9UH58; 1FLT.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; P:cell proliferation; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR002400; GF_cysknot.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR Growth factor; Mitogen.
FT NON TER 1 1
FT NON TER 78 78
SQ SEQUENCE 78 AA; 9131 MW; 7EE20DDFFC17847C CRC64;

Query Match 78.3%; Score 36; DB 2; Length 78;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db 25 CNDESLEC 32

RESULT 13
Q9MIN1 PRELIMINARY; PRT; 109 AA.
AC Q9MIN1;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Vascular endothelial growth factor 165 (Fragment).
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Corpus luteum;
RA Kawate N., Tsuji M., Tamada H., Inaba T., Sawada T.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AY114352; AAM76673.1; -.
DR HSSP; Q9UH58; 1FLT.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; P:cell proliferation; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR Growth factor; Mitogen.
FT NON TER 1 1
FT NON TER 109 AA; 12656 MW; 912657251A37E023 CRC64;

Query Match 78.3%; Score 36; DB 2; Length 109;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db 5 CNDESLEC 12

RESULT 14
Q9MZB1 PRELIMINARY; PRT; 118 AA.
AC Q9MZB1;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Vascular endothelial growth factor (Fragment).
GN Name=VEGF;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placental artery endothelium;
RA Tsai S.C.M., Wen Y.X., Chung J.Y., Chen D.B., Magness R.R., Zheng J.;
RL MEDLINE=22274477; PubMed=12385828; DOI=10.1016/S0303-7207(02)00190-9;
RT in ovine feto-placental artery endothelial growth factor and neuropilin-1 Mol. Cell. Endocrinol. 196:95-106 (2002).
CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AF250375; AAF75258.1; -.
DR HSSP; Q9UH58; 1FLT.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; P:cell proliferation; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.

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DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Growth factor; Mitogen.
FT NON_TER 1
SQ SEQUENCE 118 AA; 13931 MW; 757DC53AA56378A6 CRC64;

Query Match      78.3%; Score 36; DB 2; Length 118;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CNEESLIC 8
Db 58 CNDESLEC 65

RESULT 15
Q866G4 PRELIMINARY; PRT; 120 AA.
AC Q866G4;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Vascular endothelial growth factor (Fragment).
GN Name=VEGF;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Clausen I., Kietz S., Fischer B.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AY196796; AAC42518.1; -.
DR HSSP; Q9UH58; IFLT.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008083; P:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Growth factor; Mitogen.
FT NON_TER 1
SQ SEQUENCE 120 AA; 14032 MW; E563C54980DCE1E8 CRC64;

Query Match      78.3%; Score 36; DB 2; Length 120;
Best Local Similarity 75.0%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CNEESLIC 8
Db 74 CNDESLEC 81

Search completed: April 1, 2005, 09:25:57
Job time : 50.9863 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 07:04:23 ; Search time 28.8493 Seconds

(without alignments)
33.638 Million cell updates/sec

Title: US-09-761-636A-5

Perfect score: 72

Sequence: 1 CASELGKSTNTF 13

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	54	75.0	109	3	US-09-469-186-1
2	54	75.0	109	4	US-09-469-185-1
3	54	75.0	109	4	US-10-100-037-1
4	54	75.0	197	4	US-09-431-888-8
5	54	75.0	325	3	US-08-915-795-3
6	54	75.0	325	4	US-09-296-275-3
7	54	75.0	354	3	US-08-915-795-5
8	54	75.0	354	4	US-09-296-275-5
9	54	75.0	354	4	US-09-375-248-6
10	54	75.0	354	4	US-09-468-647A-109
11	54	75.0	354	4	US-09-169-079-22
12	54	75.0	354	4	US-09-214-982-1
13	54	75.0	362	4	US-09-949-016-11286
14	51	70.8	110	4	US-09-847-524-6
15	51	70.8	321	3	US-08-915-795-9
16	51	70.8	321	4	US-09-847-524-4
17	51	70.8	321	4	US-09-296-275-9
18	51	70.8	358	3	US-08-915-795-8
19	51	70.8	358	4	US-09-847-524-2
20	51	70.8	358	4	US-09-296-275-8
21	51	70.8	358	4	US-09-438-046-15
22	43	59.7	83	3	US-08-875-811-2
23	43	59.7	83	3	US-09-071-672-3
24	43	59.7	83	4	US-09-986-119-3
25	43	59.7	104	1	US-08-283-971-1
26	43	59.7	104	1	US-07-921-619-1
27	43	59.7	104	1	US-08-467-955-1

28 43 59.7 104 1 US-08-467-955-2 Sequence 2, Appli
29 43 59.7 104 2 US-08-891-848-13 Sequence 13, Appli
30 43 59.7 104 3 US-08-875-811-1 Sequence 1, Appli
31 43 59.7 104 3 US-03-394-268-1 Sequence 1, Appli
32 43 59.7 104 3 US-09-394-268-2 Sequence 2, Appli
33 43 59.7 104 3 US-09-071-672-1 Sequence 1, Appli
34 43 59.7 104 4 US-09-687-748-1 Sequence 1, Appli
35 43 59.7 104 4 US-09-687-748-2 Sequence 2, Appli
36 43 59.7 104 4 US-08-626-288-1 Sequence 1, Appli
37 43 59.7 104 4 US-08-626-288-2 Sequence 2, Appli
38 43 59.7 104 4 US-09-095-429-1 Sequence 1, Appli
39 43 59.7 104 4 US-09-095-429-2 Sequence 2, Appli
40 43 59.7 104 4 US-09-986-119-1 Sequence 1, Appli
41 43 59.7 105 3 US-08-875-811-24 Sequence 24, Appli
42 43 59.7 105 3 US-08-875-811-26 Sequence 26, Appli
43 43 59.7 105 3 US-08-875-811-39 Sequence 39, Appli
44 43 59.7 106 3 US-08-875-811-28 Sequence 28, Appli
45 43 59.7 107 3 US-08-875-811-20 Sequence 20, Appli

ALIGNMENTS

RESULT 1
US-09-469-186-1
; Sequence 1, Application US/09469186
; Patent No. 6383484
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; APPLICANT: STACKER, Steve A.
; TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
; FILE REFERENCE: ACHEN et al-1064-44660
; CURRENT APPLICATION NUMBER: US/09/469,186
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 60/113,254
; EARLIER FILING DATE: 1998-12-21
; EARLIER APPLICATION NUMBER: 60/134,556
; EARLIER FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-469-186-1

Query Match 75.0%; Score 54; DB 3; Length 109;
Best Local Similarity 100.0%; Pred.No. 0.065;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 ASELGKSTNTF 12
Db 29 ASELGKSTNTF 39

RESULT 2
US-09-469-185-1
; Sequence 1, Application US/09469185
; Patent No. 6531185
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; APPLICANT: STACKER, Steve A.
; TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
; FILE REFERENCE: ACHEN et al-1064-44660
; CURRENT APPLICATION NUMBER: US/09/469,185
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 60/113,254
; EARLIER FILING DATE: 1998-12-21
; EARLIER APPLICATION NUMBER: 60/134,556
; EARLIER FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1

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; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-469-185-1

Query Match          75.0%; Score 54; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASELGKSTNTF 12
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Db 29 ASELGKSTNTF 39

RESULT 3
US-10-100-037-1
; Sequence 1, Application US/10100037
; Patent No. 6730489
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; TITLE OF INVENTION: ANTIBODIES TO TRUNCATED VEGF-D AND USES THEREOF
; FILE REFERENCE: ACHEN et al-1064-44660
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/469,186
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/113,254
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/134,556
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-100-037-1

Query Match          75.0%; Score 54; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASELGKSTNTF 12
   |||||
Db 29 ASELGKSTNTF 39

RESULT 4
US-09-431-888-8
; Sequence 8, Application US/09431888A
; Patent No. 6541008
; GENERAL INFORMATION:
; APPLICANT: Wise, Lyn M
; APPLICANT: Mercer, Andrew A
; APPLICANT: Savory, Loreen J
; APPLICANT: Fleming, Stephen B
; APPLICANT: Stackner, Stephen
; TITLE OF INVENTION: VASCULAR ENOTHELIAL GROWTH FACTOR-LIKE PROTEIN FROM ORF
; TITLE OF INVENTION: VIRUS N22 BINDS AND ACTIVATES MAMMALIAN VEGF
; TITLE OF INVENTION: RECEPTOR-2, AND USES THEREOF
; FILE REFERENCE: Sequence Listing for 09/431,833
; Patent No. 6541008
; CURRENT APPLICATION NUMBER: US/09/431,888A
; CURRENT FILING DATE: 1999-11-02
; EARLIER APPLICATION NUMBER: 60/106,689
; EARLIER FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/106,800
; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 197

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-431-888-8

Query Match          75.0%; Score 54; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASELGKSTNTF 12
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Db 45 ASELGKSTNTF 55

RESULT 5
US-08-915-795-3
; Sequence 3, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,795
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Breast
US-08-915-795-3

Query Match          75.0%; Score 54; DB 3; Length 325;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASELGKSTNTF 12
   |||||
Db 92 ASELGKSTNTF 102

RESULT 6
US-09-296-275-3
; Sequence 3, Application US/09296275
; Patent No. 6689580
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GENERAL INFORMATION:
APPLICANT: MARC G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: Kari ALITALO
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Suite 700
CITY: Washington
STATE: DC
COUNTRY: United States of America
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/296,275
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/915,795
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/42983
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
TELEX: N/A
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: Human Breast
US-09-296-275-3
Query Match 75.0%; Score 54; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ASELGKSTNTF 12
Db 92 ASELGKSTNTF 102
RESULT 7
US-08-915-795-5
Sequence 5, Application US/08915795
Patent No. 6235713
GENERAL INFORMATION:
APPLICANT: MARC G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: Kari ALITALO
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Suite 700
CITY: Washington
STATE: DC
COUNTRY: United States of America
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/42983
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
TELEX: N/A
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: Human Lung
US-08-915-795-5
Query Match 75.0%; Score 54; DB 3; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ASELGKSTNTF 12
Db 121 ASELGKSTNTF 131
RESULT 8
US-09-296-275-5
Sequence 5, Application US/09296275
Patent No. 6689580
GENERAL INFORMATION:
APPLICANT: MARC G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: Kari ALITALO
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Suite 700
CITY: Washington
STATE: DC
COUNTRY: United States of America
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/296,275
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/915,795
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/42983
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
TELEX: N/A
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: Human Lung
US-08-915-795-5

; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Lung
; US-09-296-275-5

Query Match 75.0%; Score 54; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 ASELGKSTNTF 12
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Db 121 ASELGKSTNTF 131

RESULT 9

US-09-375-248-6
; Sequence 6, Application US/09375248
; Patent No. 6764820
; GENERAL INFORMATION:
; APPLICANT: Ferrell, Robert E.
; APPLICANT: Alitalo, Kari
; APPLICANT: Finegold, David N.
; APPLICANT: Karkkainen, Marika
; TITLE OF INVENTION: SCREENING AND THERAPY FOR LYMPHATIC DISORDERS INVOLVING
; FILE REFERENCE: 28967/35235A
; CURRENT APPLICATION NUMBER: US/09/375,248
; CURRENT FILING DATE: 1999-08-16
; EARLIER APPLICATION NUMBER: PCT/US99/06133
; EARLIER FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-375-248-6

Query Match 75.0%; Score 54; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 ASELGKSTNTF 12
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Db 121 ASELGKSTNTF 131

RESULT 10

US-09-468-647A-109
; Sequence 109, Application US/09468647A
; Patent No. 6783953
; GENERAL INFORMATION:
; APPLICANT: Gordon, Robert D
; APPLICANT: Sprengel, Jorg J
; APPLICANT: Von, Jeffery R
; APPLICANT: Dijkmans, Josiena J.H.
; APPLICANT: Gosiowska, Anna
; APPLICANT: Dhanaraj, Sridevi N
; APPLICANT: Xu, Jean
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-X
; FILE REFERENCE: B0192.70011US00
; CURRENT APPLICATION NUMBER: US/09/468,647A
; CURRENT FILING DATE: 1999-12-21

; PRIOR APPLICATION NUMBER: GB 9828377.3
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/124,967
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/164,131
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 109
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-468-647A-109

Query Match 75.0%; Score 54; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 ASELGKSTNTF 12
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Db 121 ASELGKSTNTF 131

RESULT 11

US-09-169-079-22
; Sequence 22, Application US/09169079
; Patent No. 6824777
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Kaipainen, Arja
; APPLICANT: Valtola, Reija
; APPLICANT: Jussila, Lotta
; TITLE OF INVENTION: Flt4 (VEGFR-3) as a Target for Tumor Imaging and Anti-Tumor Therap
; FILE REFERENCE: 28113/34891
; CURRENT APPLICATION NUMBER: US/09/169,079
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: 08/901,710
; EARLIER FILING DATE: 1997-07-28
; EARLIER APPLICATION NUMBER: 08/340,011
; EARLIER FILING DATE: 1994-11-14
; EARLIER APPLICATION NUMBER: 08/257,754
; EARLIER FILING DATE: 1994-07-09
; EARLIER APPLICATION NUMBER: 07/959,951
; EARLIER FILING DATE: 1992-10-09
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-169-079-22

Query Match 75.0%; Score 54; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 ASELGKSTNTF 12
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Db 121 ASELGKSTNTF 131

RESULT 12

US-09-214-982-1
; Sequence 1, Application US/09214982
; Patent No. 6828426
; GENERAL INFORMATION:
; APPLICANT: Hirata, Yuichi
; APPLICANT: Nezu, Junichi
; TITLE OF INVENTION: No. 6828426el VEGF-like Factor
; FILE REFERENCE: 50026/014001
; CURRENT APPLICATION NUMBER: US/09/214,982
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 8-185216 Japan

EARLIER FILING DATE: 1996-07-15
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 354
TYPE: PRT
ORGANISM: Homo sapiens
US-09-214-982-1

Query Match 75.0%; Score 54; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASELGKSTNTF 12
DB 121 ASELGKSTNTF 131

RESULT 13
US-09-949-016-11286
Sequence 11286, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11286
LENGTH: 362
TYPE: PRT
ORGANISM: Human.
US-09-949-016-11286

Query Match 75.0%; Score 54; DB 4; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASELGKSTNTF 12
DB 129 ASELGKSTNTF 139

RESULT 14
US-09-847-524-6
Sequence 6, Application US/09847524
Patent No. 6689352
GENERAL INFORMATION:
APPLICANT: ACHEN, Marc G
APPLICANT: STACKER, Steven A
TITLE OF INVENTION: A METHOD FOR ACTIVATING ONLY THE VASCULAR ENDOTHELIAL
RECEPTOR-3 AND USES THEREOF
FILE REFERENCE: Achen&Stacker-mouse VEGF-D
CURRENT APPLICATION NUMBER: US/09/847,524
CURRENT FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 110
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-09-847-524-6

Query Match 70.8%; Score 51; DB 4; Length 110;

Best Local Similarity 90.9%; Pred. No. 0.21;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASELGKSTNTF 12
DB 30 ASELGKSTNTF 40

RESULT 15
US-08-915-795-9
Sequence 9, Application US/08915795
Patent No. 6235713
GENERAL INFORMATION:
APPLICANT: Marc G. ACHEN
APPLICANT: Andrew F. WILKS
APPLICANT: Steven A. STACKER
APPLICANT: Kari ALITALO
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Suite 700
CITY: Washington
STATE: DC
COUNTRY: United States of America
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/42983
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
TELEX: N/A
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
TISSUE TYPE: Mouse Lung
US-08-915-795-9

Query Match 70.8%; Score 51; DB 3; Length 321;
Best Local Similarity 90.9%; Pred. No. 0.64;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASELGKSTNTF 12
DB 121 ASELGKSTNTF 131

Search completed: April 1, 2005, 09:36:14
Job time : 28.8493 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 06:17:29 ; Search time 11.6164 Seconds
(without alignments)
66.262 Million cell updates/sec

Title: US-09-761-636A-6

Perfect score: 46

Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	36	78.3	120	2 A33787	vascular endotheli
2	36	78.3	133	2 B49530	vascular endotheli
3	36	78.3	146	2 S57956	ovine vascular end
4	36	78.3	190	2 B40080	vascular endotheli
5	36	78.3	1115	2 A45761	Ca2+-transporting
6	35	76.1	4427	2 FN0637	polyketide synthas
7	34.5	75.0	351	2 T42421	hypothetical prote
8	34.5	75.0	1778	2 T50074	probable nucleopor
9	34	73.9	295	2 H71078	probable cation ef
10	34	73.9	501	1 A40938	cytochrome P450 ib
11	34	73.9	642	2 T51421	L-aspartate oxidas
12	34	73.9	1722	1 I78879	retinoblastoma bin
13	33	71.7	190	2 A35987	glioma-derived vas
14	33	71.7	190	2 B44881	vascular endotheli
15	33	71.7	214	2 A44881	vascular endotheli
16	33	71.7	291	2 AF0123	probable antigenic
17	33	71.7	325	2 G90130	transcription init
18	33	71.7	350	2 D69143	LPS biosynthesis R
19	33	71.7	551	2 JC7562	glioblastoma RING
20	33	71.7	1786	1 MMHUB1	laminin beta-1 cha
21	32	69.6	169	2 S76289	hypothetical prote
22	32	69.6	183	2 E72459	hypothetical prote
23	32	69.6	190	2 S52130	vascular endotheli
24	32	69.6	232	2 A41551	vascular endotheli
25	32	69.6	272	2 S13587	malate dehydrogena
26	32	69.6	290	2 G97328	uncharacterized co
27	32	69.6	338	2 E86465	hypothetical prote
28	32	69.6	358	2 A82206	protein-glutamate
29	32	69.6	376	2 B72321	conserved hypothet

30	32	69.6	399	2 H87486	1-deoxy-D-xylulose
31	32	69.6	429	2 JH0151	malate dehydrogena
32	32	69.6	429	2 S13588	malate dehydrogena
33	32	69.6	429	2 T16656	hypothetical prote
34	32	69.6	430	2 S17781	malate dehydrogena
35	32	69.6	432	1 DEMZMC	malate dehydrogena
36	32	69.6	432	2 S20743	malate dehydrogena
37	32	69.6	435	2 S52268	malate dehydrogena
38	32	69.6	441	2 S33066	malate dehydrogena
39	32	69.6	441	2 S38346	malate dehydrogena
40	32	69.6	463	2 T15416	hypothetical prote
41	32	69.6	765	2 AF0118	probable kinase yp
42	32	69.6	766	2 AG0179	hypothetical prote
43	32	69.6	1044	2 H97186	glycosyltransferas
44	32	69.6	1047	2 T21306	hypothetical prote
45	32	69.6	1124	2 H88772	protein F23B2.4 [i

ALIGNMENTS

RESULT 1

A33787

vascular endothelial growth factor (version 1) - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 09-Jul-2004

C:Accession: A33787

R:Tischer, E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Schilling, J.; Lau, K.; Crisp,

Biochem. Biophys. Res. Commun. 165, 1198-1206, 1989

A:Title: Vascular endothelial growth factor: a new member of the platelet-derived growth

A:Reference number: A33787; MUID:90121225; PMID:2610687

A:Accession: A33787

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-120 <TIS>

A:Cross-references: UNIPROT:P15691; GB:M33750; NID:G163810; PIDN:AAA30805.1; PID:G163811

C:Keywords: alternative splicing

Query Match 78.3%; Score 36; DB 2; Length 120;

Best Local Similarity 75.0%; Pred. NO. 11;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEESLIC 8

||:|||||

Db 60 CNDESLEC 67

RESULT 2

B49530

vascular endothelial growth factor homolog A2R, 14.7K - Orf virus

C:Species: Orf virus

C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999

C:Accession: B49530

R:Lyttle, D.J.; Fraser, K.M.; Fleming, S.B.; Mercer, A.A.; Robinson, A.J.

J. Virol. 68, 84-92, 1994

A:Title: Homologs of vascular endothelial growth factor are encoded by the poxvirus orf

A:Reference number: A49530; MUID:94076465; PMID:8254780

A:Contents: NZ2

A:Accession: B49530

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-133 <LYT>

A:Cross-references: GB:S67520; NID:G456897; PIDN:AAR29220.1; PID:G456899

A:Note: sequence inconsistent with nucleotide translation

A:Note: sequence extracted from NCBI backbone (NCBIN:141420, NCBIP:141425)

Query Match 78.3%; Score 36; DB 2; Length 133;

Best Local Similarity 75.0%; Pred. NO. 12;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEESLIC 8

||:|||||

Db 71 CNDESLEC 78

C>Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 09-Jul-2004

C/Accession: A45761

R/Murakami, K.; Tanabe, K.; Takada, S.

J. Cell Sci. 97, 487-495, 1990

A>Title: Structure of a Plasmodium yoelii gene-encoded protein homologous to the Ca(2+)-

A/Reference number: A45761; MUID:91161669; PMID:2150071

A/Accession: A45761

A>Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1115 <MUR>

A/Cross-references: UNIPROT:Q27764; GB:X55197; NID:g10097; PIDN:CAA38982.1; PID:g10098

C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain

C/Keywords: hydrolase

F:689-866/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 78.3%; Score 36; DB 2; Length 146;

Best Local Similarity 75.0%; Pred. No. 13;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY

1 CNEESLIC 8

|||||

86 CNEESLEC 93

DB

RESULT 4

B40080

vascular endothelial growth factor precursor (version 2) - bovine

C/Species: Bos primigenius taurus (cattle)

C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C/Accession: B40080; B33787; A33255

R/Leung, D.W.; Cachianes, G.; Kuang, W.J.; Goeddel, D.V.; Ferrara, N.

Science 246, 1306-1309, 1989

A>Title: Vascular endothelial growth factor is a secreted angiogenic mitogen.

A/Reference number: A40080; MUID:90069608; PMID:2479986

A/Accession: B40080

A/Molecule type: mRNA

A/Residues: 1-190 <LEU>

A/Cross-references: UNIPROT:P15691; NID:M32976; PIDN:AAA30502.1; PID:g163007

R/Tischer, E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Schilling, J.; Lau, K.; Crisp

Biochem. Biophys. Res. Commun. 165, 1198-1206, 1989

A>Title: Vascular endothelial growth factor: a new member of the platelet-derived growth

A/Reference number: A33787; MUID:90121225; PMID:2610687

A/Accession: B33787

A/Molecule type: mRNA

A/Residues: 27-190 <TIS>

A/Cross-references: GB:M31836; NID:g163808; PIDN:AAA30804.1; PID:g163809

R/Ferrara, N.; Hensel, W.J.

Biochem. Biophys. Res. Commun. 161, 851-858, 1989

A>Title: Pituitary follicular cells secrete a novel heparin-binding growth factor specific

A/Reference number: A33255; MUID:89286596; PMID:2735925

A/Accession: A33255

A/Molecule type: protein

A/Residues: 27-31 <FER>

C/Keywords: alternative splicing; glycoprotein

F:1-26/Domain: signal sequence #status predicted <SIG>

F:27-190/Product: vascular endothelial growth factor #status predicted <MAT>

F:100/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

78.3%; Score 36; DB 2; Length 190;

Best Local Similarity 75.0%; Pred. No. 17;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY

1 CNEESLIC 8

|||||

86 CNEESLEC 93

DB

RESULT 5

A45761

Ca2+-transporting ATPase (EC 3.6.3.8) - Plasmodium yoelii

C/Species: Plasmodium yoelii

C/Comment: This enzyme is composed of four synthase units. Unit1 comprises beta-ketosynth

acyl-carrier protein domains. Unit3 comprises beta-ketosynthase, acyl-carrier protein and

C/Genetics: pkSL; pkSX

C/Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 09-Jul-2004

C/Accession: A45761

R/Murakami, K.; Tanabe, K.; Takada, S.

J. Cell Sci. 97, 487-495, 1990

A>Title: Structure of a Plasmodium yoelii gene-encoded protein homologous to the Ca(2+)-

A/Reference number: A45761; MUID:91161669; PMID:2150071

A/Accession: A45761

A>Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1115 <MUR>

A/Cross-references: UNIPROT:Q27764; GB:X55197; NID:g10097; PIDN:CAA38982.1; PID:g10098

C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain

C/Keywords: hydrolase

F:689-866/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match

78.3%; Score 36; DB 2; Length 1115;

Best Local Similarity 62.5%; Pred. No. 76;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY

1 CNEESLIC 8

|||||

486 CNEASILC 493

DB

RESULT 6

PN0637

polyketide synthase pksL - Bacillus subtilis

C/Species: Bacillus subtilis

C/Date: 19-May-1994 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004

C/Accession: S25021; PN0637; B69679

R/Scott, C.; Piatti, M.; Cuzzoni, A.; Tognoni, A.; Grandi, G.; Galizzi, A.; Albertini, I.

submitted to the EMBL Data Library, July 1992

A/Description: A Bacillus subtilis large ORF coding for a polypeptide highly similar to

A/Reference number: S25021

A/Accession: S25021

A>Status: preliminary

A/Molecule type: DNA

A/Residues: 1-4427 <SCO>

A/Cross-references: UNIPROT:Q05470; EMBL:Z14098; NID:g40057; PIDN:CAA78479.1; PID:g40058

R/Scott, C.; Piatti, M.; Cuzzoni, A.; Perani, P.; Tognoni, A.; Grandi, G.; Galizzi, A.;

Gene 130, 65-71, 1993

A>Title: A Bacillus subtilis large ORF coding for a polypeptide highly similar to polyket

A/Reference number: PN0637; MUID:93345824; PMID:8344529

A/Accession: PN0637

A>Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 184-282;382-850;926-1115;1409-1648;1665-1761;1876-2344;2469-2560;2609-2702;28

R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero

C/ Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi

A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler

lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinols,

A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,

Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A/Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror,

akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terptrat, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.

A/Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A/Reference number: A69580; MUID:98044033; PMID:9384377

A/Accession: B69679

A>Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-4427 <KUN>

A/Cross-references: GB:Z99113; GB:AL009126; NID:g2634090; PIDN:CAB13602.1; PID:g2634102

A/Experimental source: strain 168

C/Comment: This enzyme is composed of four synthase units. Unit1 comprises beta-ketosynth

acyl-carrier protein domains. Unit3 comprises beta-ketosynthase, acyl-carrier protein and

C/Genetics:

A/Genes: pksL; pksX

C:Superfamily: Bacillus subtilis polyketide synthase pksL; 3-oxoacyl-[acyl-carrier-protein]
F:343-758/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS1>
C:Keywords: acyltransferase; carrier protein
F:1410-1591/Domain: short-chain alcohol dehydrogenase homology <SAD1>
F:1836-2252/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS2>
F:2485-2559/Domain: acyl carrier protein homology <ACP1>
F:2626-2700/Domain: acyl carrier protein homology <ACP2>
F:2783-3181/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS3>
F:3576-3774/Domain: short-chain alcohol dehydrogenase homology <SAD2>
F:3852-3922/Domain: acyl carrier protein homology <ACP3>
F:3992-4372/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS4>

Query Match 76.1%; Score 35; DB 2; Length 4427;
Best Local Similarity 62.5%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db 1205 CNEEQVC 1212
|||||
:
:
:
:
:

RESULT 7
T42421
hypothetical protein - fission yeast (Schizosaccharomyces pombe) (fragment)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: T42421
R:Yoshioaka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A:Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A:Reference number: Z17323; MUID:98162722; PMID:9501991
A:Accession: T42421
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-351 <YOS>
A:Cross-references: EMBL:D89145; NID:g1749497; PIDN:BAAL3807.1; PID:g1749498
A:Experimental source: strain PR745

Query Match 75.0%; Score 34.5; DB 2; Length 351;
Best Local Similarity 72.7%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 CNEESL---IC 8
Db 321 CNEESLTDIC 331
|||||
||
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||
||

RESULT 8
TS0074
probable nucleoporin [imported] - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C:Accession: TS0074
R:McDougall, R.C.; Rayadream, M.A.; Barrell, B.G.; Seeger, K.; Harris, D.
submitted to the EMBL Data Library, December 1999
A:Reference number: Z25034
A:Accession: TS0074
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1778 <MCD>
A:Cross-references: UNIPROT:Q9UTX4; EMBL:AL133357; PIDN:CAB62415.1; GSPDB:GN000066; SPDB:
A:Experimental source: strain 972h(-); cosmid c1486
C:Genetics:
A:Gene: SPDB:SPAC1486.05
A:Map position: 1
A:Introns: 139/2

Query Match 75.0%; Score 34.5; DB 2; Length 1778;
Best Local Similarity 72.7%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 CNEESL---IC 8
|||||
||
||
||
||

Db 1748 CNEESLTDIC 1758

RESULT 9
H71078
probable cation efflux system protein czcd - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C:Accession: H71078
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine, M.; Ohtoku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: H71078
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-295 <KAW>
A:Cross-references: UNIPROT:O58637; GB:AP000004; NID:g3236131; PIDN:BA29990.1; PID:g325:
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank C:Genetics:
A:Gene: PH0896

Query Match 73.9%; Score 34; DB 2; Length 295;
Best Local Similarity 62.5%; Pred. No. 58;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
Db 283 CKEKSMIC 290
|||||
:
:
:
:
:

RESULT 10
A40938
cytochrome P450 ib - rabbit
N:Contains: oxidoreductase (EC 1.-.-.-)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A40938
R:Kikuta, Y.; Sogawa, K.; Haniu, M.; Kinoshita, M.; Kusunose, E.; Nojima, Y.; Yamamoto, S.; J. Biol. Chem. 266, 17821-17825, 1991
A:Title: A novel species of cytochrome P-450 (P-450-ib) specific for the small intestine A:Reference number: A40938; MUID:92011499; PMID:1717443
A:Accession: A40938
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-501 <KIK>
A:Cross-references: UNIPROT:P52786; GB:D90405; NID:g217717; PIDN:BAAL4401.1; PID:g217718 C:Genetics:
A:Gene: CYP2J1
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F:308-469/Domain: cytochrome P450 homology <CYP>
F:447/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 73.9%; Score 34; DB 1; Length 501;
Best Local Similarity 85.7%; Pred. No. 90;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NEESLIC 8
Db 297 NEENLIC 303
|||||
:
:
:
:
:

RESULT 11
TS1421
L-aspartate oxidase-like protein - Arabidopsis thaliana
N:Alternate names: protein T9L3_60
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: TS1421
R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew

submitted to the Protein Sequence Database, August 2000

A:Reference number: Z25394
A:Accession: T51421
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-642 <SAT>
A:Cross-references: UNIPROT:Q9LER1; EMBL:AL391149
A:Experimental source: cultivar Columbia; BAC clone T9L3
C:Genetics:
A:Map position: 5
A:Introns: 43/2; 158/3; 239/3; 258/3; 278/3; 299/2
A:Note: T9L3_60
C:Superfamily: fumarate reductase flavoprotein; 3-oxosteroid 1-dehydrogenase homology; 4

Query Match 73.9%; Score 34; DB 1; Length 642;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
|||:|:
Db 154 CDEETWVC 161

RESULT 12

I78879
retinoblastoma binding protein 2 - human
C:Species: Homo sapiens (man)
C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
C:Accession: I78879; S16954
R:Pattaeay, A.R.; Holin, K.; Dembski, M.S.; Dyson, N.; Harlow, E.; Vuocolo, G.A.; Hanobik
Oncogene 8, 3149-3156, 1993.
A:Title: Characterization of the retinoblastoma binding proteins RBP1 and RBP2.
A:Reference number: I59383; MUID:94020841; PMID:8414517
A:Accession: I78879
A:Status: preliminary; translated from GB/EMBL/DBDJB

A:Molecule type: mRNA
A:Residues: 1-1722 <FAT>
A:Cross-references: UNIPROT:R29375; GB:S66431; NID:9435777; PIDN:AAB28544.1; PID:9435778
R:Deleo-Jones, D.; Huang, P.S.; Jones, K.M.; Haskell, K.M.; Vuocolo, G.A.; Hanobik, M.G.
Nature 352, 251-254, 1991
A:Title: Cloning of cDNAs for cellular proteins that bind to the retinoblastoma gene product.
A:Reference number: S16953; MUID:91312450; PMID:1857421
A:Accession: S16954
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1102-1562, 'KKK' <DEF>
C:Genetics:
A:Gene: GDB:RBP2
A:Cross-references: GDB:119548; OMIM:180280
A:Map position: 3q21-3qter
C:Superfamily: human retinoblastoma binding protein 2

Query Match 73.9%; Score 34; DB 1; Length 1722;
Best Local Similarity 62.5%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
|||:|:
Db 692 CNPERLVC 699

RESULT 13

A35987
glioma-derived vascular endothelial cell growth factor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 05-Nov-1999
C:Accession: A35987
R:Conn, G.; Bayne, M.L.; Soderman, D.D.; Kwok, P.W.; Sullivan, K.A.; Palisi, T.M.; Hope,
Proc. Natl. Acad. Sci. U.S.A. 87, 2628-2632, 1990
A:Title: Amino acid and cDNA sequences of a vascular endothelial cell mitogen that is homologous to the rat growth factor.
A:Reference number: A35987; MUID:90207249; PMID:2320579
A:Accession: A35987
A:Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-190 <CON>
A:Cross-references: GB:M32167; NID:g204287; PIDN:AAA41211.1; PID:g204288

Query Match 71.7%; Score 33; DB 2; Length 190;
Best Local Similarity 62.5%; Pred. No. 61;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
|||:|:
Db 86 CNDEALEC 93

RESULT 14

B44881
vascular endothelial growth factor-1 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C:Accession: B44881; A43351; A61029
R:Breier, G.; Albrecht, U.; Sterrer, S.; Risau, W.
Development 114, 521-532, 1992
A:Title: Expression of vascular endothelial growth factor during embryonic angiogenesis.
A:Reference number: A44881; MUID:92274860; PMID:1592003
A:Accession: B44881

A:Molecule type: mRNA
A:Residues: 1-190 <BRE>
A:Cross-references: UNIPROT:Q00731; GB:S38083; NID:g249858; PIDN:AAB22253.1; PID:g249859
A:Experimental source: embryo
A:Note: sequence extracted from NCBI backbone (NCBIN:107622, NCBIP:107623)
R:Claffey, K.P.; Wilkison, W.O.; Spiegelman, B.M.
J. Biol. Chem. 267, 16317-16322, 1992
A:Title: Vascular endothelial growth factor. Regulation by cell differentiation and activation.
A:Reference number: A43351; MUID:92355593; PMID:1644816
A:Accession: A43351

A:Molecule type: mRNA
A:Residues: 1-116, ER, 119-190 <CLA>
A:Cross-references: GB:M95200; NID:g202350; PIDN:AAA40547.1; PID:g202351
A:Note: sequence extracted from NCBI backbone (NCBIN:110665, NCBIP:110675)
R:Rosenthal, R.A.; Megyesi, J.F.; Henzel, W.J.; Ferrara, N.; Folkman, J.
Growth Factors 4, 53-59, 1990
A:Title: Conditioned medium from mouse sarcoma 180 cells contains vascular endothelial growth factor.
A:Reference number: A61029; MUID:91197543; PMID:2085441
A:Accession: A61029

A:Molecule type: protein
A:Residues: 27-38 <ROS>
C:Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; glycoprotein; mitogenesis

Query Match 71.7%; Score 33; DB 2; Length 190;
Best Local Similarity 62.5%; Pred. No. 61;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
|||:|:
Db 86 CNDEALEC 93

RESULT 15

A44881
vascular endothelial growth factor-3 precursor - mouse
N:Contains: vascular endothelial growth factor-2; vascular permeability factor
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C:Accession: A44881; C44881; A60932; S52136
R:Breier, G.; Albrecht, U.; Sterrer, S.; Risau, W.
Development 114, 521-532, 1992
A:Title: Expression of vascular endothelial growth factor during embryonic angiogenesis.
A:Reference number: A44881; MUID:92274860; PMID:1592003
A:Accession: A44881

A:Molecule type: mRNA
A:Residues: 1-214 <BRE>
A:Cross-references: UNIPROT:Q00731; GB:S37052; NID:g249856; PIDN:AAB22252.1; PID:g249857
A:Experimental source: embryo
A:Note: sequence extracted from NCBI backbone (NCBIN:104677, NCBIP:104678)

A;Accession: C44881
 A;Molecule type: mRNA
 A;Residues: 1-140,209-214 <BR2>
 A;Cross-references: GB:S38100; NID:g249860; PIDN:AB22254.1; PID:g249861
 A;Note: sequence extracted from NCBI backbone (NCBIN:107624, NCBI:P:107625)
 R;Clauss, M.; Gerlach, M.; Gerlach, H.; Brett, J.; Wang, F.; Familletti, P.C.; Pan, Y.C.
 J. Exp. Med. 172, 1535-1545, 1990
 A;Title: Vascular permeability factor: a tumor-derived polypeptide that induces endothelial
 A;Reference number: A60932; MUID:91079755; PMID:2258694
 A;Accession: A60932
 A;Molecule type: protein
 A;Residues: 27-33 <CLA>
 R;Sugihara, T.; Kaul, S.C.; Mitsui, Y.; Wadhwa, R.
 Biochim. Biophys. Acta 1224, 365-370, 1994
 A;Title: Enhanced expression of multiple forms of VEGF is associated with spontaneous im
 A;Reference number: S52136; MUID:95101726; PMID:7803491
 A;Accession: S52136
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 27-46 <SUG>
 C;Comment: Homodimers could be demonstrated for recombinant VEGF-2 but not VEGF-3.
 C;Keywords: alternative splicing; angiogenesis; disulfide bond; glycoprotein; homodimer;
 F;1-26/Domain: signal sequence #status predicted <SIG>
 F;27-214/Product: vascular endothelial growth factor-3 #status experimental <MAT>

Query Match 71.7%; Score 33; DB 2; Length 214;
 Best Local Similarity 62.5%; Pred.No. 67;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEESLIC 8
 Db 86 CNDEALEC 93

Search completed: April 1, 2005, 09:33:22
 Job time : 13.6164 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 06:17:29 ; Search time 18.8767 Seconds
(without alignments)
66.262 Million cell updates/sec

Title: US-09-761-636A-5

Perfect score: 72

Sequence: 1 CASELGKSTNTFC 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	43	59.7	104	A39035	ribonuclease-relat
2	41	56.9	397	AH1220	acetate kinase hom
3	41	56.9	397	AC1574	acetate kinase hom
4	40	55.6	383	TL1722	hypothetical prote
5	39	54.2	409	S42384	Kruppel-like prote
6	39	54.2	1117	C85018	hypothetical prote
7	38	52.8	378	G97177	membrane-associate
8	38	52.8	469	T46230	NAC2-like protein
9	37	51.4	319	A84947	lytB protein (impo
10	37	51.4	421	S53818	XPMC2 protein - Af
11	37	51.4	433	S70914	pectinesterase (EC
12	37	51.4	988	S35362	protein kinase C (
13	37	51.4	1174	T43051	probable membrane
14	37	51.4	1294	S77690	hypothetical prote
15	36.5	50.7	230	S09778	T-cell receptor be
16	36	50.0	35	B49046	hypothetical prote
17	36	50.0	282	A84341	hypothetical prote
18	36	50.0	372	E85170	GTP-binding regula
19	36	50.0	419	S34421	probable RNA helic
20	36	50.0	442	H71410	catalase (EC 1.11.
21	36	50.0	483	S73055	C30A5.5 protein -
22	36	50.0	683	S44780	probable allene ox
23	36	50.0	814	A71419	probable alpha-tre
24	36	50.0	944	T41711	hypothetical prote
25	36	50.0	1226	S69078	MG243 homolog H91
26	35.5	49.3	224	S73823	germin homolog F21
27	35.5	49.3	266	T01199	viral capsid prote
28	35	48.6	47	JC6158	ORF MSV185 hypothe
29	35	48.6	62	T28346	

30	35	48.6	66	2	A27406	toxin CsaII - Mexi
31	35	48.6	80	2	PC4272	cdu3 protein - Clo
32	35	48.6	155	2	D82152	conserved hypothet
33	35	48.6	182	2	H71899	hypothetical prote
34	35	48.6	207	2	AF0199	probable lipoprote
35	35	48.6	218	2	T33545	hypothetical prote
36	35	48.6	228	2	S67199	hypothetical prote
37	35	48.6	238	2	S77699	inner cell wall ma
38	35	48.6	265	2	AF2007	hypothetical prote
39	35	48.6	276	2	S27641	hypothetical prote
40	35	48.6	308	2	AF1990	hypothetical prote
41	35	48.6	375	2	H82329	alanine racemase,
42	35	48.6	393	2	E64239	acetate kinase (EC
43	35	48.6	396	2	D81339	competence-damage
44	35	48.6	415	2	A11611	protein kinase (EC
45	35	48.6	483	1	T43234	

ALIGNMENTS

RESULT 1

A39035

ribonuclease-related anti-tumor protein - northern leopard frog (fragment)

C:Species: Rana pipiens [northern leopard frog]

C>Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 09-Jul-2004

C:Accession: A39035

R:Ardelet, W.; Mikulecki, S.M.; Shogen, K.

J. Biol. Chem. 266, 245-251, 1991

A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early

A:Reference number: A39035; MUID:91093131; PMID:1985896

A:Accession: A39035

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-104 <ARD>

A:Cross-references: UNIPROT:O8UVK5; UNIPROT:O918V8

C:Superfamily: pancreatic ribonuclease

Query Match 59.7%; Score 43; DB 2; Length 104;

Best Local Similarity 61.5%; Pred. No. 2;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13

DB 75 CKYLUKRSNTKFC 87

RESULT 2

AH1220

acetate kinase homolog AckA2 [imported] - Listeria monocytogenes (strain EGD-e)

C:Species: Listeria monocytogenes

C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 16-Aug-2004

C:Accession: AH1220

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,

D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitouran, A.; Mat

ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AH1220

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-397 <GLA>

A:Cross-references: UNIPROT:Q8Y7V1; GB:NC_003210; PIDN:CAC99246.1; PID:gl6410584; GSPDB:S:

A:Experimental source: strain EGD-e

C:Genetics:

A:Gene: AckA2

C:Superfamily: Acetate/propionate kinase

Query Match 56.9%; Score 41; DB 2; Length 397;

Best Local Similarity 72.7%; Pred. No. 16;

Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CASELGKSTNT 11
||| ||| |||
Db 214 CAIEAGKSVNT 224

RESULT 3
AC1574
acetate kinase homolog AckA2 [imported] - Listeria innocua (strain Clip11262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 16-Aug-2004
C:Accession: AC1574
R:Glaeser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1574
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-397 <GLA>
A:Cross-references: UNIPROT:Q92CN9; GB:AL592022; PIDN:CAC96363.1; PID:g16413591; GSPDB:G
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: AckA2
C:Superfamily: Acetate/propionate kinase

Query Match 56.9%; Score 41; DB 2; Length 397;
Best Local Similarity 72.7%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CASELGKSTNT 11
||| ||| |||
Db 214 CAIEAGKSVNT 224

RESULT 4
TI1722
hypothetical protein A231L - Chlorella virus PBCV-1
C:Species: Chlorella virus PBCV-1
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: TI1722
R:Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A:Reference number: Z18806
A:Accession: TI1722
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-383 <GRA>
A:Cross-references: UNIPROT:Q84551; EMBL:U02580; NID:G4028896; PIDN:AAC96599.1
A:Experimental source: specific host Chlorella strain NC64A
C:Genetics:
A:Note: A231L

Query Match 55.6%; Score 40; DB 2; Length 383;
Best Local Similarity 46.2%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
||| ||| |||
Db 304 CVMNIGKKKNEFC 316

RESULT 5
S42384
Kruppel-like protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Sep-1997
C:Accession: S42384

R:Smith, A.
submitted to the EMBL Data Library, March 1994
A:Reference number: S42368
A:Accession: S42384
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-409 <SMI>
A:Cross-references: EMBL:Z30662; NID:G459581; PID:G459587
C:Genetics:
A:Introns: 10/3; 48/3; 182/3; 315/3; 360/3

Query Match 54.2%; Score 39; DB 2; Length 409;
Best Local Similarity 58.3%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CASELGKSTNTF 12
||| ||| |||
Db 229 CKSDLGSPQTTF 240

RESULT 6
C85018
hypothetical protein AT4G01400 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: C85018
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: C85018
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1117 <STO>
A:Cross-references: UNIPROT:Q9M133; GB:NC_001268; NID:g7267637; PIDN:CAB80949.1; GSPDB:G
C:Genetics:
A:Gene: AT4G01400
A:Map position: 4

Query Match 54.2%; Score 39; DB 2; Length 1117;
Best Local Similarity 58.3%; Pred. No. 93;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELGKSTNTF 12
||| ||| |||
Db 922 CLSELGELSSTF 933

RESULT 7
G97177
membrane-associated sensory histidine kinase-like ATPase [imported] - Clostridium acetob
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: G97177
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: G97177
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-378 <KUR>
A:Cross-references: UNIPROT:Q97GW2; GB:AE001437; PIDN:AAK80210.1; PID:GI5025255; GSPDB:G
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC2253

Query Match 52.8%; Score 38; DB 2; Length 378;
Best Local Similarity 63.6%; Pred. No. 51;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELGKSTNT 11

Db 278 CASDIEKSTTT 288
||||: |||||

RESULT 8
T46230
NAC2-like protein - Arabidopsis thaliana
N:Alternate names: protein T9C5.120
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
R:Accession: T46230
R:Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23026
A:Accession: T46230
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-469 <RIE>
A:Cross-references: UNIPROT:Q9SCK6; EMBL:AL132964
A:Experimental source: cultivar Columbia; BAC clone T9C5
C:Genetics:
A:Map position: 3
A:Introns: 60/1; 153/3; 233/3; 332/3; 402/3
A>Note: T9C5.120

Query Match 52.8%; Score 38; DB 2; Length 469;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 SELGKSTNTF 12
||||| |||||

Db 260 SELGSSYNTF 269

RESULT 9
A84947
lytB protein [imported] - Buchnera sp. (strain APS)
C:Species: Buchnera sp.
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
R:Accession: A84947
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A>Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.
A:Reference number: A84930; MUID:20445173; PMID:10993077
A:Accession: A84947
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-319 <STO>
A:Cross-references: GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: lytB; BU147
C:Superfamily: penicillin tolerance protein

Query Match 51.4%; Score 37; DB 2; Length 319;
Best Local Similarity 70.0%; Pred. No. 66;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SELGKSTNTF 12
: ||||| |||||

Db 232 AELGKETGTF 241

RESULT 10
S53818
XPMC2 protein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
R:Accession: S53818
R:Su, J.Y.; Waller, J.L.
Mol. Gen. Genet. 246, 387-396, 1995
A>Title: Cloning and expression of a Xenopus gene that prevents mitotic catastrophe in
A:Reference number: S53818; MUID:95157530; PMID:7854324

A:Accession: S53818
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-421 <SUJ>
A:Cross-references: UNIPROT:Q91560; GB:U10185; NID:G595379; PIDN:AAA82179.1; PID:G595380

Query Match 51.4%; Score 37; DB 2; Length 421;
Best Local Similarity 54.5%; Pred. No. 86;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CASELGKSTNT 11
: ||||| |||||

Db 13 CSGSLGKTANT 23

RESULT 11
S70914
pectinesterase (EC 3.1.1.11) precursor - Erwinia chrysanthemi
N:Alternate names: pectin methyltransferase
C:Species: Erwinia chrysanthemi
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
R:Accession: S70914; S70913
R:Shevchik, V.E.; Condemine, G.; Hugouvieux-Cotte-Pattat, N.; Robert-Baudouy, J.
submitted to the EMBL Data Library, February 1995
A:Description: Characterization of pectin methyltransferase B, an outer membrane lipoprotein
A:Reference number: S70914
A:Accession: S70914
A:Molecule type: DNA
A:Residues: 1-433 <SHE>
A:Cross-references: UNIPROT:Q47474; EMBL:X84665; NID:G1212890; PIDN:CAA59151.1; PID:G1212890
R:Shevchik, V.E.; Condemine, G.; Hugouvieux-Cotte-Pattat, N.; Robert-Baudouy, J.
Mol. Microbiol. 19, 455-466, 1996
A>Title: Characterization of pectin methyltransferase B, an outer membrane lipoprotein of
A:Reference number: S70913; MUID:96228695; PMID:8830237
A:Accession: S70913
A:Status: nucleic acid sequence not shown

A:Molecule type: DNA
A:Residues: 1-53; 234-361 <SHA>
A:Cross-references: EMBL:X84665; NID:G1212890; PIDN:CAA59151.1
A:Experimental source: strain 3937
C:Genetics:
A:Gene: pectB
A:Start codon: GTG
C:Superfamily: pectinesterase pectB
C:Keywords: carboxylic ester hydrolase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-433/Product: pectinesterase #status predicted <MAT>

Query Match 51.4%; Score 37; DB 2; Length 433;
Best Local Similarity 46.2%; Pred. No. 88;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
: ||||| |||||

Db 192 CATKAGATINTTC 204

RESULT 12
S35362
protein kinase C (EC 2.7.1.1-) pck1 - fission yeast (Schizosaccharomyces pombe)
N:Alternate names: pombe C-kinase 1
C:Species: Schizosaccharomyces pombe
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 06-Oct-2000
R:Accession: S35362; T37866; T38203
R:Toda, T.; Shimanuki, M.; Yanagida, M.
EMBO J. 12, 1987-1995, 1993
A>Title: Two novel protein kinase C-related genes of fission yeast are essential for cell
A:Reference number: S35362; MUID:93259141; PMID:8491190
A:Accession: S35362
A:Molecule type: DNA

A:Residues: 1-988 <TOD>
A:Cross-references: EMBL:D14337; NID:G303938; PIDN:BA03267.1; PID:G303939
R:Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, February 1996

A:Reference number: Z21750
A:Accession: T37866
A:Molecule type: DNA
A:Residues: 93-988 <DEV>
A:Cross-references: EMBL:Z69795; PIDN:CAA93697.1; GSPDB:GN000066; SPDB:SPAC17G8.14c
R:Grishchuk, K.; McIntosh, J.R.; Devlin, K.; Churcher, C.; Barrell, B.G.; Rajandream, M.
submitted to the EMBL Data Library, February 1996

A:Reference number: Z21778
A:Accession: T38203

A:Molecule type: DNA
A:Residues: 1-26, 'AMVASTKNP', 36-137 <GRI>
A:Cross-references: EMBL:Z69730; PIDN:CAA93602.1; GSPDB:GN000066; SPDB:SPAC22H10.01c
A:Experimental source: strain 97zh-; cosmid c22H10

C:Genetics:
A:Gene: pck1
A:Map position: 1L
A:Introns: 767/2; 834/3; 897/3; 959/1
C:Superfamily: yeast protein kinase C; protein kinase C zinc-binding repeat homology; p
C:Keywords: ATP; duplication; phospholipid binding; phosphotransferase; serine/threonine
F:414-461/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F:481-530/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F:662-923/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F:670-678/Region: protein kinase ATP-binding motif

Query Match 51.4%; Score 37; DB 1; Length 988;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 LCKSTNTFC 13

||| :|||

DB 817 LGNTTSTFC 825

RESULT 13

protein kinase C (EC 2.7.1.1-) PKC1 - fungus (Cochliobolus heterostrophus)
C:Species: Cochliobolus heterostrophus, Bipolaris maydis
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43051

R:Oeser, B.M.
FEMS Microbiol. Lett. 165, 273-280, 1998
A:Title: PKC1, encoding a protein kinase C, and PAT1, encoding a fatty acid transporter
A:Reference number: Z22303; MUID:98415124; PMID:9742699

A:Accession: T43051
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-1174 <ORS>
A:Cross-references: UNIPROT:O42632; EMBL:Y15839; NID:g2687848; PIDN:CAA75801.1; PID:g268

A:Experimental source: strain C2 (ATCC 48329)
C:Genetics:
A:Gene: pkc1

A:Introns: 146/1; 234/1; 559/1; 952/2; 1019/3; 1155/1
C:Superfamily: yeast protein kinase C; protein kinase C zinc-binding repeat homology; p
C:Keywords: ATP; phospholipid binding; phosphotransferase; serine/threonine-specific pro
F:459-506/Domain: protein kinase C zinc-binding repeat homology <KZNI>
F:527-576/Domain: protein kinase C zinc-binding repeat homology <KZN2>

Query Match 51.4%; Score 37; DB 2; Length 1174;
Best Local Similarity 46.7%; Pred. No. 2.2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 1 CASEL--GKSTNTFC 13

||| :|||

DB 996 CKEEWYGSTTSTFC 1010

RESULT 14

probable membrane protein YOL075c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein O1125; hypothetical protein O1130; hypothetical
C:Species: Saccharomyces cerevisiae
C:Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text_change 16-Aug-2004

C:Accession: S77690; S66767; S66768
R:Alexandraki, D.; Katsoulou, C.; Tzermia, M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66756
A:Accession: S77690
A:Molecule type: DNA
A:Residues: 1-1294 <ALE>
A:Cross-references: UNIPROT:Q08234; EMBL:Z74816; MIPS:YOL075c
A:Note: this is a revision to the sequence from reference S66756

A:Accession: S66767
A:Molecule type: DNA
A:Residues: 1-179, 'TTRTGVLVVKRED' <ALW>
A:Cross-references: EMBL:Z74816
A:Experimental source: strain S288C
A:Note: this sequence has been revised in reference S77690

A:Accession: S66768
A:Molecule type: DNA
A:Residues: 200-1294 <ALF>

A:Cross-references: EMBL:Z74817
A:Experimental source: strain S288C
A:Note: this sequence has been revised in reference S77690

A:Note: this was assumed to be the complete sequence of protein YOL075c
C:Genetics:

A:Cross-references: SGD:S0005435

A:Map position: 15L

A:Note: YOL075c

C:Superfamily: ATP-binding cassette homology
C:Keywords: ATP; nucleotide binding; P-loop; transmembrane protein
F:45-263/Domain: ATP-binding cassette homology <ABCI>
F:62-69/Region: nucleotide-binding motif A (P-loop)

F:376-392/Domain: transmembrane #status predicted <TM1>

F:469-485/Domain: transmembrane #status predicted <TM2>

F:496-512/Domain: transmembrane #status predicted <TM3>

F:606-622/Domain: transmembrane #status predicted <TM4>

F:710-916/Domain: ATP-binding cassette homology <ABC2>

F:727-734/Region: nucleotide-binding motif A (P-loop)

F:1042-1058/Domain: transmembrane #status predicted <TM5>

F:1125-1141/Domain: transmembrane #status predicted <TM6>

F:1177-1193/Domain: transmembrane #status predicted <TM7>

F:1269-1285/Domain: transmembrane #status predicted <TM8>

Query Match 51.4%; Score 37; DB 2; Length 1294;
Best Local Similarity 58.3%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASELKGSTNTNF 12

||| :|||

DB 1161 CGERLGIMTNTF 1172

RESULT 15

S09778

hypothetical protein UL16 precursor - human cytomegalovirus (strain AD169)

C:Species: human cytomegalovirus, human herpesvirus 5

A:Note: host Homo sapiens (man)

C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C:Accession: S09778

R:Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.;

M.; Barrell, B.G.

Curr. Top. Microbiol. Immunol. 154, 125-169, 1990

A:Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus

A:Reference number: S09749; MUID:90269039; PMID:2161319

A:Accession: S09778

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-230 <CHE>

A:Cross-references: UNIPROT:P16757; EMBL:X17403; NID:g59591; PIDN:CAA35448.1; PID:g59620

A:Note: this sequence was submitted to the EMBL Data Library, December 1989

C:Superfamily: human cytomegalovirus hypothetical protein UL16

C:Keywords: glycoprotein; transmembrane protein

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-230/Product: hypothetical protein UL16 #status predicted <MAT>

F:189-206/Domain: transmembrane #status predicted <TMM>
 F:35,41,88,84,95,101,132,145/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 50.7%; Score 36.5; DB 2; Length 230;
 Best Local Similarity 57.1%; Pred. No. 60;
 Matches 8; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
 QY 1 CASELG-KSTNTFC 13
 DB 25 CAVDLGSKSNSTC 38

Search completed: April 1, 2005, 09:33:20
 Job time : 20.8767 secs

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2005, 03:33:32 ; Search time 79.6027 Seconds
(without alignments)
83.628 Million cell updates/sec

Title: US-09-761-636A-5

Perfect score: 72

Sequence: 1 CASELGKSTNTFC 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	54	75.0	354	1	VEGD HUMAN	O43915 homo sapien
2	51	70.8	326	1	VEGD_RAT	O35251 rattus norv
3	51	70.8	326	1	O91ZE4	O91ZE4 rattus norv
4	51	70.8	358	1	VEGD MOUSE	P97946 mus musculus
5	49	68.1	127	2	O918V8	O918V8 rana pipien
6	43	59.7	104	1	RN30 RANPI	P22069 rana pipien
7	43	59.7	127	2	O8UVX5	O8UVX5 rana pipien
8	43	59.7	997	2	O967Z1	O967Z1 trypanosoma
9	42	58.3	1011	2	O9FP94	O9FP94 pneumocysti
10	42	58.3	1086	2	O6UB96	O6UB96 cryptococcu
11	42	58.3	1086	2	O6UB97	O6UB97 cryptococcu
12	41	56.9	316	2	O90ZB2	O90ZB2 brachydanio
13	41	56.9	397	1	ACK2_LISIN	O92CN9 listeria in
14	41	56.9	397	1	ACK2_LISMO	O8Y7V1 listeria mo
15	41	56.9	397	2	O720R2	O720R2 listeria mo
16	41	56.9	611	2	O65NS9	O65NS9 bacillus li
17	40	55.6	283	2	O7UWU5	O7UWU5 rhodopirell
18	40	55.6	297	2	O7RC90	O7RC90 plasmodium
19	40	55.6	297	2	O7R7C30	O7R7C30 plasmodium
20	40	55.6	354	2	O7NOR6	O7NOR6 photorhabdu
21	40	55.6	383	2	O84551	O84551 paramecium
22	40	55.6	605	2	O630E7	O630E7 bacillus ce
23	40	55.6	605	2	O72WY2	O72WY2 bacillus ce
24	40	55.6	605	2	O81410	O81410 bacillus ce
25	40	55.6	605	2	O81J98	O81J98 bacillus an
26	40	55.6	605	2	O6HAH9	O6HAH9 bacillus th
27	40	55.6	681	2	O7X816	O7X816 oryza sativ
28	40	55.6	394	2	O6TQF5	O6TQF5 crimean-con
29	40	55.6	394	2	O6B835	O6B835 crimean-con
30	40	55.6	394	2	O6TFZ7	O6TFZ7 crimean-con
31	40	55.6	394	2	O6TFZ8	O6TFZ8 crimean-con

RESULT 1	VEGD HUMAN	STANDARD;	PRT;	354 AA.
AC	O43915;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced growth factor) (FIGF).			
DE	Name=FIGF; Synonyms=VEGFD;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RC	MEDLINE=97349118; PubMed=9205122; DOI=10.1006/geno.1997.4774;			
RA	Yamada Y., Nezu J.-I., Shimane M., Hirata Y.;			
RT	"Molecular cloning of a novel vascular endothelial growth factor,			
RT	VEGF-D.";			
RL	Genomics 42:483-488(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RC	MEDLINE=98140120; PubMed=9479493; DOI=10.1006/geno.1997.5079;			
RA	Rocchigliani M., Lestingi M., Luddi A., Orlandini M., Franco B.,			
RA	Rossi E., Ballabio A., Zuffardi O., Oliviero S.;			
RT	"Human FIGF: cloning, gene structure, and mapping to chromosome Xp22.1			
RT	between the FIGA and the GRPR genes.";			
RL	Genomics 47:207-216(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=98118549; PubMed=9435229; DOI=10.1073/pnas.95.2.548;			
RA	Achen M.G., Jeltsch M., Kukk E., Maekinen T., Vitali A., Wilks A.F.,			
RA	Alitalo K., Stacker S.A.;			
RT	"Vascular endothelial growth factor D (VEGF-D) is a ligand for the			
RT	tyrosine kinases VEGF receptor 2 (Flk1) and VEGF receptor 3 (Flt4).";			
RL	Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RC	MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,			
RA	Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,			

ALIGNMENTS

FAHEY J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E., Scherch A., Schein J.E., Jones S.D.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[5]

RP PROCESSING, AND SEQUENCE OF 89-94; 100-105 AND 206-213.

RX MEDLINE=20011413; PubMed=10542248; DOI=10.1074/jbc.274.45.32127;

RA Stacker S.A., Stenvers K.L., Caesar C., Vitali A., Domagala T., Rice E.C., Roufail S., Simpson R.J., Moritz R., Karpanen T., Alitalo K., Achen M.G.;

RA "Bioynthesis of vascular endothelial growth factor-D involves proteolytic processing which generates non-covalent homodimers.";

RL J. Biol. Chem. 274:32127-32136 (1999).

CC -!- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis and endothelial cell growth, stimulating their proliferation and migration and also has effects on the permeability of blood vessels. May function in the formation of the venous and lymphatic vascular systems during embryogenesis, and also in the maintenance of differentiated lymphatic endothelium in adults. Binds and activates VEGFR-2 (Flk1) and VEGFR-3 (Flt4) receptors.

CC -!- SUBUNIT: Homodimer; non-covalent and antiparallel.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Highly expressed in lung, heart, small intestine and fetal lung, and at lower levels in skeletal muscle, colon, and pancreas.

CC -!- PTM: Undergoes a complex proteolytic maturation which generates a variety of processed secreted forms with increased activity toward VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer linked by disulfide bonds before secretion. The fully processed VEGF-D is composed mostly of two VEGF homology domains (VHDs) bound by non-covalent interactions.

CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.

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DR EMBL; D89630; BAA24264.1; -

DR EMBL; Y12863; CAA73370.1; -

DR EMBL; Y12864; CAA73371.1; -

DR EMBL; Y12865; CAA73371.1; JOINED.

DR EMBL; Y12866; CAA73371.1; JOINED.

DR EMBL; Y12867; CAA73371.1; JOINED.

DR EMBL; Y12868; CAA73371.1; JOINED.

DR EMBL; Y12869; CAA73371.1; JOINED.

DR EMBL; Y12870; CAA73371.1; JOINED.

DR EMBL; A000185; CAA03942.1; -

DR EMBL; BC027948; AAH27948.1; -

DR HSSP; P01127; LPDG.

DR H-InvDB; HGNC:3708; FIGF.

DR MIM; 300091; -

DR GO; GO:0005615; Cxetracellular space; TAS.

DR GO; GO:0005161; F:platelet-derived growth factor receptor bin. .; TAS.

DR GO; GO:0005102; F:receptor binding; TAS.

DR GO; GO:0008284; F:positive regulation of cell proliferation; TAS.

DR InterPro; IPR0004153; CXXC_repeat

DR InterPro; IPR000072; PD_growth_factor.

DR Pfam; PF03128; CXXC; 3.

DR Pfam; PF00341; PDGF; 1.

DR ProDom; PD001629; PD_growth_factor; 1.

DR SMART; SM00141; PDGF; 1.

DR PROSITE; PS00249; PDGF_1; 1.

DR PROSITE; PS0278; PDGF_2; 1.

KW Angiogenesis; Cleavage on pair of basic residues;

KW Direct protein sequencing; Glycoprotein; Growth factor; Mitogen;

KW Multigene family; Repeat; Signal.

FT SIGNAL 1 21 Potential.

FT PROPEP 22 88 Or 99 (in a minor form).

FT CHAIN 89 205 Vascular endothelial growth factor D.

FT PROPEP 206 354

FT DOMAIN 222 318 4 X 16 AA repeats of C-X(10)-C-X-C-X(1,3)-C.

FT REPEAT 222 237 1 (approximate).

FT REPEAT 258 273 2.

FT REPEAT 277 293 3.

FT REPEAT 301 318 4.

FT DISULFID 111 153 By similarity.

FT DISULFID 142 189 By similarity.

FT DISULFID 146 191 By similarity.

FT DISULFID 136 136 Interchain (By similarity).

FT DISULFID 145 145 Interchain (By similarity).

FT CARBOHYD 155 155 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 185 185 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 287 287 N-linked (GlcNAc...) (Potential).

SQ SEQUENCE 354 AA; 40444 MW; 2048D769D735173E CRC64;

Query Match 75.0%; Score 54; DB 1; Length 354;

Best Local Similarity 100.0%; Pred. No. 0.18;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASELGKSTNTF 12

DB 121 ASELGKSTNTF 131

RESULT 2

VEGD_RAT STANDARD; PRT; 326 AA.

ID_VEGD_RAT

AC O39251;

DT 28-FEB-2003 (Rel. 41, Created)

DT 08-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced growth factor) (FIGF).

GN Name=Figf; Synonyms=vegfd;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OC NCBI_TaxID=10116;

OX [1]

RN [1] SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley;

RA Yamada Y., Hirata Y., Nezu J., Shimane M.;

RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis and endothelial cell growth, stimulating their proliferation and migration and also has effects on the permeability of blood vessels. May function in the formation of the venous and lymphatic vascular systems during embryogenesis, and also in the maintenance of differentiated lymphatic endothelium in adults. Binds and activates VEGFR-3 (Flt4) receptor (By similarity).

CC -!- SUBUNIT: Homodimer; non-covalent and antiparallel (By similarity).

CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -!- PTM: Undergoes a complex proteolytic maturation which generates a variety of processed secreted forms with increased activity toward VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer linked by disulfide bonds before secretion. The fully processed VEGF-D is composed mostly of two VEGF homology domains (VHDs) bound by non-covalent interactions (By similarity).

CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.

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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF014827; AAB66557.1; --
DR HSSP; P01127; IPDG.
DR RGD; 620695; Figf.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1; PD_growth_factor.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Angiogenesis; Cleavage_on pair of basic residues; Glycoprotein;
Growth factor; Mitogen; Multigene family; Repeat; Signal.
FT SIGNAL 1 21 Potential.
FT PROPEP 22 93 Potential.
FT CHAIN 94 210 Vascular endothelial growth factor D.
FT PROPEP 211 326 Potential.
FT DOMAIN 227 317 4 X 16 AA repeats of C-X(10)-C-X-C-X(1,3)-C.
FT REPEAT 227 242 1 (approximate).
FT REPEAT 263 278 2.
FT REPEAT 282 298 3.
FT REPEAT 306 317 4 (incomplete).
FT DISULFID 116 158 By similarity.
FT DISULFID 147 194 By similarity.
FT DISULFID 151 196 By similarity.
FT DISULFID 141 141 Interchain (By similarity).
FT DISULFID 150 150 Interchain (GlcNAc. .) (Potential).
FT CARBOHYD 160 160 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 190 190 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 292 292 N-linked (GlcNAc. .) (Potential).
SQ SEQUENCE 326 AA; 37112 MW; 1261AFA373596C00 CRC64;

Query Match 70.8%; Score 51; DB 1; Length 326;
Best Local Similarity 90.9%; Pred. No. 0.61;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASELGKSTNTF 12
Db 126 ASELGKTTNTF 136

RESULT 3
Q91ZE4 PRELIMINARY; PRT; 326 AA.
AC Q91ZE4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE VEGF-D.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21541129; PubMed=11683876;
RA Kirkin V., Mazitschek R., Krishnan J., Steffen A., Waltenberger J., Pepper M.S., Giannis A., Sleeman J.P.;
RT "Characterization of indolinones which preferentially inhibit VEGF-C- and VEGF-D-induced activation of VEGFR-3 rather than VEGFR-2.";
RL Eur. J. Biochem. 268:5530-5540(2001).
CC -1- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
DR EMBL; AF032728; AAK96008.1; --
DR HSSP; P01127; IPDG.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0008083; F.growth factor activity; IEA.
DR GO; GO:0008283; P.cell proliferation; IEA.
DR GO; GO:0000074; P.regulation of cell cycle; IEA.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.

DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Growth factor; Mitogen.
SQ SEQUENCE 326 AA; 37106 MW; D7CAEBA6C9FABB7D CRC64;

Query Match 70.8%; Score 51; DB 2; Length 326;
Best Local Similarity 90.9%; Pred. No. 0.61;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASELGKSTNTF 12
Db 126 ASELGKTTNTF 136

RESULT 4
VEGD MOUSE STANDARD; PRT; 358 AA.
AC P97946;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced growth factor) (FIGF).
GN Name=Figf; Synonyms=Vegfd;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Fibroblast;
RX MEDLINE=97030254; PubMed=8876195; DOI=10.1073/pnas.93.21.11675;
RA Orlandini M., Marconini L., Ferruzzi R., Oliviero S.;
RT "Identification of a c-fos-induced gene that is related to the platelet-derived growth factor/vascular endothelial growth factor family.";
RT Proc. Natl. Acad. Sci. U.S.A. 93:11675-11680(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=97349118; PubMed=9205122; DOI=10.1006/geno.1997.4774;
RA Yamada Y., Nezu J.-I., Shimane M., Hirata Y.;
RT "Molecular cloning of a novel vascular endothelial growth factor, VEGF-D.";
RL Genomics 42:483-488(1997).
RN [3]
RP DEVELOPMENTAL STAGE.
RX MEDLINE=98288130; PubMed=9622638; DOI=10.1016/S0925-4773(98)00049-5;
RA Avantiaggio V., Orlandini M., Acampora D., Oliviero S., Simeone A.;
RT "Embryonic expression pattern of the murine figf gene, a growth factor belonging to platelet-derived growth factor/vascular endothelial growth factor family.";
RT Mech. Dev. 73:221-224(1998).
RN [4]
RP RECEPTOR SPECIFICITY.
RX MEDLINE=21276411; PubMed=11279005; DOI=10.1074/jbc.M100097200;
RA Baldwin M.E., Catimel B., Nice E.C., Roufail S., Hall N.E., Stevens K.L., Karkkainen M.J., Alitalo K., Stacker S.A., Achen M.G.;
RT "The specificity of receptor binding by vascular endothelial growth factor-d is different in mouse and man.";
RL J. Biol. Chem. 276:19166-19171(2001).
CC -1- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis and endothelial cell growth, stimulating their proliferation and migration and also has effects on the permeability of blood vessels. May function in the formation of the venous and lymphatic vascular systems during embryogenesis, and also in the maintenance of differentiated lymphatic endothelium in adults. Binds and activates VEGFR-3 (Flt4) receptor.
CC -1- SUBUNIT: Homodimer; non-covalent and antiparallel.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Highly expressed in fetal and adult lung.
CC -1- DEVELOPMENTAL STAGE: Expressed in a dynamic pattern in several

body structures and organs of the embryo such as limb buds, acoustic ganglion, teeth, heart, anterior pituitary as well as lung and kidney mesenchyme, liver, derma, and periosteum of the vertebral column.

CC -!- INDUCTION: By the transcription factor c-fos.

CC -!- PTM: Undergoes a complex proteolytic maturation which generates a variety of processed secreted forms with increased activity toward VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer linked by disulfide bonds before secretion. The fully processed VEGF-D is composed mostly of two VEGF homology domains (VHDS) bound by non-covalent interactions (By similarity).

CC -!- SIMILARITY: Belongs to the PDGF/VEGF growth factor family.

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CC -----

DR EMBL; X99572; CAA67892.1; -.

DR EMBL; D89628; BAAL4002.1; -.

DR HSSP; P01127; PDGF.

DR PMMA-2DPAGE; P97946; -.

DR MGD; MGI:108037; Fgf.

DR GO; GO:0005576; C:extracellular; IDA.

DR GO; GO:0008083; F:growth factor activity; IDA.

DR GO; GO:0005515; P:protein binding; IPI.

DR GO; GO:0008283; P:cell proliferation; IDA.

DR InterPro; IPR004153; CXKC-repeat.

DR InterPro; IPR000072; PD_growth_factor.

DR Pfam; PF03128; CXKC; 2.

DR Pfam; PF00341; PDGF; 1.

DR ProDom; PD001629; PD_growth_factor; 1.

DR SMART; SM00141; PDGF_1; 1.

DR PROSITE; PS00249; PDGF_1; 1.

DR PROSITE; PS0278; PDGF_2; 1.

CC Angiogenesis; Cleavage on pair of basic residues; Glycoprotein; Growth factor; Mitogen; Multigene family; Repeat; Signal.

FT SIGNAL 1 21 Potential.

FT PROPEP 22 93 Potential.

FT CHAIN 94 210 Vascular endothelial growth factor D.

FT PROPEP 211 358 Potential.

FT DOMAIN 227 323 4 X 16 AA repeats of C-X(10)-C-X-C-X(1,3)-C.

FT REPEAT 227 242 1 (approximate).

FT REPEAT 263 278 2.

FT REPEAT 282 298 3.

FT REPEAT 306 323 4.

FT DISULFID 116 158 By similarity.

FT DISULFID 147 194 By similarity.

FT DISULFID 151 196 By similarity.

FT DISULFID 141 141 Interchain (By similarity).

FT DISULFID 150 150 Interchain (By similarity).

FT CARBOHYD 160 160 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 190 190 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 292 292 N-linked (GlcNAc...) (Potential).

CC SEQUENCE 358 AA; 40908 MW; 6636B17FBF07037C CRC64;

Query Match 70.8%; Score 51; DB 1; Length 358;
Best Local Similarity 90.9%; Pred. No. 0.67;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASELGKSTNTF 12
|||||

Db 126 ASELGKSTNTF 136

RESULT 5

Q918V8 PRELIMINARY; PRT; 127 AA.

ID Q918V8

AC Q918V8;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Onconase variant rapR1 precursor.

OS Rana pipiens (Northern leopard frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

OX NCBI_TaxID=8404;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=20330357; PubMed=10871370; DOI=10.1093/nar/28.12.2375;

RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;

RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a 3' UTR of unusual length and structure.";

RL Nucleic Acids Res. 28:2375-2382(2000).

CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.

DR EMBL; AF165133; AAF76935.1; -.

DR PIR; A39035; A39035.

DR HSSP; P22069; 10NC.

DR GO; GO:0004519; F:endonuclease activity; IEA.

DR GO; GO:0016787; F:hydrolase activity; IEA.

DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.

DR InterPro; IPR001427; RNaseA.

DR Pfam; PF00074; RNaseA; 1.

DR ProDom; PD000535; RNaseA; 1.

DR SMART; SM00092; RNase Pc; 1.

DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.

KW Endonuclease; Hydrolase; Nuclease; Signal.

FT SIGNAL 1 23 Potential.

CC SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 68.1%; Score 49; DB 2; Length 127;
Best Local Similarity 69.2%; Pred. No. 0.56;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
|:|||||

Db 98 CKYKLGKSTNTFC 110

RESULT 6

RN30_RANPI

ID RN30_RANPI STANDARD; PRT; 104 AA.

AC P22069;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

DE P-30 protein (EC 3.1.27.-) (Onconase).

OS Rana pipiens (Northern leopard frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

OX NCBI_TaxID=8404;

RN [1]

RP SEQUENCE.

RC TISSUE=Embryo;

RX MEDLINE=91093131; PubMed=1985896;

RA Ardelit W., Mikulski S.M., Shogen K.;

RT "Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos. Homology to pancreatic ribonucleases.";

RN J. Biol. Chem. 266:245-251(1991).

RN [2]

RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).

RX MEDLINE=94166079; PubMed=8120892;

RA Mosimann S.C., Ardelit W., James M.N.G.;

RT "Refined 1.7 A X-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity.";

RL J. Mol. Biol. 236:1141-1153(1994).

CC -!- FUNCTION: Basic protein with antiproliferative/cytotoxic activity against several tumor cell lines in vitro, as well as antitumor in vivo. It exhibits a ribonuclease-like activity against high molecular weight ribosomal RNA.

CC -!- DEVELOPMENTAL STAGE: Early embryos (up to four blastomere stage).
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PDB; 1ONC; X-ray; @=1-104.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW 3D-structure; Direct protein sequencing; Endonuclease; Hydrolase;
KW Nuclease; Pyridoxal carboxylic acid.
FT SITE 31 35 Substrate binding.
FT MOTIF 1 1 Pyridoxal carboxylic acid.
FT ACT_SITE 10 10 Proton acceptor.
FT ACT_SITE 97 97 Proton donor.
FT DISULFID 19 68
FT DISULFID 30 75
FT DISULFID 48 90
FT DISULFID 87 104
FT HELIX 3 10
FT STRAND 11 12
FT STRAND 19 22
FT TURN 23 24
FT TURN 26 30
FT STRAND 33 38
FT HELIX 41 45
FT HELIX 46 48
FT TURN 49 50
FT STRAND 55 58
FT STRAND 63 70
FT TURN 74 75
FT STRAND 77 84
FT STRAND 86 91
FT TURN 92 93
FT STRAND 94 101
SQ SEQUENCE 104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;

Query Match 59.7%; Score 43; DB 1; Length 104;
Best Local Similarity 61.5%; Pred. No. 6.1;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
| : | | | | |
Db 75 CKYKLLKSTNKF 87

RESULT 7
Q8UVX5 PRELIMINARY; PRT; 127 AA.
AC Q8UVX5;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Onconase precursor.
GN Name=rpr;
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2836040; PubMed=12954760; DOI=10.1093/nar/gkg746;
RA Liao Y.-D., Wang S.-C., Leu Y.-J., Wang C.F., Chang S.T., Hong Y.T.,
RA Pan Y.R., Chen C.;
RT "The structural integrity exerted by N-terminal pyroglutamate is
RT crucial for the cytotoxicity of frog ribonuclease from Rana pipiens."
RL Nucleic Acids Res. 31:5247-5255(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR EMBL; AF332139; AAL54383.1; -.
DR FIR; A39035; A39035.

DR HSSP; P22069; 1ONC.
DR GO; GO:0004519; P:endonuclease activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN 1.
KW Endonuclease; Hydrolase; Nuclease; Signal.
FT SIGNAL 1 23 Potential.
SQ SEQUENCE 127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 127;
Best Local Similarity 61.5%; Pred. No. 7.4;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
| : | | | | |
Db 98 CKYKLLKSTNKF 110

RESULT 8
Q967Z1 PRELIMINARY; PRT; 997 AA.
AC Q967Z1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Putative mismatch repair protein MSH8.
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MITat1.2;
RX PubMed=14651619;
RA Bell J.S., Harvey T.I., Sims A.M., McCulloch R.;
RT "Characterization of components of the mismatch repair machinery in
RT Trypanosoma brucei";
RL Mol. Microbiol. 51:159-173(2004).
CC -!- SIMILARITY: Belongs to the DNA mismatch repair mutS family.
DR EMBL; AF350880; AAK51796.1; -.
DR HSSP; Q56215; IEWQ.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003684; F:damaged DNA binding; IEA.
DR GO; GO:0006259; P:DNA metabolism; IEA.
DR GO; GO:0006298; P:mismatch repair; IEA.
DR InterPro; IPR000432; Muts_C.
DR InterPro; IPR007696; Muts_III.
DR InterPro; IPR007695; Muts_N.
DR Pfam; PF01624; Muts_I; 1.
DR Pfam; PF05192; Muts_III; 1.
DR Pfam; PF00488; Muts_V; 1.
DR SMART; SM00534; MutsAc; 1.
DR SMART; SM00533; Mutsd; 1.
DR PROSITE; PS00486; DNA_MISMATCH_REPAIR_2; 1.
KW DNA-binding.
SQ SEQUENCE 997 AA; 110416 MW; DBFCA3D8D2642A3 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 997;
Best Local Similarity 58.3%; Pred. No. 58;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELGKSTNTF 12
| : | | | | |
Db 460 CGSKRGRTNTF 471

RESULT 9
Q9P944 PRELIMINARY; PRT; 1011 AA.
ID Q9P944
AC Q9P944;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Kexin-like protease KEX1.
 GN Name=kex1;
 OS *Pneumocystis carinii* f. sp. muris.
 OC Eukaryota; Fungi; Ascomycota; Pneumocystidaceae; Pneumocystidaceae;
 OC Pneumocystis.
 OX NCBI_TaxID=42066;
 RN [1]
 RY SEQUENCE FROM N.A.
 RP MEDLINE=20184731; PubMed=10721706; DOI=10.1016/S0378-1119(99)00533-8;
 RA Lee L.H., Gigliotti F., Wright T.W., Simpson-Haidaris P.J.,
 RA Weinberg G.A., Haidaris C.G.;
 RT "Molecular characterization of KEX1, a kexin-like protease in mouse
 RT *Pneumocystis carinii*.";
 RL Gene 242:141-150(2000).
 DR EMBL; AF093132; AAF32493.1; --
 DR HSP; P13134; 1075.
 DR MEROPS; S08.011; --
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004289; F:subtilase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR008979; Gal bind like.
 DR InterPro; IPR000209; Pept_S8_S53.
 DR InterPro; IPR002884; Protonconvertsp.
 DR InterPro; IPR006970; PT.
 DR Pfam; PF00082; Peptidase_S8; 1.
 DR Pfam; PF04886; PT; 4.
 DR Pfam; PF01483; P:proteoin; 1.
 DR PRINTS; PR00723; SUBTILISIN.
 DR ProDom; PD000717; Protonconvertsp; 1.
 DR PROSITE; PS00137; SUBTILASE_HIS; UNKNOWN_1.
 KW Protease.
 SQ SEQUENCE 1011 AA; 112020 MW; FBE472C8F65864E8 CRC64;

Query Match 58.3%; Score 42; DB 2; Length 1011;
 Best Local Similarity 53.8%; Pred. No. 91;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 CASELGKSTNTFC 13
 |||:|:|:|:|
 DB 246 CAGEIVAANKTFC 258

RESULT 10

Q6UB96
 ID Q6UB96 PRELIMINARY; PRT; 1086 AA.
 AC Q6UB96;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Protein kinase C 1.
 GN Name=PKC1;
 OS *Cryptococcus neoformans* var. *neoformans*.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
 OX NCBI_TaxID=40410;
 RN [1]
 RY SEQUENCE FROM N.A.
 RP STRAIN=B3501;
 RC PubMed=15014071; DOI=10.1074/jbc.M312995200;
 RA Heung L.J., Luberto C., Plowden A., Hannun Y.A., Del Poeta M.;
 RT "The Sphingolipid Pathway Regulates Pkc1 through the Formation of
 RT Diacylglycerol in *Cryptococcus neoformans*.";
 RL J. Biol. Chem. 279:21144-21153(2004).
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AY373759; AAQ84896.1; --
 DR HSP; P05132; 1APM.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR002219; DAG PE-bind.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR011072; PKN_effector.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR000861; REM_repeat.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR000217; Tubulin.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00130; C1.1; 2.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF02185; HR1; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00433; Pkinase_C; 1.
 DR PRINTS; PR00008; DAGPEDOMAIN.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00109; C1; 2.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00220; S_TK; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00479; DAG PE BIND DOM 1; 2.
 DR PROSITE; PS0081; DAG PE BIND DOM 2; 2.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
 DR PROSITE; PS00227; TUBULIN; UNKNOWN_1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 1086 AA; 120346 MW; 55AEF737EFBE1F9E CRC64;

Query Match 58.3%; Score 42; DB 2; Length 1086;
 Best Local Similarity 53.3%; Pred. No. 97;
 Matches 8; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

OY 1 CASEL--GKSTNTFC 13
 |||:|:|:|:|
 DB 904 CKEEMWFGKTTSTFC 918

RESULT 11

Q6UB97
 ID Q6UB97 PRELIMINARY; PRT; 1086 AA.
 AC Q6UB97;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Protein kinase C 1.
 GN Name=PKC1;
 OS *Cryptococcus neoformans* var. *grubii* (Filobasidiella neoformans var. *grubii*).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
 OX NCBI_TaxID=178876;
 RN [1]
 RY SEQUENCE FROM N.A.
 RP STRAIN=H99;
 RC PubMed=15014071; DOI=10.1074/jbc.M312995200;
 RA Heung L.J., Luberto C., Plowden A., Hannun Y.A., Del Poeta M.;
 RT "The Sphingolipid Pathway Regulates Pkc1 through the Formation of
 RT Diacylglycerol in *Cryptococcus neoformans*.";
 RL J. Biol. Chem. 279:21144-21153(2004).
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AY373758; AAQ84895.1; --
 DR HSP; P05132; 1APM.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0008468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG PE-bind.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000961; Kinase C.
DR InterPro; IPR011072; PKN effector.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR000861; REM_repeat.
DR InterPro; IPR002290; Ser thr kinase.
DR InterPro; IPR008271; Ser thr pkin_AS.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00130; C1_1; 2.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF02185; HRI; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00220; S_TK_X; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00811; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1086 AA; 120767 MW; 5700CFD9E1D27BB CRC64;

Query Match 58.3%; Score 42; DB 2; Length 1086;
Best Local Similarity 53.3%; Pred. No. 97;
Matches 8; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 1 CASEL--GKSTNTFC 13
DB 904 CKEMWFGKTTSTFC 918

RESULT 12
Q90ZB2 PRELIMINARY; PRT; 316 AA.
ID Q90ZB2;
AC Q90ZB2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transcription factor Gbx1.
GN Name=gbx1;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22844360; PubMed=12963112; DOI=10.1016/S0925-4773(03)00135-7;
RA Rhinn M., Lun K., Amores A., Yan Y.L., Postlethwait J.H., Brand M.;
RT "Cloning, expression and relationship of zebrafish gbx1 and gbx2 genes
RT to Fgf signaling."
RL Mech. Dev. 120:919-936(2003).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AF288763; AAK83070.1; -.
DR HSSP; P14653; 1B72.
DR ZFIN; ZDB-GENE-020117-2; gbx1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.

DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 316 AA; 34409 MW; DC32955EA5430D8A CRC64;

Query Match 56.9%; Score 41; DB 2; Length 316;
Best Local Similarity 56.7%; Pred. No. 44;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 ASELGKSTNTFC 13
DB 63 ASFAGRLNTTFC 74

RESULT 13
ACK2 LISIN
ID ACK2 LISIN STANDARD; PRT; 397 AA.
AC Q92CN9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Acetate kinase 2 (EC 2.7.2.1) (Acetokinase 2).
GN Name=ackA2; OrderedLocusNames=lin1132;
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAINS=CLIP 11262 / Setovar 6a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaeser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Donann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kref J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehlant J., Cossart P.;
RT "Comparative genomics of Listeria species";
RL Science 294:849-852(2001).
CC -1- CATALYTIC ACTIVITY: ATP + acetate = ADP + acetyl phosphate.
CC -1- PATHWAY: Conversion of acetate to acetyl-CoA; first step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the acetokinase family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL; AL596167; CAC96363.1; -.
DR PIR; AC1574; AC1574.
DR HSSP; P38502; 1G99.
DR Listlist; LN01132; -.
DR HAMAP; MF_00020; -; 1.
DR InterPro; IPR000890; Acetate_kin.
DR InterPro; IPR004372; ACKA.
DR Pfam; PF00871; Acetate_kinase; 1.
DR PRINTS; PR00471; ACETATEKINASE.
DR TIGRPFAM; TIGR00016; ackA; 1.
DR PROSITE; PS01075; ACETATE_KINASE_1; 1.
DR PROSITE; PS01076; ACETATE_KINASE_2; 1.
KW Complete proteome; Kinase; Transferase.
SQ SEQUENCE 397 AA; 43115 MW; 5822544EF92CBF51 CRC64;

Query Match 56.9%; Score 41; DB 1; Length 397;

```
Best Local Similarity 72.7%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CASELGKSTNT 11
Db 214 CAIEAGKSVNT 224

RESULT 14
ACK2 LISMO
ID ACK2 LISMO STANDARD; PRT; 397 AA.
AC Q8V7V1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Acetate kinase 2 (EC 2.7.2.1) (Acetokinase 2).
GN Name=ackA2; OrderedLocusNames=lmol168;
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetoui F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fshi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkut G.,
RA Madueno E., Maltounam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -!- CATALYTIC ACTIVITY: ATP + acetate = ADP + acetyl phosphate.
CC -!- PATHWAY: Conversion of acetate to acetyl-CoA; first step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the acetokinase family.
CC -----
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CC -----
DR EMBL; AL591978; CAC99246.1; -.
DR PIR; AH1220; AH1220.
DR HSP; P38502; IG99.
DR ListList; LMO01168; -.
DR HAMAP; MF_00020; ; 1.
DR InterPro; IPR000890; Acetate_kin.
DR InterPro; IPR004372; ACKA.
DR Pfam; PF00871; Acetate_kinase; 1.
DR PRINTS; PR00471; ACETATE_KINASE.
DR TIGRFAMs; TIGR00016; ackA; 1.
DR PROSITE; PS01075; ACETATE_KINASE_1; 1.
DR PROSITE; PS01076; ACETATE_KINASE_2; 1.
DR Complete proteome; Kinase; Transferase.
KW SEQUENCE 397 AA; 43132 MW; 6E295A59A5FD5C5B CRC64;

Query Match 56.9%; Score 41; DB 1; Length 397;
Best Local Similarity 72.7%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CASELGKSTNT 11
Db 214 CAIEAGKSVNT 224
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RESULT 15
Q72OR2
ID Q72OR2;
AC Q72OR2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Propionate/acetate kinase, putative.
GN OrderedLocusNames=LMOF2365.1176;
OS Listeria monocytogenes (serotype 4b / strain F2365).
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=265669;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15115801; DOI=10.1093/nar/gkh562;
RX Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
RA Kolonay J.P., Rasko D.A., Anguoli S.V., Gill S.R., Paulsen I.T.,
RA Peterson J.D., White O., Nelson W.C., Nierman W.C., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
RA Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,
RA Forberger H.A., Tran B., Kathariou S., Wonderling L.D., Uhlir G.A.,
RA Bayles D.O., Luchansky J.B., Fraser C.M.;
RT "Whole genome comparisons of serotype 4b and 1/2a strains of the food-
RT borne pathogen Listeria monocytogenes reveal new insights into the
RT core genome components of this species.";
RL Nucleic Acids Res. 32:2386-2395(2004).
CC -!- SIMILARITY: Belongs to the acetokinase family.
DR EMBL; AE017325; AAT03952.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016774; F:phosphotransferase activity, carboxyl group. .; IEA.
DR GO; GO:0006082; P:organic acid metabolism; IEA.
DR GO; GO:0016310; P:phosphorylation; IEA.
DR InterPro; IPR000890; Acetate_kin.
DR InterPro; IPR004372; ACKA.
DR Pfam; PF00871; Acetate_kinase; 1.
DR PRINTS; PR00471; ACETATE_KINASE.
DR TIGRFAMs; TIGR00016; ackA; 1.
DR PROSITE; PS01075; ACETATE_KINASE_1; 1.
DR PROSITE; PS01076; ACETATE_KINASE_2; 1.
DR Complete proteome; Kinase; Transferase.
KW SEQUENCE 397 AA; 43149 MW; CCD3F60C4ABBF533 CRC64;

Query Match 56.9%; Score 41; DB 2; Length 397;
Best Local Similarity 72.7%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CASELGKSTNT 11
Db 214 CAIEAGKSVNT 224
```

Search completed: April 1, 2005, 09:25:55
Job time : 82.6027 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 03:27:37 ; Search time 98.1233 Seconds
(without alignments)
51.240 Million cell updates/sec

Title: US-09-761-636A-5

Perfect score: 72

Sequence: 1 CASELGRKSTNTFC 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	13	AAU04524	AAU04524 VEGF base
2	72	100.0	17	AAU04527	AAU04527 VEGF base
3	69	95.8	13	AAU04534	AAU04534 VEGF base
4	69	95.8	17	AAU04550	AAU04550 VEGF base
5	69	95.8	17	AAU04546	AAU04546 VEGF base
6	65	90.3	13	AAU04535	AAU04535 VEGF base
7	65	90.3	13	AAU04537	AAU04537 VEGF base
8	65	90.3	17	AAU04547	AAU04547 VEGF base
9	65	90.3	17	AAU04551	AAU04551 VEGF base
10	65	90.3	17	AAU04549	AAU04549 VEGF base
11	61	84.7	13	AAU04536	AAU04536 VEGF base
12	61	84.7	17	AAU04548	AAU04548 VEGF base
13	54	75.0	73	AAU04522	AAU04522 Human VEG
14	54	75.0	96	AAU04520	AAU04520 Human VEG
15	54	75.0	109	AAU04523	AAU04523 Human VEG
16	54	75.0	109	AAU04531	AAU04531 Human VEG
17	54	75.0	109	AAU04535	AAU04535 Human VEG
18	54	75.0	109	AAU04537	AAU04537 Human VEG
19	54	75.0	109	AAU04547	AAU04547 Human VEG
20	54	75.0	109	AAU04551	AAU04551 Human VEG
21	54	75.0	109	AAU04549	AAU04549 Human VEG
22	54	75.0	109	AAU04536	AAU04536 Human VEG
23	54	75.0	109	AAU04548	AAU04548 Human VEG
24	54	75.0	109	AAU04535	AAU04535 Human VEG
25	54	75.0	109	AAU04537	AAU04537 Human VEG

26	54	75.0	354	3	AAU04524	AAU04524 standard; peptide; 13 AA.
27	54	75.0	354	3	AAU04527	AAU04527 standard; peptide; 13 AA.
28	54	75.0	354	3	AAU04534	AAU04534 standard; peptide; 13 AA.
29	54	75.0	354	4	AAU04550	AAU04550 standard; peptide; 13 AA.
30	54	75.0	354	4	AAU04546	AAU04546 standard; peptide; 13 AA.
31	54	75.0	354	4	AAU04535	AAU04535 standard; peptide; 13 AA.
32	54	75.0	354	4	AAU04537	AAU04537 standard; peptide; 13 AA.
33	54	75.0	354	5	AAU04547	AAU04547 standard; peptide; 13 AA.
34	54	75.0	354	5	AAU04551	AAU04551 standard; peptide; 13 AA.
35	54	75.0	354	6	AAU04549	AAU04549 standard; peptide; 13 AA.
36	54	75.0	354	7	AAU04536	AAU04536 standard; peptide; 13 AA.
37	54	75.0	354	7	AAU04548	AAU04548 standard; peptide; 13 AA.
38	54	75.0	354	8	AAU04535	AAU04535 standard; peptide; 13 AA.
39	54	75.0	354	8	AAU04537	AAU04537 standard; peptide; 13 AA.
40	54	75.0	354	8	AAU04547	AAU04547 standard; peptide; 13 AA.
41	54	75.0	354	8	AAU04551	AAU04551 standard; peptide; 13 AA.
42	51	70.8	110	5	AAU04524	AAU04524 standard; peptide; 13 AA.
43	51	70.8	178	2	AAU04527	AAU04527 standard; peptide; 13 AA.
44	51	70.8	321	2	AAU04534	AAU04534 standard; peptide; 13 AA.
45	51	70.8	321	5	AAU04550	AAU04550 standard; peptide; 13 AA.

ALIGNMENTS

RESULT 1
AAU04524
ID AAU04524 standard; peptide; 13 AA.
XX
AC AAU04524;
XX
DT 26-SEP-2001 (first entry)
XX
DE VEGF based monocyclic peptide 1.
XX
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
KW diabetes induced neovascular sequelae; rheumatoid arthritis;
KW diabetic retinopathy; chronic inflammation; cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..13 /note= "This bond cyclises the peptide"
XX
PN WO200152875-A1.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-US001533.
XX
PR 18-JAN-2001; 2000US-0176293P.
PR 16-MAY-2000; 2000US-0204590P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Achen MG, Hughes RA, Stacker S, Cendron A;
XX
DR WPI; 2001-442248/47.
XX
PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
PT from an exposed loop of a growth factor protein by oxidizing the cysteine
PT residues.
XX
PS Claim 49; Page 32; 102pp; English.
XX
CC The sequence represents a monomeric monocyclic peptide of the invention,
CC whose 3-dimensional structure is modelled on the exposed loop of human
CC VEGF (vascular endothelial growth factor). The invention relates to a
CC method of producing a monomeric monocyclic peptide by a measuring beta-
CC beta carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 13 AA;

Query Match 100.0%; Score 72; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
 |||||

DB 1 CASELGKSTNTFC 13
 |||||

RESULT 2

AAU04527
 ID AAU04527 standard; protein; 17 AA.

AC AAU04527;

DT 26-SEP-2001 (first entry)

XX VEGF based bicyclic dimeric peptide #1.

XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.

XX Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 1..13 /note= "This bond cyclises the peptide"

FT Disulfide-bond 17

FT /note= "A disulfide bond forms between residue 17 and
 residue 17 of an identical peptide to form a dimeric
 peptide, or to residue 1 of the sequence appearing as
 AAU04528, also forming a dimeric peptide"

XX WO200152875-A1.

PN 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

PR 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Hughes RA, Stacker S, Cendron A;

XX

DR WPI; 2001-442248/47.
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclising a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.

XX Claim 59; Page 32; 102pp; English.

XX The sequence represents a dimeric bicyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the exposed loop of human
 CC VEGF (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 72; DB 4; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.7e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
 |||||

DB 1 CASELGKSTNTFC 13
 |||||

RESULT 3

AAU04534

ID AAU04534 standard; peptide; 13 AA.

AC AAU04534;

DT 26-SEP-2001 (first entry)

XX VEGF based monocyclic peptide 12.

XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.

XX Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 1..13

FT /note= "This bond cyclises the peptide"

XX WO200152875-A1.

XX 26-JUL-2001.

XX

PF 18-JAN-2001; 2001WO-US001533.
 XX
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Achen MG, Hughes RA, Stacker S, Cendron A;
 XX
 DR WPI; 2001-442248/47.
 XX
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX
 PS Example 25; Page 47; 102pp; English.
 XX
 CC The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain). The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 13 AA;
 Query Match 95.8%; Score 69; DB 4; Length 13;
 Best Local Similarity 92.3%; Pred. No. 9e-05;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CASELGKSTNTFC 13
 Db ||:|||||:|
 1 CATELGKSTNTFC 13
 RESULT 4
 AAU04550
 ID AAU04550 standard; peptide; 17 AA.
 XX
 AC AAU04550;
 XX
 XX 26-SEP-2001 (first entry)
 DT
 DE VEGF based bicyclic dimeric peptide #7.
 XX
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 FT Disulfide-bond 1..13
 FT Disulfide-bond 17
 FT /note= "This bond cyclises the peptide"
 FT /note= "A disulfide bond forms between residue 17 and
 FT residue 1 of the sequence appearing as AAU04528, forming
 FT a dimeric peptide"
 XX
 PN WO200152875-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 18-JAN-2001; 2001WO-US001533.
 XX
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 PI Achen MG, Hughes RA, Stacker S, Cendron A;
 XX
 XX WPI; 2001-442248/47.
 XX
 PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX
 PS Example 26; Page 49; 102pp; English.
 XX
 CC The sequence represents a dimeric bicyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the expose loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain). The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 17 AA;
 Query Match 95.8%; Score 69; DB 4; Length 17;
 Best Local Similarity 92.3%; Pred. No. 0.00012;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CASELGKSTNTFC 13
 Db ||:|||||:|
 1 CASELGKSTNTFC 13
 RESULT 5
 AAU04546
 ID AAU04546 standard; peptide; 17 AA.

XX AAU04546;
XX 26-SEP-2001 (first entry)
XX VEGF based bicyclic dimeric peptide #3.
XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
XX neovascularisation; lymphangiogenesis; psoriasis; tumour;
XX diabetes induced neovascular sequelae; rheumatoid arthritis;
XX diabetic retinopathy; chronic inflammation; cyclic.
XX Synthetic.
XX Key Location/Qualifiers
XX Disulfide-bond 1..13
XX Disulfide-bond 17 /note= "This bond cyclises the peptide"
XX /note= "A disulfide bond forms between residue 17 and
XX residue 17 of an identical peptide to form a dimeric
XX peptide"
XX WO200152875-A1.
XX 26-JUL-2001.
XX 18-JAN-2001; 2001WO-US001533.
XX 18-JAN-2000; 2000US-0176293P.
XX 16-MAY-2000; 2000US-0204590P.
XX (LUDW-) LUDWIG INST CANCER RES.
XX Achen MG, Hughes RA, Stackler S, Cendron A;
XX WPI; 2001-442248/47.
XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
XX from an exposed loop of a growth factor protein by oxidizing the cysteine
XX residues.
XX Example 26; Page 49; 102pp; English.
XX The sequence represents a dimeric bicyclic peptide of the invention,
XX whose 3-dimensional structure is modelled on the expose loop of human
XX VEGFD (vascular endothelial growth factor). The invention relates to a
XX method of producing a monomeric monocyclic peptide by a measuring beta-
XX beta carbon separation distances on opposite antiparallel strands of a
XX peptide loop fragment from an exposed loop of a growth factor protein and
XX cyclising the peptide by oxidising the cysteine residues. The monocyclic
XX peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
XX peptides) and a cyclic peptide with at least one amino acid deleted prior
XX to cyclisation are used to interfere with angiogenesis,
XX neovascularisation or lymphangiogenesis in a mammal with a condition
XX characterised by angiogenesis, neovascularisation or lymphangiogenesis.
XX The condition is diabetic retinopathy, psoriasis, arthropathy,
XX hemangioma, vascularised malignant or benign tumour, post-recovery
XX cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
XX trauma, substance-induced neovascularisation of the liver, excessive
XX hormone-related angiogenic dysfunction, diabetes induced neovascular
XX sequelae, hypertension induced neovascular sequelae, or chronic liver
XX infection. The peptides are also used to modulate vascular permeability
XX in a mammal (the mammal has a condition characterised by fluid
XX accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
XX or brain. The peptides are used to image blood vessels and lymphatic
XX vasculature. The monomeric and bicyclic peptides are used to interfere
XX with at least one biological activity induced by VEGF, VEGF-C or -D and
XX are also used in combination with an anti-inflammatory agent, to treat a
XX chronic inflammation, especially rheumatoid arthritis, psoriasis and
XX diabetic retinopathy
XX Sequence 17 AA;

Query Match 95.8%; Score 69; DB 4; Length 17;
Best Local Similarity 92.3%; Pred. NO. 0.00012;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CASLGLKSTNTFC 13
DB 1 CATELGKSTNTFC 13
RESULT 6
AAU04535
ID AAU04535 standard; peptide; 13 AA.
XX AAU04535;
XX 26-SEP-2001 (first entry)
XX VEGF based monocyclic peptide 13.
XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
XX neovascularisation; lymphangiogenesis; psoriasis; tumour;
XX diabetes induced neovascular sequelae; rheumatoid arthritis;
XX diabetic retinopathy; chronic inflammation; cyclic.
XX Synthetic.
XX Key Location/Qualifiers
XX Disulfide-bond 1..13 /note= "This bond cyclises the peptide"
XX WO200152875-A1.
XX 26-JUL-2001.
XX 18-JAN-2001; 2001WO-US001533.
XX 18-JAN-2000; 2000US-0176293P.
XX 16-MAY-2000; 2000US-0204590P.
XX (LUDW-) LUDWIG INST CANCER RES.
XX Achen MG, Hughes RA, Stackler S, Cendron A;
XX WPI; 2001-442248/47.
XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
XX from an exposed loop of a growth factor protein by oxidizing the cysteine
XX residues.
XX Example 25; Page 47; 102pp; English.
XX The sequence represents a monomeric monocyclic peptide of the invention,
XX whose 3-dimensional structure is modelled on the expose loop of human
XX VEGFD (vascular endothelial growth factor). The invention relates to a
XX method of producing a monomeric monocyclic peptide by a measuring beta-
XX beta carbon separation distances on opposite antiparallel strands of a
XX peptide loop fragment from an exposed loop of a growth factor protein and
XX cyclising the peptide by oxidising the cysteine residues. The monocyclic
XX peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
XX peptides) and a cyclic peptide with at least one amino acid deleted prior
XX to cyclisation are used to interfere with angiogenesis,
XX neovascularisation or lymphangiogenesis in a mammal with a condition
XX characterised by angiogenesis, neovascularisation or lymphangiogenesis.
XX The condition is diabetic retinopathy, psoriasis, arthropathy,
XX hemangioma, vascularised malignant or benign tumour, post-recovery
XX cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
XX trauma, substance-induced neovascularisation of the liver, excessive
XX hormone-related angiogenic dysfunction, diabetes induced neovascular
XX sequelae, hypertension induced neovascular sequelae, or chronic liver
XX infection. The peptides are also used to modulate vascular permeability
XX in a mammal (the mammal has a condition characterised by fluid

CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 13 AA;
 Query Match 90.3%; Score 65; DB 4; Length 13;
 Best Local Similarity 84.6%; Pred. No. 0.00043;
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CASELGKSTNTFC 13
 DB 1 CASELGKSTNTFC 13
 RESULT 7
 AAU04537
 ID AAU04537 standard; peptide; 13 AA.
 XX
 AC AAU04537;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE VEGF based monocyclic peptide 15.
 XX
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..13 /note= "This bond cyclises the peptide"
 FT
 PN WO200152875-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 18-JAN-2001; 2001WO-US001533.
 XX
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Achen MG, Hughes RA, Stackers S, Cendron A;
 XX
 DR WPI; 2001-442248/47.
 XX
 PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX
 PS Example 25; Page 47; 102pp; English.
 XX
 CC The sequence represents a monomeric monocyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the exposed loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition

CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy
 XX
 SQ Sequence 13 AA;
 Query Match 90.3%; Score 65; DB 4; Length 13;
 Best Local Similarity 84.6%; Pred. No. 0.00043;
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CASELGKSTNTFC 13
 DB 1 CASELGKSTNTFC 13
 RESULT 8
 AAU04547
 ID AAU04547 standard; peptide; 17 AA.
 XX
 AC AAU04547;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE VEGF based bicyclic dimeric peptide #4.
 XX
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..13 /note= "This bond cyclises the peptide"
 FT Disulfide-bond 17 /note= "A disulfide bond forms between residue 17 and
 FT residue 17 of an identical peptide to form a dimeric
 FT peptide"
 XX
 PN WO200152875-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 18-JAN-2001; 2001WO-US001533.
 XX
 PR 18-JAN-2000; 2000US-0176293P.
 PR 16-MAY-2000; 2000US-0204590P.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Achen MG, Hughes RA, Stackers S, Cendron A;
 XX
 DR WPI; 2001-442248/47.
 XX
 PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX

PS Example 26; Page 49; 102pp; English.

XX The sequence represents a dimeric bicyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the exposed loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy

XX SQ Sequence 17 AA;
 Query Match 90.3%; Score 65; DB 4; Length 17;
 Best Local Similarity 84.6%; Pred. No. 0.00058;
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
 |||||:|||||
 Db 1 CASELGKSTNTFC 13

RESULT 9
 AAU04551
 ID AAU04551 standard; peptide; 17 AA.
 AC AAU04551;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE VEGF based bicyclic dimeric peptide #8.
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 1..13 /note= "This bond cyclises the peptide"
 FT Disulfide-bond 17 /note= "A disulfide bond forms between residue 17 and
 FT residue 1 of the sequence appearing as AAU04528, forming
 FT a dimeric peptide"
 XX
 XX WO200152875-A1.
 FN
 XX 26-JUL-2001.
 XX
 XX 18-JAN-2001; 2001WO-US001533.
 PF
 XX 18-JAN-2000; 2000US-0176293P.
 PR

PR 16-MAY-2000; 2000US-0204590P.
 XX (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Achen MG, Hughes RA, Stacker S, Cendron A;
 XX WPI; 2001-442248/47.
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclising a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.
 XX
 XX Example 26; Page 49; 102pp; English.

PS The sequence represents a dimeric bicyclic peptide of the invention,
 CC whose 3-dimensional structure is modelled on the exposed loop of human
 CC VEGFD (vascular endothelial growth factor). The invention relates to a
 CC method of producing a monomeric monocyclic peptide by a measuring beta-
 CC beta carbon separation distances on opposite antiparallel strands of a
 CC peptide loop fragment from an exposed loop of a growth factor protein and
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior
 CC to cyclisation are used to interfere with angiogenesis,
 CC neovascularisation or lymphangiogenesis in a mammal with a condition
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,
 CC hemangioma, vascularised malignant or benign tumour, post-recovery
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
 CC trauma, substance-induced neovascularisation of the liver, excessive
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver
 CC infection. The peptides are also used to modulate vascular permeability
 CC in a mammal (the mammal has a condition characterised by fluid
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
 CC or brain. The peptides are used to image blood vessels and lymphatic
 CC vasculature. The monomeric and bicyclic peptides are used to interfere
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and
 CC are also used in combination with an anti-inflammatory agent, to treat a
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and
 CC diabetic retinopathy

XX SQ Sequence 17 AA;
 Query Match 90.3%; Score 65; DB 4; Length 17;
 Best Local Similarity 84.6%; Pred. No. 0.00058;
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
 |||||:|||||
 Db 1 CASELGKSTNTFC 13

RESULT 10
 AAU04549
 ID AAU04549 standard; peptide; 17 AA.
 XX
 AC AAU04549;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE VEGF based bicyclic dimeric peptide #6.
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation; cyclic.
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 1..13


```

FT Disulfide-bond 17 /note= "This bond cyclises the peptide"
FT /note= "A disulfide bond forms between residue 17 and
FT residue 17 of an identical peptide to form a dimeric
FT peptide"
XX WO200152875-A1.
XX 26-JUL-2001.
XX
XX 18-JAN-2001; 2001WO-US001533.
XX
XX 18-JAN-2000; 2000US-0176293P.
XX 16-MAY-2000; 2000US-0204590P.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Achen MG, Hughes RA, Stacker S, Cendron A;
XX WPI; 2001-442248/47.
XX
XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
XX from an exposed loop of a growth factor protein by oxidizing the cysteine
XX residues.
XX
XX Example 26; Page 49; 102pp; English.
XX
XX The sequence represents a dimeric bicyclic peptide of the invention,
XX whose 3-dimensional structure is modelled on the exposed loop of human
XX VEGFD (vascular endothelial growth factor). The invention relates to a
XX method of producing a monomeric monocyclic peptide by a measuring beta-
XX carbon separation distances on opposite antiparallel strands of a
XX peptide loop fragment from an exposed loop of a growth factor protein and
XX cyclising the peptide by oxidising the cysteine residues. The monocyclic
XX peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
XX peptides) and a cyclic peptide with at least one amino acid deleted prior
XX to cyclisation are used to interfere with angiogenesis,
XX neovascularisation or lymphangiogenesis in a mammal with a condition
XX characterised by angiogenesis, neovascularisation or lymphangiogenesis.
XX The condition is diabetic retinopathy, psoriasis, arthropathy,
XX hemangioma, vascularised malignant or benign tumour, post-recovery
XX cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
XX trauma, substance-induced neovascularisation of the liver, excessive
XX hormone-related angiogenic dysfunction, diabetes induced neovascular
XX sequelae, hypertension induced neovascular sequelae, or chronic liver
XX infection. The peptides are also used to modulate vascular permeability
XX in a mammal (the mammal has a condition characterised by fluid
XX accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
XX or brain. The peptides are used to image blood vessels and lymphatic
XX vasculature. The monomeric and bicyclic peptides are used to interfere
XX with at least one biological activity induced by VEGF, VEGF-C or -D and
XX are also used in combination with an anti-inflammatory agent, to treat a
XX chronic inflammation, especially rheumatoid arthritis, psoriasis and
XX diabetic retinopathy
XX
XX Sequence 17 AA;
XX
XX Query Match 90.3%; Score 65; DB 4; Length 17;
XX Best Local Similarity 84.6%; Pred. No. 0.00058; Indels 0; Gaps 0;
XX Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CASELGKSTNTFC 13
XX |||||:||||:|
XX 1 CASELGRSTNSFC 13
XX
XX RESULT 11
XX AAU04536
XX ID AAU04536 standard; peptide; 13 AA.
XX
XX AC AAU04536;
XX

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```

DT 26-SEP-2001 (first entry)
XX
XX VEGF based monocyclic peptide 14.
XX
XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
XX neovascularisation; lymphangiogenesis; psoriasis; tumour;
XX diabetes induced neovascular sequelae; rheumatoid arthritis;
XX diabetic retinopathy; chronic inflammation; cyclic.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Disulfide-bond 1..13 /note= "This bond cyclises the peptide"
XX
XX WO200152875-A1.
XX
XX 26-JUL-2001.
XX
XX 18-JAN-2001; 2001WO-US001533.
XX
XX 18-JAN-2000; 2000US-0176293P.
XX 16-MAY-2000; 2000US-0204590P.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Achen MG, Hughes RA, Stacker S, Cendron A;
XX WPI; 2001-442248/47.
XX
XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
XX from an exposed loop of a growth factor protein by oxidizing the cysteine
XX residues.
XX
XX Example 25; Page 47; 102pp; English.
XX
XX The sequence represents a monomeric monocyclic peptide of the invention,
XX whose 3-dimensional structure is modelled on the exposed loop of human
XX VEGFD (vascular endothelial growth factor). The invention relates to a
XX method of producing a monomeric monocyclic peptide by a measuring beta-
XX carbon separation distances on opposite antiparallel strands of a
XX peptide loop fragment from an exposed loop of a growth factor protein and
XX cyclising the peptide by oxidising the cysteine residues. The monocyclic
XX peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
XX peptides) and a cyclic peptide with at least one amino acid deleted prior
XX to cyclisation are used to interfere with angiogenesis,
XX neovascularisation or lymphangiogenesis in a mammal with a condition
XX characterised by angiogenesis, neovascularisation or lymphangiogenesis.
XX The condition is diabetic retinopathy, psoriasis, arthropathy,
XX hemangioma, vascularised malignant or benign tumour, post-recovery
XX cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
XX trauma, substance-induced neovascularisation of the liver, excessive
XX hormone-related angiogenic dysfunction, diabetes induced neovascular
XX sequelae, hypertension induced neovascular sequelae, or chronic liver
XX infection. The peptides are also used to modulate vascular permeability
XX in a mammal (the mammal has a condition characterised by fluid
XX accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
XX or brain. The peptides are used to image blood vessels and lymphatic
XX vasculature. The monomeric and bicyclic peptides are used to interfere
XX with at least one biological activity induced by VEGF, VEGF-C or -D and
XX are also used in combination with an anti-inflammatory agent, to treat a
XX chronic inflammation, especially rheumatoid arthritis, psoriasis and
XX diabetic retinopathy
XX
XX Sequence 13 AA;
XX
XX Query Match 84.7%; Score 61; DB 4; Length 13;
XX Best Local Similarity 76.9%; Pred. No. 0.0021;
XX Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CASELGKSTNTFC 13
XX |||||:||||:|
XX

```

Db 1 CASDVKGSTNTWC 13

RESULT 12

AAU04548

ID AAU04548 standard; peptide; 17 AA.

AC AAU04548;

DT 26-SEP-2001 (first entry)

DE VEGF based bicyclic dimeric peptide #5.

XX Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Disulfide-bond 1..13

FT Disulfide-bond 17 /note= "This bond cyclises the peptide"

FT Disulfide-bond 17 /note= "A disulfide bond forms between residue 17 and residue 17 of an identical peptide to form a dimeric peptide"

FT

PN WO200152875-A1.

XX

PD 26-JUL-2001.

XX

PF 18-JAN-2001; 2001WO-US001533.

XX

PR 18-JAN-2000; 2000US-0176293P.

PR 16-MAY-2000; 2000US-0204590P.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Achen MG, Hughes RA, Stacker S, Cendron A;

XX WPI; 2001-442248/47.

DR

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

PS Example 26; Page 49; 102pp; English.

XX

CC The sequence represents a dimeric bicyclic peptide of the invention, whose 3-dimensional structure is modelled on the exposed loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere

CC with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy

XX

SQ Sequence 17 AA;

Query Match 84.7%; Score 61; DB 4; Length 17;

Best Local Similarity 76.9%; Pred. No. 0.0028;

Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13

DB 1 CASDVKGSTNTWC 13

||||:|||||:

RESULT 13

AAU04522

ID AAU04522 standard; protein; 73 AA.

XX

AC AAU04522;

XX

DT 26-SEP-2001 (first entry)

XX

DE Human VEGF-D amino acids Val101-Thr 173.

XX

KW Human; VEGF-D; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation.

XX

OS Homo sapiens.

XX

PN WO200152875-A1.

XX

PD 26-JUL-2001.

XX

PF 18-JAN-2001; 2001WO-US001533.

XX

PR 18-JAN-2000; 2000US-0176293P.

PR 16-MAY-2000; 2000US-0204590P.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Achen MG, Hughes RA, Stacker S, Cendron A;

XX WPI; 2001-442248/47.

DR

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

PS Example 1; Page 90-91; 102pp; English.

XX

CC The sequence represents Human VEGF-D (vascular endothelial growth factor) amino acids Val101-Thr 173, used together with the C-terminal 23 residues of VEGF to make a hybrid theoretical molecule for 3 dimensional modelling. The sequence is used in a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere

CC neovascular sequelae, or chronic liver infection. The peptides are also
 CC used to modulate vascular permeability in a mammal (the mammal has a
 CC condition characterised by fluid accumulation in peripheral limbs or in
 CC lungs, peritoneal cavity, pleura, or brain. The peptides are used to
 CC image blood vessels and lymphatic vasculature. The monomeric and bicyclic
 CC peptides are used to interfere with at least one biological activity
 CC induced by VEGF, VEGF-C or -D and are also used in combination with an
 CC anti-inflammatory agent, to treat a chronic inflammation, especially
 CC rheumatoid arthritis, psoriasis and diabetic retinopathy

XX Sequence 73 AA;

Query Match 75.0%; Score 54; DB 4; Length 73;
 Best Local Similarity 100.0%; Pred. No. 0.2; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0;

Qy 2 ASELGKSTNTF 12
 Db 21 ASELGKSTNTF 31
 |||||

RESULT 14

AAU04520
 ID AAU04520 standard; protein; 96 AA.

XX AAU04520;

XX 26-SEP-2001 (first entry)

XX Human VEGF-D amino acids Val101-PRO186.

XX Human; VEGF-D; vascular endothelial growth factor; angiogenesis;
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;
 KW diabetic retinopathy; chronic inflammation.

XX Homo sapiens.

XX WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

XX 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Hughes RA, Stacker S, Cendron A;

XX WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine
 PT residues.

XX Example 1; Page 89; 102pp; English.

XX The sequence represents Human VEGF-D (vascular endothelial growth factor)
 CC amino acids Val101-PRO186. The sequence is used in a method of producing
 CC a monomeric monocyclic peptide by a measuring beta-beta carbon separation
 CC distances on opposite antiparallel strands of a peptide loop fragment
 CC from an exposed loop of a growth factor protein and cyclising the peptide
 CC by oxidising the cysteine residues. The monocyclic peptides, dimeric
 CC bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic
 CC peptide with at least one amino acid deleted prior to cyclisation are
 CC used to interfere with angiogenesis, neovascularisation or
 CC lymphangiogenesis in a mammal with a condition characterised by
 CC angiogenesis, neovascularisation or lymphangiogenesis. The condition is
 CC diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised
 CC malignant or benign tumour, post-recovery cerebrovascular accident, post-

CC angioplasty restenosis, head, heat or cold trauma, substance-induced
 CC neovascularisation of the liver, excessive hormone-related angiogenic
 CC dysfunction, diabetes induced neovascular sequelae, hypertension induced
 CC neovascular sequelae, or chronic liver infection. The peptides are also
 CC used to modulate vascular permeability in a mammal (the mammal has a
 CC condition characterised by fluid accumulation in peripheral limbs or in
 CC lungs, peritoneal cavity, pleura, or brain. The peptides are used to
 CC image blood vessels and lymphatic vasculature. The monomeric and bicyclic
 CC peptides are used to interfere with at least one biological activity
 CC induced by VEGF, VEGF-C or -D and are also used in combination with an
 CC anti-inflammatory agent, to treat a chronic inflammation, especially
 CC rheumatoid arthritis, psoriasis and diabetic retinopathy

XX Sequence 96 AA;

Query Match 75.0%; Score 54; DB 4; Length 96;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASELGKSTNTF 12
 Db 21 ASELGKSTNTF 31
 |||||

RESULT 15

AAU23889
 ID AAY23889 standard; protein; 109 AA.

XX AAY23889;

XX 21-SEP-1999 (first entry)

XX Human vascular endothelial growth factor (VEGF)-D.

XX Vascular endothelial growth factor; VEGF; VEGF-D; malignant melanoma;
 KW tumour; psoriasis; angiogenesis; lymphangiogenesis; skin graft;
 KW wound healing; lymphedema; scleroderma; anhydrotic ectodermal dysplasia.

XX Homo sapiens.

XX WO9933485-A1.

XX 08-JUL-1999.

XX 23-DEC-1998; 98WO-US027373.

XX 24-DEC-1997; 97AU-00001131.

XX 29-MAY-1998; 98US-0087392P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Stacker SA, Alitalo K;

XX WPI; 1999-405368/34.

XX A human cell line stably expressing vascular endothelial growth factor D,
 PT useful for treating melanomas or tumors expressing VEGF-D.

XX Claim 6; Page 72; 79pp; English.

XX The present sequence represents human vascular endothelial growth factor
 CC (VEGF)-D. The specification describes a human cell line which stably
 CC expresses VEGF-D, or fragments/analogs having VEGF-D biological
 CC activity. VEGF-D antagonists, e.g. antisense nucleic acids or triplex
 CC DNA, VEGF-D variants or antibodies (especially chimeric antibodies), are
 CC useful for the treatment or alleviation of malignant melanomas, tumours
 CC or psoriasis. Angiogenesis and lymphangiogenesis stimulating amounts of
 CC VEGF-D can be administered to enhance the acceptance and/or healing of
 CC skin grafts or to stimulate the healing of a surgical or traumatic wound
 CC to the skin. Lymphangiogenesis stimulating amounts of VEGF-D can be used
 CC to treat lymphedema. Endothelial proliferation stimulating amounts of
 CC VEGF-D are used to treat scleroderma. Vascularisation stimulating amounts
 CC of VEGF-D can be used to treat anhydrotic ectodermal dysplasia. VEGF-D

CC antibodies are useful for detecting tumours expressing VEGF-D. Fully-
 CC processed VEGF-D can be used to stimulate at least one VEGF-D bioactivity
 CC chosen from endothelial cell proliferation, migration, survival and
 CC differentiation and lymphangiogenesis without inducing vascular
 CC permeability
 XX
 SQ Sequence 109 AA;

Query Match 75.0%; Score 54; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASELGKSTNTF 12
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 Db 29 ASELGKSTNTF 39

Search completed: April 1, 2005, 09:18:15
 Job time : 100.123 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 09:26:18 ; Search time 319.479 Seconds
(without alignments)
13.493 Million cell updates/sec

Title: US-09-761-636A-5
Perfect score: 72
Sequence: 1 CASELGKSTNTFC 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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2: /cgn2_6/ptodata/2/pubpaa/FCT_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	72	100.0	17	9 US-09-761-636A-8	Sequence 8, Appli
3	69	95.8	13	9 US-09-761-636A-15	Sequence 15, Appl
4	69	95.8	17	9 US-09-761-636A-27	Sequence 27, Appl
5	69	95.8	17	9 US-09-761-636A-31	Sequence 31, Appl
6	65	90.3	13	9 US-09-761-636A-16	Sequence 16, Appl
7	65	90.3	13	9 US-09-761-636A-18	Sequence 18, Appl
8	65	90.3	17	9 US-09-761-636A-28	Sequence 28, Appl
9	65	90.3	17	9 US-09-761-636A-30	Sequence 30, Appl
10	65	90.3	17	9 US-09-761-636A-32	Sequence 32, Appl
11	61	84.7	13	9 US-09-761-636A-17	Sequence 17, Appl
12	61	84.7	17	9 US-09-761-636A-29	Sequence 29, Appl
13	54	75.0	73	9 US-09-761-636A-3	Sequence 3, Appli

14	54	75.0	96	9 US-09-761-636A-1	Sequence 1, Appli
15	54	75.0	109	9 US-09-956-095-3	Sequence 3, Appli
16	54	75.0	109	9 US-09-219-345A-1	Sequence 1, Appli
17	54	75.0	109	16 US-10-779-731-1	Sequence 10, Appli
18	54	75.0	134	17 US-10-868-549-10	Sequence 8, Appli
19	54	75.0	197	15 US-10-352-153-8	Sequence 1, Appli
20	54	75.0	280	13 US-10-044-622-1	Sequence 3, Appli
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22	54	75.0	325	14 US-10-161-694-3	Sequence 3, Appli
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25	54	75.0	354	9 US-09-219-345A-11	Sequence 119, App
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27	54	75.0	354	10 US-09-375-248-6	Sequence 22, Appli
28	54	75.0	354	11 US-09-785-534B-22	Sequence 26, Appli
29	54	75.0	354	14 US-10-262-538-26	Sequence 5, Appli
30	54	75.0	354	14 US-10-274-953-5	Sequence 5, Appli
31	54	75.0	354	14 US-10-161-694-5	Sequence 1, Appli
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34	54	75.0	354	16 US-10-705-476-5	Sequence 4, Appli
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40	51	70.8	81	14 US-10-260-539-18	Sequence 6, Appli
41	51	70.8	110	10 US-09-847-524-6	Sequence 4, Appli
42	51	70.8	321	10 US-09-847-524-6	Sequence 9, Appli
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44	51	70.8	321	14 US-10-161-694-9	Sequence 9, Appli
45	51	70.8	321	16 US-10-705-476-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-761-636A-5
; Sequence 5, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-5

Query Match 100.0%; Score 72; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.8e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
Db 1 CASELGKSTNTFC 13

RESULT 2
US-09-761-636A-8

; Sequence 8, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-8

Query Match 100.0%; Score 72; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
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Db 1 CASELGKSTNTFC 13

RESULT 3

US-09-761-636A-15
; Sequence 15, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-15

Query Match 95.8%; Score 69; DB 9; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e-05;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
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Db 1 CASELGKSTNTFC 13

RESULT 4

US-09-761-636A-27
; Sequence 27, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven

; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; NUMBER OF SEQ ID NOS: 34
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; ORGANISM: synthetic construct
US-09-761-636A-27

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Best Local Similarity 92.3%; Pred. No. 4.3e-05;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
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Db 1 CASELGKSTNTFC 13

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; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-31

Query Match 95.8%; Score 69; DB 9; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.3e-05;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
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Db 1 CASELGKSTNTFC 13

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US-09-761-636A-16
; Sequence 16, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A

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; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-16

Query Match          90.3%; Score 65; DB 9; Length 13;
Best Local Similarity 84.6%; Pred. No. 0.00016;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTFC 13
Db 1 CASELGKSTNTFC 13

RESULT 7
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; Sequence 18, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-18

Query Match          90.3%; Score 65; DB 9; Length 13;
Best Local Similarity 84.6%; Pred. No. 0.00016;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTFC 13
Db 1 CASELGKSTNTFC 13

RESULT 8
US-09-761-636A-28
; Sequence 28, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-28

Query Match          90.3%; Score 65; DB 9; Length 17;
Best Local Similarity 84.6%; Pred. No. 0.00022;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTFC 13
Db 1 CASELGKSTNTFC 13

RESULT 9
US-09-761-636A-30
; Sequence 30, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-30

Query Match          90.3%; Score 65; DB 9; Length 17;
Best Local Similarity 84.6%; Pred. No. 0.00022;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTFC 13
Db 1 CASELGKSTNTFC 13

RESULT 10
US-09-761-636A-32
; Sequence 32, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-32
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; ORGANISM: synthetic construct
US-09-761-636A-32

Query Match          90.3%; Score 65; DB 9; Length 17;
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Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
Db 1 CASELGRSTNSFC 13
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RESULT 11
US-09-761-636A-17
; Sequence 17, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-17

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QY 1 CASELGKSTNTFC 13
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RESULT 12
US-09-761-636A-29
; Sequence 29, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-29

Query Match          84.7%; Score 61; DB 9; Length 17;
Best Local Similarity 76.9%; Pred. No. 0.0011;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
Db 1 CASELGRSTNSFC 13
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RESULT 13
US-09-761-636A-3
; Sequence 3, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Amino acid residues Val101-Thr173 of VEGF-D
US-09-761-636A-3

Query Match          75.0%; Score 54; DB 9; Length 73;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASELGKSTNTF 12
Db 21 ASELGKSTNTF 31
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RESULT 14
US-09-761-636A-1
; Sequence 1, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Amino acid residues of Val101-Pro196 of VEGF-D
US-09-761-636A-1

Query Match          75.0%; Score 54; DB 9; Length 96;
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Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

QY 2 ASELGKSTNTF 12
Db 21 ASELGKSTNTF 31

RESULT 15

US-09-956-095-3
; Sequence 3, Application US/09956095
; Patent No. US20020102260A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; APPLICANT: STACKER, Steven A.
; TITLE OF INVENTION: METHODS FOR TREATING NEOPLASTIC DISEASE CHARACTERIZED BY
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR D EXPRESSION, FOR SCREENING
; TITLE OF INVENTION: FOR NEOPLASTIC DISEASE OR METASTATIC RISK AND FOR MAINTAINING
; TITLE OF INVENTION: VASCULARIZATION OF TISSUE
; FILE REFERENCE: 1064/48666PC
; CURRENT APPLICATION NUMBER: US/09/956,095
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 09/796,714
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/234,196
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-956-095-3

Query Match 75.0%; Score 54; DB 9; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

QY 2 ASELGKSTNTF 12
Db 29 ASELGKSTNTF 39

Search completed: April 1, 2005, 10:36:33
Job time : 319.479 secs

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